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OM protein - protein search, using sw model

Run on: November 15, 2004, 14:01:34 ; Search time 43.0833 Seconds
(without alignments)
391.341 Million cell updates/sec

Title: US-10-032-376A-8
Perfect score: 258
Sequence: 1 LQXQLSLPETGELDSATLKA.....VPDLGRFQTFEGDLKWHHNN 47

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 1022821

Minimum DB seq length: 47
Maximum DB seq length: 660

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:.*
1: geneseqp1980s:.*
2: geneseqp1990s:.*
3: geneseqp2000s:.*
4: geneseqp2001s:.*
5: geneseqp2002s:.*
6: geneseqp2003as:.*
7: geneseqp2003bs:.*
8: geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	258	100.0	47	6	ABP971130 Human mat
2	258	100.0	47	6	ABG76316 Human mat
3	258	100.0	47	8	ADQ17091 Human mat
4	258	100.0	47	5	ABP69247 Human pol
5	150	58.1	54	5	ABG31461 Peptidase
6	141	54.7	54	6	ABP971127 Human mat
7	141	54.7	54	6	ABG76313 Human mat
8	141	54.7	54	8	ADQ17088 Human mat
9	141	54.7	460	1	AAP93629 Sequence
10	141	54.7	477	2	AAY21993 Human mat
11	141	54.7	477	2	AAY21994 Human mat
12	141	54.7	477	4	AAB84608 Amino aci
13	141	54.7	477	4	AAE10420 Human mat
14	141	54.7	477	4	AAO20482 Prostrone
15	141	54.7	477	5	ABO4752 Human MMP
16	141	54.7	477	6	ABP72353 Matrix me
17	141	54.7	477	6	ABU03473 Angiogene
18	141	54.7	477	6	ABR58544 Human can
19	141	54.7	477	6	ABR32114 Human cer
20	141	54.7	477	6	ABP54461 Matrix me
21	141	54.7	477	7	ADG3273 Human Pro
22	141	54.7	477	7	ADD46343 Human Pro
23	141	54.7	477	7	ADG16014 G-coupled
24	141	54.7	477	7	ADN38704 Cancer/an
25	141	54.7	477	8	ADH42533 Novel hum

26	141	54.7	477	8	ADH42533 Novel hum
27	141	54.7	477	8	ADH42537 Novel hum
28	141	54.7	477	8	ADL93953 Human G-c
29	141	54.7	477	8	ADN07699 Human mat
30	141	54.7	482	8	ADH42531 Novel hum
31	138	53.5	170	1	AAP81873 Partial s
32	135	52.3	173	7	ADL16018 G-coupled
33	135	52.3	173	8	ADL93957 Human G-c
34	135	52.3	477	7	ADL16016 G-coupled
35	135	52.3	477	8	ADH42529 Novel hum
36	135	52.3	477	8	ADH42539 Novel hum
37	135	52.3	477	8	ADL93955 Human G-c
38	134	51.9	463	1	AAP93630 Sequence
39	134	51.9	475	7	ADD46341 Rat Prote
40	134	51.9	475	7	ADE63271 Rat Prote
41	133	51.6	55	6	ABP97128 Human mat
42	133	51.6	55	6	ABG76314 Human mat
43	133	51.6	55	8	ADQ17089 Human mat
44	133	51.6	475	5	ABJ05574 Breast ca
45	133	51.6	475	6	ABU56595 Lung canc

ALIGNMENTS

RESULT 1
ABP971130
ID ABP971130 standard; peptide; 47 AA.

XX AC ABP971130;

XX 24-JUN-2003 (first entry)

XX DE Human matrix metalloproteinase 9 cleavage region peptide SEQ ID NO:8.

XX KW Human; matrix metalloproteinase; MMP; anticancer; wound healing;
XX KW matrix metalloproteinase inhibitor; antitumor; antiangiogenic; cardiant;
XX KW vascular endothelial growth factor inhibitor; VEGF inhibitor; cytostatic;
XX KW vulnary; cerebroprotective; antidiabetic; ophthalmological; tumour;
XX KW dermatological; metastatic; non-metastatic; vascular; heart disease;
XX KW non-vascularised; surgical incision; chronic wound; stroke; angiogenesis;
XX KW macular degeneration; diabetic retinopathy; cleavage region.

XX OS Homo sapiens.

XX PN WC2003018748-A2.

XX PD 06-MAR-2003.

XX PF 15-AUG-2002; 2002WO-US026319.

XX PR 16-AUG-2001; 2001US-0312726P.

XX PR 21-DEC-2001; 2001US-00032376.

XX PR 21-MAY-2002; 2002US-00153185.

XX XX (KIMB) KIMBERLY-CLARK WORLDWIDE INC.

XX PI Quirk S. Weart IF.

XX XX WPI; 2003-381408/36.

XX PT Anti-angiogenic composition comprising peptide inhibitor of matrix

XX PT metalloproteinase, useful for decreasing the expression of vascular

XX PT endothelial growth factor and treating cancers and tissue injuries.

XX PS Claim 17; Page 16; 103pp; English.

XX CC The present invention describes an anti-angiogenic composition (I) for

XX CC inhibiting expression of vascular endothelial growth factor (VEGF). (I)

XX CC comprises an effective amount of a peptide inhibitor of matrix

XX CC metalloproteinase (MMP), where the peptide can inhibit the expression of

XX CC VEGF. (I) has cytostatic, vulnary cardiant, cerebroprotective,

XX CC antidiabetic, ophthalmological and dermatological activities. (I) can be

1757 RAL (1329 5.71)

CC used for inhibiting expression of VEGF, and so can be used for inhibiting
 CC growth of tumours and diminishing tumours size. The tumour can be
 CC metastatic, non-metastatic, vascularised, non-vascularised, hard or soft.
 CC (I) is also useful for treating injuries including wounds, surgical
 CC incisions, chronic wounds, heart diseases and stroke. (I) is also useful
 CC for treating disorders characterised by excessive angiogenesis e.g.
 CC macular degeneration and diabetic retinopathy. The present sequence
 CC represents a human MMP cleavage region peptide, which is used in the
 CC exemplification of the present invention
 XX
 XX Sequence 47 AA;

Query Match 100.0%; Score 258; DB 6; Length 47;
 Best Local Similarity 100.0%; Pred. NO. 3.2e-29;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQKLSLPETGEISATLKAMRTPCGVDPDLGRFQTFEGDLKWHHN 47
 Db 1 LQKLSLPETGEISATLKAMRTPCGVDPDLGRFQTFEGDLKWHHN 47

RESULT 2

ABG76316
 ID ABG76316 standard; protein; 47 AA.

XX AC ABG76316;

XX DT 10-MAY-2003 (first entry)

XX DE Human matrix metalloproteinase (MMP) peptide inhibitor #8.

XX KW Human; peptide inhibitor; matrix metalloproteinase-9; MMP-9;
 KW Cleavage region; proenzyme form; cellular proliferation; fibroblast;
 KW Keratinocyte; healthy skin development; wound healing; scarring;
 KW skin tone; wrinkle; anti-aging; vulnerary.

XX OS Homo sapiens.

XX PN W0203016520-A1.

XX PD 27-FEB-2003.

XX PF 15-AUG-2002; 2002WO-US026198.

XX PR 16-AUG-2001; 2001US-0312726P.

XX PR 21-DEC-2001; 2001US-00032376.

XX PR 21-MAY-2002; 2002US-00153185.

XX PA (KIMB) KIMBERLY-CLARK WORLDWIDE INC.

XX PI Quirk S, Malik S, Villanueva-JM;

XX DR WPI; 2003-289980/28.

XX Novel peptide inhibitor of proteinase activity of matrix
 PT metalloproteinases, e.g. matrix metalloproteinase-2, useful for
 PT stimulating cellular proliferation of fibroblasts or keratinocytes.
 PS Claim 1; Page 16; 120pp; English.

XX The present invention relates to peptide inhibitors of metalloproteinases
 CC (MMPs), particularly metalloproteinase-2 (MMP-2). The inhibitors have
 CC peptide sequences related to the cleavage regions of the proenzyme forms
 CC of the MMPs. The peptide inhibitors are useful for stimulating cellular
 CC proliferation of fibroblasts or keratinocytes, promoting healthy skin
 CC development, treating wounds, preventing scarring, improving skin tone,
 CC reducing wrinkling and for stimulating the development of smooth, healthy
 CC skin. The peptide inhibitors are useful as anti-aging and wound healing
 CC compounds. ABG76309-ABG76321 represent peptide inhibitors of MMPs
 XX
 XX Sequence 47 AA;

Query Match 100.0%; Score 258; DB 6; Length 47;

Best Local Similarity 100.0%; Pred. NO. 3.2e-29;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQKLSLPETGEISATLKAMRTPCGVDPDLGRFQTFEGDLKWHHN 47
 Db 1 LQKLSLPETGEISATLKAMRTPCGVDPDLGRFQTFEGDLKWHHN 47

RESULT 3

ADQ17091
 ID ADQ17091 standard; peptide; 47 AA.

XX AC ADQ17091;

XX DT 23-SEP-2004 (first entry)

XX DE Human matrix metalloproteinase-9 (MMP9) cleavage region peptide.

XX KW Fibronectin; healthy skin; wrinkle; wound; vulnerary; dermatological;
 KW human; matrix metalloproteinase; MMP.

XX OS Homo sapiens.

XX PN US2004127421-A1.

XX PD 01-JUL-2004.

XX PF 30-DEC-2002; 2002US-00335207.

XX PR 30-DEC-2002; 2002US-00335207.

XX PA (MALI/) MALIK S.

XX PA (QUIR/) QUIRK S.

XX PI Malik S, Quirk S;

XX DR WPI; 2004-506456/48.

XX Composition used for preventing and treating wrinkles and treating wounds
 PT comprises peptide having sequence related to matrix metalloproteinase
 PT proenzyme.

XX Example 1; SEQ ID NO 8; 60pp; English.

XX The present invention provides peptides and compositions containing such
 CC peptides that are useful as agents to maintain healthy skin and to
 CC promote the condition of the skin. The invention is useful for increasing
 CC the amount of fibronectin in tissue. The invention is also useful for
 CC encouraging the maintenance and development of healthy skin, preventing
 CC and treating wrinkles and for treating wounds. The invention acts as
 CC vulnerary and dermatological agents. The present sequence is human matrix
 CC metalloproteinase (MMP) cleavage region peptide. This sequence is used in
 CC the exemplification of the invention.

XX Sequence 47 AA;

Query Match 100.0%; Score 258; DB 8; Length 47;
 Best Local Similarity 100.0%; Pred. NO. 3.2e-29;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQKLSLPETGEISATLKAMRTPCGVDPDLGRFQTFEGDLKWHHN 47
 Db 1 LQKLSLPETGEISATLKAMRTPCGVDPDLGRFQTFEGDLKWHHN 47

RESULT 4

ABP69247
 ID ABP69247 standard; protein; 432 AA.

XX AC ABP69247;

XX DT 20-JAN-2003 (first entry)

DE Human polypeptide SEQ ID NO 1294.
XX
KW Human; genome mapping; gene therapy; food supplement; virus; fungus;
KW cell-proliferative disorder; neurodegenerative disease; bacterial;
KW Parkinson's disease; Alzheimer's disease; autoimmune disease;
KW multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
KW arthritis; cytostatic; immunomodulator; nootropic; neuroprotective;
KW antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
KW hemostatic; vulnery; fungicide; antibacterial; virucide; protozoacide;
KW antiarthritic.
XX
OS Homo sapiens.
XX
PN WO200270539-A2.
XX
PD 12-SEP-2002.
XX
XX 05-MAR-2002; 2002WO-US0005095.
XX
XX 05-MAR-2001; 2001US-00799451.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;
PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;
PI Wehrman T, Wang J, Wang D, Dermanac RT;
XX
XX WPI: 2002-759812/82.
DR N-PSDB; ABZ11464.
XX
XX New polynucleotides comprising sequences assembled from expressed
PT sequence tags (ESTs), useful for treating cell-proliferative,
PT neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
PT or coagulation disorders.
XX
XX
PS Claim 9; SEQ ID NO 1294; 1012pp + Sequence Listing; English.
XX
XX The invention relates to an isolated polynucleotide (I) comprising a
CC nucleotide sequence selected from any of 948 sequences (ABZ11119-
CC ABZ12066) or their mature protein coding portion, active domain coding
CC protein or complementary sequences. The polynucleotides are useful for
CC identifying expressed genes or for physical mapping of human genome. The
CC encoded polypeptides (ABZ68902-ABZ69849) are useful as molecular weight
CC markers, as a food supplement, for generating antibodies, in medical
CC imaging, screening and diagnostic assays and for treating cell-
CC proliferative disorders (cancer), neurodegenerative diseases (Parkinson's
CC or Alzheimer's disease), autoimmune diseases (multiple sclerosis,
CC diabetes, lupus) genetic disorders, wound, burns, incision, ulcers, liver
CC platelet or coagulation disorders, myeloid or lymphoid disorders,
CC or lung fibrosis, infections (bacterial, viral, fungal, parasitic),
CC arthritis, etc. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 432 AA;
Query Match 100.0%; Score 258; DB 5; Length 432;
Best Local Similarity 100.0%; Pred. No. 4.8e-28;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LQKQLSLPTGELDSATLKAMRTPCGVPDLGRFQTFEGDLKWHHN 47
DB 74 LQKQLSLPTGELDSATLKAMRTPCGVPDLGRFQTFEGDLKWHHN 120
RESULT 5
ABG31461
ID ABG31461 standard; protein; 171 AA.
XX
XX
AC ABG31461;
XX
XX 29-NOV-2002 (first entry)
DT
XX

DE Peptidase M10 domain characteristic of metalloproteinases.
XX
KW Matrix metalloproteinase; MMP 46798; cell proliferation disorder;
KW cell differentiation disorder; carcinoma; sarcoma; leukaemia;
KW breast cancer; lung cancer; neurological disorder; schizophrenia;
KW ischaemia; infarction; Parkinson's disease; Huntington's disease;
KW inflammatory disorder; Crohn's disease; immune disorder; arthritis;
KW diabetes mellitus; cardiovascular disorder; restenosis; tachycardia;
KW rheumatic heart disease; motility disorder; developmental disorder;
KW lung disorder; chronic bronchitis; pulmonary congestion; oedema;
KW blood disorder; blood clotting disorder; cytostatic; immunomodulator;
KW anti-inflammatory; cardiant; antiparkinsonian; nootropic; thrombolytic;
KW neuroprotective; antidiabetic; antirheumatic; antithrombotic; vasotropic;
KW peptidase M10 domain.
XX
OS Synthetic.
XX
XX WO200266670-A2.
XX
XX 29-AUG-2002.
XX
XX 16-JAN-2002; 2002WO-US001546.
XX
XX 16-JAN-2001; 2001US-0262252P.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Curtis RAJ, Lora JM;
PI
XX WPI: 2002-674955/72.
XX
XX New human matrix metalloproteinase nucleic acid and polypeptide
PT molecules, designated 46798, useful for diagnosing, preventing or
PT treating cancers, ischemia, Parkinson's disease heart disease or edema.
XX
XX Disclosure; Page 108; 117pp; English.
XX
XX The present invention relates to the isolation of novel human matrix
CC metalloproteinases (MMP), designated 46798, and the polynucleotide
CC sequences encoding them. The MMP 46798 polypeptide and polynucleotide
CC sequences are useful for diagnosing, preventing, alleviating or treating
CC metalloproteinase-associated disorders such as cell proliferation and/or
CC differentiation disorders (e.g. carcinoma, sarcoma, leukaemia, breast
CC cancer, or lung cancer), neurological disorders (e.g. schizophrenia,
CC ischaemia, infarction, Parkinson's disease or Huntington's disease),
CC inflammatory disorders (e.g. Crohn's disease), immune disorders (e.g.
CC diabetes mellitus or arthritis), cardiovascular disorders (e.g.
CC restenosis, tachycardia or rheumatic heart disease), motility disorders,
CC developmental disorders, lung disorders (e.g. chronic bronchitis,
CC pulmonary congestion or oedema), and blood/blood clotting disorders. The
CC present sequence represents a peptidase M10 domain which is
CC characteristic of extracellular MMPs
XX
SQ Sequence 171 AA;
Query Match 58.1%; Score 150; DB 5; Length 171;
Best Local Similarity 57.4%; Pred. No. 5.1e-13;
Matches 27; Conservative 7; Mismatches 13; Indels 0; Gaps 0;
QY 1 LQKQLSLPTGELDSATLKAMRTPCGVPDLGRFQTFEGDLKWHHN 47
DB 32 MCKFFGLPVTGKLDSTNLVKNKPRCGVPDLGRFQTFEGSPKWSKN 78
RESULT 6
ABP97127
ID ABP97127 standard; peptide; 54 AA.
XX
XX
AC ABP97127;
XX
XX 24-JUN-2003 (first entry)
DT
XX
XX Human matrix metalloproteinase 3 cleavage region peptide SEQ ID NO:5.

```

XX Human; matrix metalloproteinase; MMP; anticancer; wound healing;
XX matrix metalloproteinase inhibitor; antitumour; antiangiogenic; cardiant;
XX vascular endothelial growth factor inhibitor; VEGF inhibitor; cytostatic;
XX vulnary; cerebroprotective; antidiabetic; ophthalmological; tumour;
XX dermatological; metastatic; non-metastatic; vascularised; heart disease;
XX non-vascularised; surgical incision; chronic wound; stroke; angiogenesis;
XX macular degeneration; diabetic retinopathy; cleavage region.
XX
XX Homo sapiens.
XX
XX WO2003018748-A2.
XX
XX 06-MAR-2003.
XX
XX 15-AUG-2002; 2002WO-US026319.
XX
XX 16-AUG-2001; 2001US-0312726P.
XX
XX 21-DEC-2001; 2001US-00032376.
XX
XX 21-MAY-2002; 2002US-00153185.
XX
XX (KIMB ) KIMBERLY-CLARK WORLDWIDE INC.
XX
XX Quirk S, Weart IF;
XX
XX WPI; 2003-381408/36.
XX
XX Anti-angiogenic composition comprising peptide inhibitor of matrix
XX metalloproteinase, useful for decreasing the expression of vascular
XX endothelial growth factor and treating cancers and tissue injuries.
XX
XX Claim 17; Page 15; 103pp; English.
XX
XX The present invention describes an anti-angiogenic composition (I) for
XX inhibiting expression of vascular endothelial growth factor (VEGF). (I)
XX comprises an effective amount of a peptide inhibitor of matrix
XX metalloproteinase (MMP), where the peptide can inhibit the expression of
XX VEGF. (I) has cytostatic, vulnary, cardiant, cerebroprotective,
XX antidiabetic, ophthalmological and dermatological activities. (I) can be
XX used for inhibiting expression of VEGF, and so can be used for inhibiting
XX growth of tumours and diminishing tumours size. The tumour can be
XX metastatic, non-metastatic, vascularised, non-vascularised, hard or soft.
XX (I) is also useful for treating injuries including wounds, surgical
XX incisions, chronic wounds, heart diseases and stroke. (I) is also useful
XX for treating disorders characterised by excessive angiogenesis e.g.
XX macular degeneration and diabetic retinopathy. The present sequence
XX represents a human MMP cleavage region peptide, which is used in the
XX exemplification of the present invention
XX
XX Sequence 54 AA;
XX
XX Query Match 54.7%; Score 141; DB 6; Length 54;
XX Best Local Similarity 62.8%; Pred. No. 2.4e-12;
XX Matches 27; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
XX
XX Qy 1 LQKLSLPETGELDSATLKAMRPRCGVPDLGRFOTPEGDLKW 43
XX :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
XX Db 1 MQKFLGLEVTGKLDSDTLEVMKPRCGVPDVGHFRTPFGIPKW 43
XX
XX RESULT 7
XX ABG76313
XX ID ABG76313 standard; protein; 54 AA.
XX
XX AC ABG76313;
XX
XX 10-MAY-2003 (first entry)
XX
XX Human matrix metalloproteinase (MMP) peptide inhibitor #5.
XX
XX Human; peptide inhibitor; matrix metalloproteinase-3; MMP-3;
XX cleavage region; proenzyme form; cellular proliferation; fibroblast;
XX keratinocyte; healthy skin development; wound healing; scarring;
XX

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XX skin tone; wrinkle; anti-aging; vulnary.
XX
XX Homo sapiens.
XX
XX WO2003016520-A1.
XX
XX 27-FEB-2003.
XX
XX 15-AUG-2002; 2002WO-US026198.
XX
XX 16-AUG-2001; 2001US-0312726P.
XX
XX 21-DEC-2001; 2001US-00032376.
XX
XX 21-MAY-2002; 2002US-00153185.
XX
XX (KIMB ) KIMBERLY-CLARK WORLDWIDE INC.
XX
XX Quirk S, Malik S, Villanueva JM;
XX
XX WPI; 2003-289980/28.
XX
XX Novel peptide inhibitor of proteinase activity of matrix
XX metalloproteinases, e.g. matrix metalloproteinase-2, useful for
XX stimulating cellular proliferation of fibroblasts or keratinocytes.
XX
XX Claim 1; Page 16; 120pp; English.
XX
XX The present invention relates to peptide inhibitors of metalloproteinases
XX (MMPs), particularly metalloproteinase-2 (MMP-2). The inhibitors have
XX peptide sequences related to the cleavage regions of the proenzyme forms
XX of the MMPs. The peptide inhibitors are useful for stimulating cellular
XX proliferation of fibroblasts or keratinocytes, promoting healthy skin
XX development, treating wounds, preventing scarring, improving skin tone,
XX reducing wrinkling and for simulating the development of smooth, healthy
XX skin. The peptide inhibitors are useful as anti-aging and wound healing
XX compounds. ABG76309-ABG76321 represent peptide inhibitors of MMPs
XX
XX Sequence 54 AA;
XX
XX Query Match 54.7%; Score 141; DB 6; Length 54;
XX Best Local Similarity 62.8%; Pred. No. 2.4e-12;
XX Matches 27; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
XX
XX Qy 1 LQKLSLPETGELDSATLKAMRPRCGVPDLGRFOTPEGDLKW 43
XX :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
XX Db 1 MQKFLGLEVTGKLDSDTLEVMKPRCGVPDVGHFRTPFGIPKW 43
XX
XX RESULT 8
XX ADQ17088
XX ID ADQ17088 standard; peptide; 54 AA.
XX
XX AC ADQ17088;
XX
XX 23-SEP-2004 (first entry)
XX
XX Human matrix metalloproteinase-3 (MMP3) cleavage region peptide.
XX
XX Fibronectin; healthy skin; wrinkle; wound; vulnary; dermatological;
XX Human; matrix metalloproteinase; MMP.
XX
XX Homo sapiens.
XX
XX US2004127421-A1.
XX
XX 01-JUL-2004.
XX
XX 30-DEC-2002; 2002US-00335207.
XX
XX 30-DEC-2002; 2002US-00335207.
XX
XX (MALI/) MALIK S.
XX (QUIR/) QUIRK S.
XX

```

PI Malik S, Quirk S;
 XX WPI; 2004-506456/48.
 XX
 PT Composition used for preventing and treating wrinkles and treating wounds
 PT comprises peptide having sequence related to matrix metalloproteinases
 XX proenzyme.
 XX
 XX Example 1; SEQ ID NO 5; 60pp; English.
 XX
 CC The present invention provides peptides and compositions containing such
 CC peptides that are useful as agents to maintain healthy skin and to
 CC promote the condition of the skin. The invention is useful for increasing
 CC the amount of fibronectin in tissue. The invention is also useful for
 CC encouraging the maintenance and development of healthy skin, preventing
 CC and treating wrinkles and for treating wounds. The invention acts as
 CC a vulnerary and dermatological agents. The present sequence is human matrix
 CC metalloproteinase (MMP) cleavage region peptide. This sequence is used in
 CC the exemplification of the invention.
 XX
 SQ Sequence 54 AA;
 Query Match 54.7%; Score 141; DB 8; Length 54;
 Best Local Similarity 62.8%; Pred. No. 2.4e-12;
 Matches 27; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
 QY 1 LQKLSLPTGELDSATLKAMRTPRCVDPDLGRFTQTEGDLKW 43
 :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 DB 1 MQKFLGLEVTGKLDSDTLEVMRKPRCGVDPDVGHFTPTPGIPKW 43
 :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 RESULT 9
 AAP93629
 ID AAP93629 standard; protein; 460 AA.
 AC
 XX AAP93629;
 XX
 DT 25-MAR-2003 (revised)
 DT 19-AUG-1991 (first entry)
 XX
 DE Sequence of human prostromelysin.
 XX
 KW Hypertrophic scar; keloid; intervertebral disc disease; enzyme.
 XX
 OS Homo sapiens.
 XX
 XX GB2209526-A.
 XX
 PD 17-MAY-1989.
 XX
 PF 02-SEP-1988; 88GB-00820803.
 XX
 PR 04-SEP-1987; 87US-00093421.
 XX
 PA (UNIW) UNIV WASHINGTON.
 XX
 PI Eisen AZ, Goldberg GI;
 XX
 DR WPI; 1989-147011/20.
 XX
 PT DNA encoding human type IV collagenase (gelatinase) - for use in the
 PT treatment of hypertrophic scars, keloids and intervertebral disc disease.
 XX
 XX Example; Fig 6; 36pp; English.
 XX
 CC The original source of the protein material was H-ras transformed human
 CC bronchial epithelial cells (HBE-1). The AA sequence was then used to
 CC develop oligonucleotide probes which were used to screen a cDNA library
 CC of human skin fibroblast mRNA. The longest clone, pGEL 186.2, represented
 CC almost the full gelatinase mRNA sequence except the leader sequence
 CC encoding the first few AA's of the signal peptide. Figure 6 compares the
 CC SOS of human type IV procollagenase AAP96143, human prostromelysin
 CC (AAP93629), human interstitial procollagenase (AAP93628) and rat transin

CC (AAP93630). (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-
 CC MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI
 CC field.)
 XX
 SQ Sequence 460 AA;
 Query Match 54.7%; Score 141; DB 1; Length 460;
 Best Local Similarity 62.8%; Pred. No. 3.3e-11;
 Matches 27; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
 QY 1 LQKLSLPTGELDSATLKAMRTPRCVDPDLGRFTQTEGDLKW 43
 :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 DB 55 MQKFLGLEVTGKLDSDTLEVMRKPRCGVDPDVGHFTPTPGIPKW 97
 :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 RESULT 10
 AAY21993
 ID AAY21993 standard; protein; 477 AA.
 XX
 AC AAY21993;
 XX
 DT 13-SEP-1999 (first entry)
 XX
 DE Human matrix metalloproteinase-3 (MMP-3).
 XX
 KW Matrix metalloproteinase-3; MMP-3; modified; human; therapeutic.
 XX
 OS Homo sapiens.
 XX
 PN JP11169176-A.
 XX
 PD 29-JUN-1999.
 XX
 PF 15-DEC-1997; 97JP-00345008.
 XX
 PR 15-DEC-1997; 97JP-00345008.
 XX
 XX (YAMA) YAMANOUCHI PHARM CO LTD.
 XX
 DR WPI; 1999-422616/36.
 DR N-PSDB; AAX89009.
 XX
 PT A modified matrix metalloproteinase-3 - used in the production of
 PT therapeutics.
 XX
 PS Disclosure; Page 8-10; 17pp; Japanese.
 XX
 CC The invention describes a modified matrix metalloproteinase-3 (MMP-3) that
 CC has an amino acid (aa) sequence (AAY21994) in which the (i) the aa
 CC residue at position 172 (Xaa) from the N terminal is modified by -ile- or
 CC -Tyr-; (ii) the aa residue at position 239 (Xaa) is modified by -Val- or
 CC -Leu-; (iii) the aa residues at position from 241 to 243 (-Xaa-Xaa-Xaa-) are
 CC modified by continuous -His-Ser-Leu- or -Asn-Ala-Phe- and have an
 CC active domain or an active domain in which the aa residues of the
 CC sequence are replaced, deleted or inserted at at least aa residues from
 CC 100 to 274 from the N terminal and being stable, provided that a case is
 CC not selected in which the aa residue: 172 (Xaa) is -Tyr, the 239 (Xaa) is
 CC -Leu- and 241 to 243 (-Xaa-Xaa-Xaa-) are -His-Ser-Leu-. A host cell
 CC transfected by a vector comprising the DNA encoding the MMP-3 can be used
 CC for the recombinant preparation of MMP-3. The MMP-3 or its fragment have
 CC high stability and can be used in the production of therapeutics. The
 CC present sequence represents a human MMP-3
 XX
 SQ Sequence 477 AA;
 Query Match 54.7%; Score 141; DB 2; Length 477;
 Best Local Similarity 62.8%; Pred. No. 3.5e-11;
 Matches 27; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
 QY 1 LQKLSLPTGELDSATLKAMRTPRCVDPDLGRFTQTEGDLKW 43
 :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 DB 67 MQKFLGLEVTGKLDSDTLEVMRKPRCGVDPDVGHFTPTPGIPKW 109
 :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||


```

FH Key Location/Qualifiers
FT Peptide 1..17
FT /label= Signal_peptide
FT Protein 18..477
FT /label= Mature_MMP_3_protein
FT Domain 90..96
FT /label= Cysteine_switch_domain
FT Domain 161..185
FT /note= "Zinc and calcium binding domain"
XX
XX WO200166766-A2.
XX
XX 13-SEP-2001.
XX
XX 06-MAR-2001; 2001WO-US007167.
XX
XX 06-MAR-2000; 2000US-0187196P.
XX
XX (DARW-) DARWIN MOLECULAR CORP.
XX (SCHA/) SCHATZMAN R.
XX
XX Fajardo M, Wang K, Smith R, Moss P;
XX
XX WPI; 2001-582276/65.
XX
XX Novel isolated matrix metalloproteinase-25 nucleic acid molecule and
XX proteins encoded by them whose inhibition is useful for modulation of
XX hair growth in mammals.
XX
XX Example 2; Fig 3; 119pp; English.
XX
XX The present sequence is human matrix metalloproteinase (MMP)-3 protein
XX used in the exemplification of the invention. MMP-25 DNA is located on
XX chromosome 11q22. Matrix metalloproteinases are a family of zinc
XX dependent endopeptidases that function extracellularly to degrade
XX proteins typically found in the extracellular matrix. MMP-25 is expressed
XX in skin cells of mammals, particularly in breast cells and hair
XX follicles. MMP-25 DNA is useful for identifying a nucleic acid molecule
XX encoding all or part of MMP by hybridising MMP-25 to a nucleic acid
XX sample and identifying a sequence that hybridises in the nucleic acid
XX sample. The identification step involves performing polymerase chain
XX reaction (PCR) to amplify the hybridising sequence. MMP-25 antibody is
XX useful for identifying type 25 MMP. MMP-25 protein inhibitors may be used
XX to modulate hair growth and breast cancer in a mammal
XX
XX Sequence 477 AA;
XX
XX Query Match 54.7%; Score 141; DB 4; Length 477;
XX Best Local Similarity 62.8%; Pred. No. 3.5e-11;
XX Matches 27; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
XX
XX QY 1 LQKQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKW 43
XX :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 67 MQKFLGLEVTGKLDSDTLEVMRKPRCGVPDVGHFRTFPGIPKW 109

RESULT 14
AAO20482
ID AAO20482 standard; protein; 477 AA.
XX
XX AAO20482;
XX
XX 27-JUN-2002 (first entry)
XX
XX Prostromelysin protein.
XX
XX Osteopathic; dermatological; vulnery; catalytic domain; propeptide;
XX human; stromelysin; matrix metalloproteinase; SCD; scar tissue formation;
XX herniated vertebral disc; dermal ulcer; joint disease; protein therapy;
XX prostromelysin.
XX
XX Homo sapiens.
XX
XX OS
XX PD
XX XX

```

```

FH Key Location/Qualifiers
FT Peptide 1..17
FT /note= "Signal peptide"
FT Peptide 18..99
FT /note= "Propeptide"
FT Protein 100..273
FT /note= "Mature stromelysin catalytic domain protein"
XX
XX US6284513-B1.
XX
XX 04-SEP-2001.
XX
XX 27-JUL-1994; 94US-00281313.
XX
XX 03-FEB-1993; 93US-00012705.
XX (WARN ) WARNER LAMBERT CO.
XX
XX Ye Q, Johnson LL, Hupe DJ, Baragi V;
XX
XX WPI; 2001-615435/71.
XX
XX One step in vivo process for producing stromelysin catalytic domain,
XX which is useful in treating e.g. dermal ulcers or herniated vertebral
XX discs, by culturing transformed Escherichia coli having a gene encoding
XX the catalytic domain.
XX
XX Disclosure; Fig 1; 16pp; English.
XX
XX The invention relates to a one-step in vivo process for producing a
XX catalytic domain, without propeptide, of human stromelysin, comprising
XX culturing transformed Escherichia coli host cells comprising a DNA
XX sequence encoding the catalytic domain. For producing the catalytic
XX domain, without propeptide, of a matrix metalloproteinase, particularly
XX of the stromelysin catalytic domain. The stromelysin catalytic domain
XX (SCD) protein is useful in treating herniated vertebral discs, dermal
XX ulcers or joint diseases, or modifying scar tissue formation by means of
XX protein therapy. This sequence represents the prostromelysin protein of
XX the invention
XX
XX Sequence 477 AA;
XX
XX Query Match 54.7%; Score 141; DB 4; Length 477;
XX Best Local Similarity 62.8%; Pred. No. 3.5e-11;
XX Matches 27; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
XX
XX QY 1 LQKQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKW 43
XX :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 67 MQKFLGLEVTGKLDSDTLEVMRKPRCGVPDVGHFRTFPGIPKW 109

RESULT 15
ABB04752
ID ABB04752 standard; protein; 477 AA.
XX
XX ABB04752;
XX
XX 12-MAR-2002 (first entry)
XX
XX Human MMP3 protein SEQ ID NO:3.
XX
XX Human; matrix metalloproteinase 3; MMP3; chromosome 11q22.3; SNP;
XX haplotype; polymorphism; polymorphic; single nucleotide polymorphism;
XX probe; primer; detection; genotyping; vulnery; cytostatic; cancer;
XX antiarteriosclerotic; gene therapy; coronary atherosclerosis;
XX wound healing.
XX
XX Homo sapiens.
XX
XX WO200179238-A2.
XX
XX 25-OCT-2001.
XX
XX OS
XX PD
XX XX

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PF 17-APR-2001; 2001WO-US012452.
XX
PR 17-APR-2000; 2000US-0197911P.
PR 13-JUL-2000; 2000US-0218092P.
XX
XX (GENA-) GENAISSANCE PHARM INC.
XX
XX Bentivegna SC, Chew A, Choi JY, Koshy B, Stephens JC;
XX
XX NPI; 2002-075067/10.
DR N-PSDB; ABL01224.
XX
XX Genotyping human matrix metalloproteinase 3 gene of an individual for
PT determining the haplotype of the individual, comprises determining the
PT identity of a nucleotide pair at specific polymorphic sites for two
PT copies of the gene.
XX
XX Claim 27; Fig 3; 83pp; English.

XX The present invention describes a method for genotyping a human matrix
XX metalloproteinase 3 (MMP3) gene of an individual. MMP3 has vulnerary,
CC cytostatic and antiarteriosclerotic activity, and can be used in gene
CC therapy. The method can be used for improving the efficacy and
CC reliability of several steps in the discovery and development of drugs
CC for treating diseases associated with MMP3 activity, e.g., wound healing,
CC cancer and coronary atherosclerosis; to validate MMP3 as a candidate
CC agent for treating a specific condition or disease predicted to be
CC associated with MMP3 activity; and in the design of clinical trials of
CC candidate drugs for treating a specific condition or disease predicted to
CC be associated with MMP3 activity. Polymorphic variants of a reference
CC sequence for MMP3 (see ABL01223) are useful in studying the expression
CC and function of MMP3, and in expressing MMP3 protein for use in screening
CC for candidate drugs to treat diseases related to MMP3 activity. The human
CC MMP3 gene is located on chromosome 11q22.3. ABL01225 to ABL01246 and
CC ABL01247 to ABL01290 represent allele-specific oligonucleotide (ASO)
CC probes and primers used in the detection of polymorphisms in the human
CC MMP3 gene. ABL01291 to ABL01334 represent preferred primers used in the
CC detection of polymorphisms in the human MMP3 gene. The present sequence
CC represents the human MMP3 protein, as given in the present invention
XX

SQ Sequence 477 AA;

Query Match 54.7%; Score 141; DB 5; Length 477;
Best Local Similarity 62.8%; Pred. No. 3.5e-11;
Matches 27; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 LQQLSLPETGELDSATLKAMTRPCGVPDLGRFQTFEGDLKW 43
:|||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 67 MQKFLGLEVTGKLDSDTLEVMKRCGVPDVGHFRFFGIPKW 109

Search completed: November 15, 2004, 14:04:07
Job time : 45.0833 secs

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OM protein - protein search, using sw model

Run on: November 15, 2004, 14:01:35 ; Search time 12.6538 Seconds
(without alignments)
246.324 Million cell updates/sec

Title: US-10-032-376A-8
Perfect score: 258
Sequence: 1 LQKLSLPTGELDSATLKA.....VPLGRFQTFEGDLKWHHN 47

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 205538

Minimum DB seq length: 47
Maximum DB seq length: 660

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	141	54.7	477	3	US-08-704-711A-20
2	141	54.7	477	3	US-08-448-489-15
3	141	54.7	477	3	US-08-281-313-1
4	141	54.7	477	3	US-09-521-220-20
5	141	54.7	477	3	US-09-391-104-21
6	133	51.6	476	3	US-08-704-711A-21
7	133	51.6	476	3	US-08-448-489-14
8	133	51.6	476	3	US-09-521-220-21
9	133	51.6	476	3	US-09-391-104-22
10	117	45.3	471	3	US-09-391-104-25
11	115	44.6	136	4	US-09-513-999C-4639
12	114	44.2	631	3	US-08-448-489-17
13	114	44.2	660	3	US-08-704-711A-18
14	114	44.2	660	3	US-09-521-220-18
15	114	44.2	660	3	US-09-391-104-19
16	114	44.2	660	4	US-09-517-254-89
17	113	43.8	470	3	US-08-068-392-2
18	113	43.8	470	3	US-08-396-988-2
19	113	43.8	470	3	US-09-391-104-26
20	110	42.6	469	3	US-08-704-711A-16
21	110	42.6	469	3	US-08-448-489-12
22	110	42.6	469	3	US-09-521-220-16
23	110	42.6	469	3	US-09-391-104-23
24	109	42.2	513	4	US-10-140-002-192
25	109	42.2	513	4	US-09-862-631-4
26	108	41.9	471	4	US-08-994-689C-1
27	107	41.5	135	4	US-09-513-999C-4163

Sequence 18, Appl
Sequence 27, Appl
Sequence 2, Appl
Sequence 6, Appl
Sequence 21, Appl
Sequence 2, Appl
Sequence 1, Appl
Sequence 9, Appl
Sequence 2, Appl
Sequence 28, Appl
Sequence 84, Appl
Sequence 2, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 4, Appl
Sequence 24, Appl
Sequence 13, Appl

28 106 41.1 267 3 US-08-448-489-18
29 106 41.1 267 3 US-09-391-104-27
30 106 41.1 271 3 US-08-896-062-2
31 105 40.7 264 3 US-09-009-156-6
32 105 40.7 264 3 US-09-372-154-6
33 101 39.1 471 4 US-08-994-689C-21
34 100.5 39.0 582 3 US-08-704-711A-2
35 100.5 39.0 582 3 US-08-448-489-1
36 100.5 39.0 582 3 US-09-211-704A-9
37 100.5 39.0 582 3 US-09-521-220-2
38 100.5 39.0 582 3 US-09-391-104-28
39 100.5 39.0 582 4 US-09-919-497-84
40 100 38.8 444 1 US-09-178-002-2
41 100 38.8 466 3 US-08-704-711A-17
42 100 38.8 466 3 US-09-521-220-17
43 100 38.8 467 1 US-09-178-002-4
44 100 38.8 467 3 US-09-391-104-24
45 100 38.8 468 3 US-08-448-489-13

ALIGNMENTS

RESULT 1
US-08-704-711A-20
; Sequence 20, Application US/08704711A
; Patent No. 6114159
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; APPLICANT: HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,711A
; FILING DATE: 20-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/DE95/00357
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 477 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-704-711A-20


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;
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-704-711A-21

Query Match 51.6%; Score 133; DB 3; Length 476;
Best Local Similarity 58.1%; Pred. No. 3.6e-11;
Matches 25; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

Qy 1 LQKLSLPETGELDSATLKAMRTPRCGVDPDLGRFOTFEGDLKW 43
Db 66 MQKFLGLEVTGKLDTDLEVMRKPRCGVDPDVGHFSFGMPKW 108

RESULT 7
US-08-448-489-14
; Sequence 14, Application US/08448489
; Patent No. 6184022
; GENERAL INFORMATION:
; APPLICANT: SEIKI, Motoharu
; APPLICANT: SATO, Hiroshi
; APPLICANT: SHINAGAWA, Akira
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
; FILE REFERENCE: 35-290P
; CURRENT APPLICATION NUMBER: US/08/448,489
; CURRENT FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Known Member of
; OTHER INFORMATION: Matrix Metalloproteinase Family
; US-08-448-489-14

Query Match 51.6%; Score 133; DB 3; Length 476;
Best Local Similarity 58.1%; Pred. No. 3.6e-11;
Matches 25; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

Qy 1 LQKLSLPETGELDSATLKAMRTPRCGVDPDLGRFOTFEGDLKW 43
Db 66 MQKFLGLEVTGKLDTDLEVMRKPRCGVDPDVGHFSFGMPKW 108

RESULT 8
US-09-521-220-21
; Sequence 21, Application US/09521220
; Patent No. 6399348
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; APPLICANT: HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/09/521,220
; FILING DATE: 08-Mar-2000
; CLASSIFICATION: <Unknown>
; 21-OCT-1994
; 17-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/704,711
; FILING DATE: <Unknown>
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-521-220-21

Query Match 51.6%; Score 133; DB 3; Length 476;
Best Local Similarity 58.1%; Pred. No. 3.6e-11;
Matches 25; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

Qy 1 LQKLSLPETGELDSATLKAMRTPRCGVDPDLGRFOTFEGDLKW 43
Db 66 MQKFLGLEVTGKLDTDLEVMRKPRCGVDPDVGHFSFGMPKW 108

RESULT 9
US-09-391-104-22
; Sequence 22, Application US/09391104
; Patent No. 6399371
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Falduto, Michael T.
; APPLICANT: Magnuson, Scott R.
; APPLICANT: Morgan, Douglas W.
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE
; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
; FILE REFERENCE: 6073.US.P1
; CURRENT APPLICATION NUMBER: US/09/391,104
; CURRENT FILING DATE: 1999-09-07
; PRIOR APPLICATION NUMBER: US 08/814,394
; PRIOR FILING DATE: 1997-03-11
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-391-104-22

Query Match 51.6%; Score 133; DB 3; Length 476;
Best Local Similarity 58.1%; Pred. No. 3.6e-11;
Matches 25; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

Qy 1 LQKLSLPETGELDSATLKAMRTPRCGVDPDLGRFOTFEGDLKW 43
Db 66 MQKFLGLEVTGKLDTDLEVMRKPRCGVDPDVGHFSFGMPKW 108

RESULT 10
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```
US-09-391-104-25
; Sequence 25, Application US/09391104
; Patent No. 6399371
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Falduto, Michael T.
; APPLICANT: Magnuson, Scott R.
; APPLICANT: Morgan, Douglas W.
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEINASE GENE,
; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
; TITLE OF INVENTION: OF USING SAME
; FILE REFERENCE: 6073.US.P1
; CURRENT APPLICATION NUMBER: US/09/391,104
; CURRENT FILING DATE: 1999-09-07
; PRIOR APPLICATION NUMBER: US 08/814,394
; PRIOR FILING DATE: 1997-03-11
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 471
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-391-104-25

Query Match 45.3%; Score 117; DB 3; Length 471;
Best Local Similarity 46.8%; Pred. No. 8.5e-09;
Matches 22; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

QY 1 LQKQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 47
DB 71 MQSFFGLEVTGKLDNDTLDVMKPRCGVDPDVGSEYVNFRTLKWSQXN 117

RESULT 11
US-09-513-999C-4639
; Sequence 4639, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4639
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -29...-1
; OTHER INFORMATION: score 11.4
; OTHER INFORMATION: seq LCLLGCLLSHAAA/AP
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 16
; OTHER INFORMATION: Xaa=Lys or Thr
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 17
; OTHER INFORMATION: Xaa=Asp or Val
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 19
; OTHER INFORMATION: Xaa=Glu or Lys
; FEATURE:
; NAME/KEY: UNSURE

US-09-513-999C-4639
; Sequence 4639, Application US/08448489
; Patent No. 6184022
; GENERAL INFORMATION:
; APPLICANT: SEIKI, Motoharu
; APPLICANT: SATO, Hiroshi
; APPLICANT: SHINAGAWA, Akira
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
; FILE REFERENCE: 55-290P
; CURRENT APPLICATION NUMBER: US/08/448,489
; CURRENT FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 631
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: UNSURE

US-08-448-489-17
; Sequence 17, Application US/08448489
; Patent No. 6184022
; GENERAL INFORMATION:
; APPLICANT: SEIKI, Motoharu
; APPLICANT: SATO, Hiroshi
; APPLICANT: SHINAGAWA, Akira
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
; FILE REFERENCE: 55-290P
; CURRENT APPLICATION NUMBER: US/08/448,489
; CURRENT FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 631
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: UNSURE

Query Match 44.6%; Score 115; DB 4; Length 136;
Best Local Similarity 46.5%; Pred. No. 3.4e-09;
Matches 20; Conservative 6; Mismatches 17; Indels 0; Gaps 0;

QY 1 LQKQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKW 43
DB 77 MQKFFGLPQTGLDQNTIXXMRKPRCGXPVDVAXYFPRKXKW 119

RESULT 12
US-08-448-489-17
; Sequence 17, Application US/08448489
; Patent No. 6184022
; GENERAL INFORMATION:
; APPLICANT: SEIKI, Motoharu
; APPLICANT: SATO, Hiroshi
; APPLICANT: SHINAGAWA, Akira
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
; FILE REFERENCE: 55-290P
; CURRENT APPLICATION NUMBER: US/08/448,489
; CURRENT FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 631
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: UNSURE
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; OTHER INFORMATION: Description of Unknown Organism: Known Member of
; OTHER INFORMATION: Matrix Metalloproteinase Family
US-08-448-489-17

Query Match 44.2%; Score 114; DB 3; Length 660;
Best Local Similarity 46.5%; Pred. No. 3.5e-08;
Matches 20; Conservative 7; Mismatches 16; Indels 0; Gaps 0;

Qy 1 LQKLSLPETGELDSATLKAMRTRCGVPLGRFQTFEGDLKW 43
Db 48 MQKFFGLPQTGDDLDQNTIETMRKPCGPNPDVANYNFFPRKPKW 90

RESULT 13
US-08-704-711A-18
; Sequence 18, Application US/08704711A
; Patent No. 6114159
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; APPLICANT: HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,711A
; FILING DATE: 20-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/DE95/00357
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; APPLICATION DATA:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 660 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-704-711A-18
Query Match 44.2%; Score 114; DB 3; Length 660;
Best Local Similarity 46.5%; Pred. No. 3.7e-08;
Matches 20; Conservative 7; Mismatches 16; Indels 0; Gaps 0;
Qy 1 LQKLSLPETGELDSATLKAMRTRCGVPLGRFQTFEGDLKW 43
Db 77 MQKFFGLPQTGDDLDQNTIETMRKPCGPNPDVANYNFFPRKPKW 119
RESULT 15
US-09-391-104-19
; Sequence 19, Application US/09391104
; Patent No. 6399371
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Falduto, Michael T.
; APPLICANT: Magnuson, Scott R.
; APPLICANT: Morgan, Douglas W.
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,
; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
; TITLE OF INVENTION: OF USING SAME

RESULT 14
US-09-521-220-18
; Sequence 18, Application US/09521220
; Patent No. 6399348
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; APPLICANT: HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/521,220
; FILING DATE: 08-Mar-2000
; CLASSIFICATION: <Unknown>
; FILING DATE: 21-OCT-1994
; FILING DATE: 17-MAR-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/704,711
FILING DATE: <Unknown>
APPLICATION NUMBER: DE 4438838.1
FILING DATE: 21-OCT-1994
APPLICATION NUMBER: DE 4409663.1
FILING DATE: 17-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 26083/124
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 660 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

US-09-521-220-18
Query Match 44.2%; Score 114; DB 3; Length 660;
Best Local Similarity 46.5%; Pred. No. 3.7e-08;
Matches 20; Conservative 7; Mismatches 16; Indels 0; Gaps 0;
Qy 1 LQKLSLPETGELDSATLKAMRTRCGVPLGRFQTFEGDLKW 43
Db 77 MQKFFGLPQTGDDLDQNTIETMRKPCGPNPDVANYNFFPRKPKW 119

RESULT 15
US-09-391-104-19
; Sequence 19, Application US/09391104
; Patent No. 6399371
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Falduto, Michael T.
; APPLICANT: Magnuson, Scott R.
; APPLICANT: Morgan, Douglas W.
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,
; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
; TITLE OF INVENTION: OF USING SAME

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; FILE REFERENCE: 6073-US.P1
; CURRENT APPLICATION NUMBER: US/09/391,104
; CURRENT FILING DATE: 1999-09-07
; PRIOR APPLICATION NUMBER: US 08/814,394
; PRIOR FILING DATE: 1997-03-11
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-391-104-19
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Best Local Similarity 46.5%; Pred. No. 3.7e-08;
Matches 20; Conservative 7; Mismatches 16; Indels 0; Gaps 0;

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       :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      77 MQKFFGLPQTGDLDDQNTIETMRKPCGNDVANYNFFPRKPKW 119
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Search completed: November 15, 2004, 14:08:07
Job time : 13.6538 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 15, 2004, 14:06:45 ; Search time 121.718 Seconds
(without alignments)
136.623 Million cell updates/sec

Title: US-10-032-376A-8

Perfect score: 258

Sequence: 1 LOKLSLPETGELDSATLKA.....VPLGRFQTFEGDLKWHHN 47

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1568699 seqs, 353819137 residues

Total number of hits satisfying chosen parameters: 1077212

Minimum DB seq length: 47

Maximum DB seq length: 660

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

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- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
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- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09D_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	258	100.0	47	14 US-10-219-329-8	Sequence 8, Appli
2	258	100.0	47	14 US-10-153-185-8	Sequence 8, Appli
3	258	100.0	47	14 US-10-219-561-8	Sequence 8, Appli
4	258	100.0	47	16 US-10-032-376A-8	Sequence 8, Appli
5	258	100.0	47	16 US-10-335-207-8	Sequence 8, Appli
6	150	58.1	171	14 US-10-050-216B-4	Sequence 4, Appli
7	141	54.7	54	14 US-10-219-329-5	Sequence 5, Appli
8	141	54.7	54	14 US-10-153-185-5	Sequence 5, Appli
9	141	54.7	54	14 US-10-219-561-5	Sequence 5, Appli
10	141	54.7	54	16 US-10-032-376A-5	Sequence 5, Appli
11	141	54.7	54	16 US-10-335-207-5	Sequence 5, Appli
12	141	54.7	267	14 US-10-133-797-3	Sequence 73, Appli
13	141	54.7	477	9 US-09-391-104-21	Sequence 21, Appli

14	141	54.7	477	9	US-09-801-196-24	Sequence 24, Appli
15	141	54.7	477	14	US-10-171-311-137	Sequence 137, Appli
16	141	54.7	477	14	US-10-301-822-127	Sequence 127, Appli
17	141	54.7	477	14	US-10-131-985-27	Sequence 27, Appli
18	141	54.7	477	14	US-10-295-027-22	Sequence 22, Appli
19	141	54.7	477	15	US-10-115-479-44	Sequence 44, Appli
20	141	54.7	477	15	US-10-211-462-36	Sequence 36, Appli
21	141	54.7	477	15	US-10-447-315-5	Sequence 5, Appli
22	135	52.3	173	15	US-10-115-479-48	Sequence 48, Appli
23	135	52.3	477	15	US-10-115-479-46	Sequence 46, Appli
24	133	51.6	55	14	US-10-219-329-6	Sequence 6, Appli
25	133	51.6	55	14	US-10-153-185-8	Sequence 6, Appli
26	133	51.6	55	14	US-10-219-561-6	Sequence 6, Appli
27	133	51.6	55	16	US-10-032-376A-6	Sequence 6, Appli
28	133	51.6	55	16	US-10-335-207-6	Sequence 6, Appli
29	133	51.6	475	14	US-10-295-027-8	Sequence 8, Appli
30	133	51.6	475	15	US-10-058-270A-78	Sequence 78, Appli
31	133	51.6	476	9	US-09-391-104-22	Sequence 22, Appli
32	133	51.6	476	9	US-09-801-196-25	Sequence 25, Appli
33	133	51.6	476	14	US-10-021-860-72	Sequence 72, Appli
34	133	51.6	476	14	US-10-131-985-35	Sequence 35, Appli
35	133	51.6	476	15	US-10-211-462-10	Sequence 10, Appli
36	133	51.6	476	15	US-10-188-832-4	Sequence 4, Appli
37	123	47.7	477	9	US-09-920-455-260	Sequence 260, Appli
38	117	45.3	50	14	US-10-219-329-3	Sequence 3, Appli
39	117	45.3	50	14	US-10-153-185-3	Sequence 3, Appli
40	117	45.3	50	14	US-10-219-561-3	Sequence 3, Appli
41	117	45.3	50	16	US-10-032-376A-3	Sequence 3, Appli
42	117	45.3	50	16	US-10-335-207-3	Sequence 3, Appli
43	117	45.3	464	14	US-10-409-643-21	Sequence 21, Appli
44	117	45.3	471	9	US-09-391-104-25	Sequence 25, Appli
45	117	45.3	471	9	US-09-801-196-21	Sequence 21, Appli

ALIGNMENTS

RESULT 1

US-10-219-329-8
; Sequence 8, Application US/10219329
; Publication No. US20030096757A1
; GENERAL INFORMATION:
; APPLICANT: Quirk, Stephen
; TITLE OF INVENTION: Anti-Cancer and Wound Healing Compounds
; FILE REFERENCE: 1443.035W01
; CURRENT APPLICATION NUMBER: US/10/219,329
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-219-329-8

Query Match 100.0%; Score 258; DB 14; Length 47;
Best Local Similarity 100.0%; Pred. No. 1.1e-27;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOKLSLPETGELDSATLKA M R T P C G V P D I G R F Q T F E G D L K W H H N 47
DB 1 LOKLSLPETGELDSATLKA M R T P C G V P D I G R F Q T F E G D L K W H H N 47

RESULT 2

US-10-153-185-8
; Sequence 8, Application US/10153185
; Publication No. US20030148959A1

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; GENERAL INFORMATION:
; APPLICANT: Quirk, Stephen
; APPLICANT: Malik, Schail
; TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds
; FILE REFERENCE: 1443.034US1
; CURRENT APPLICATION NUMBER: US/10/153,185
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-185-8

Query Match      100.0%; Score 258; DB 14; Length 47;
Best Local Similarity 100.0%; Pred. No. 1.1e-27;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 LQKQLSPETGELDSATLKAMRTPCGVPDLGRFQTFEGDLKWHHN 47

RESULT 3
US-10-219-561-8
; Sequence 8, Application US/10219561
; Publication No. US20030166567A1
; GENERAL INFORMATION:
; APPLICANT: Quirk, Stephen
; APPLICANT: Malik, Schail
; APPLICANT: Villanueva, Julie M.
; TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds
; FILE REFERENCE: 1443.008US2
; CURRENT APPLICATION NUMBER: US/10/219,561
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 10/153,185
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-219-561-8

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Best Local Similarity 100.0%; Pred. No. 1.1e-27;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
US-10-032-376A-8
; Sequence 8, Application US/10032376A
; Publication No. US20040127420A1
; GENERAL INFORMATION:
; APPLICANT: Quirk, Steven
; TITLE OF INVENTION: Metalloproteinase Inhibitors for Wound Healing
; FILE REFERENCE: 1443.008US1
; CURRENT APPLICATION NUMBER: US/10/032,376A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US/10/032,376
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus
US-10-050-216B-4

Query Match      58.1%; Score 150; DB 14; Length 171;
Best Local Similarity 57.4%; Pred. No. 3e-12;
Matches 27; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

; GENERAL INFORMATION:
; APPLICANT: Quirk, Stephen
; APPLICANT: Villanueva, Julie M.
; TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds
; FILE REFERENCE: 1443.008US2
; CURRENT APPLICATION NUMBER: US/10/219,561
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 10/153,185
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-219-561-8

Query Match      100.0%; Score 258; DB 14; Length 47;
Best Local Similarity 100.0%; Pred. No. 1.1e-27;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQKQLSPETGELDSATLKAMRTPCGVPDLGRFQTFEGDLKWHHN 47
Db 1 LQKQLSPETGELDSATLKAMRTPCGVPDLGRFQTFEGDLKWHHN 47

RESULT 5
US-10-335-207-8
; Sequence 8, Application US/10335207
; Publication No. US20040127421A1
; GENERAL INFORMATION:
; APPLICANT: Quirk, Stephen
; APPLICANT: Malik, Schail
; TITLE OF INVENTION: Method to Increase Fibronectin
; FILE REFERENCE: 1443.047US1
; CURRENT APPLICATION NUMBER: US/10/335,207
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-335-207-8

Query Match      100.0%; Score 258; DB 16; Length 47;
Best Local Similarity 100.0%; Pred. No. 1.1e-27;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQKQLSPETGELDSATLKAMRTPCGVPDLGRFQTFEGDLKWHHN 47
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RESULT 6
US-10-050-216B-4
; Sequence 4, Application US/10050216B
; Publication No. US20030039991A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J., Lora, Jose M.
; TITLE OF INVENTION: 46798, A Human Matrix Metalloprotease and
; FILE REFERENCE: MPI2001-014PIRNM
; CURRENT APPLICATION NUMBER: US/10/050,216B
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 60/262,252
; PRIOR FILING DATE: 2001-01-16
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus
US-10-050-216B-4

Query Match      58.1%; Score 150; DB 14; Length 171;
Best Local Similarity 57.4%; Pred. No. 3e-12;
Matches 27; Conservative 7; Mismatches 13; Indels 0; Gaps 0;
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SECRETED COPY INFORMATION

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Best Local Similarity 62.8%; Pred. No. 1.7e-10;
Matches 27; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
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Db	67	M	Q	K	F	L	G	L	E	V	T	G	K	L	D	S	T	L	E	V	N	K	P	R	C	G	V	P	D	V	C	H	F	T	F	T	F	P	G	I	P	K	109

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 15, 2004, 14:01:35 ; Search time 10.5449 Seconds
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Title: US-10-032-376A-8

Perfect score: 258

Sequence: 1 LQQLSLPFGELDSATLKA.....VPLGRFQTFEGDLKWHHN 47

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Maximum DB seq length: 660

Post-processing: Minimum Match 0%

Maximum Match 100%

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3: PIR2:*

4: PIR3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	141	54.7	477	1 KCHUS1	stromelysin 1 (EC
2	138	53.5	478	1 KCRBS1	stromelysin 1 (EC
3	134	51.9	475	1 KCRTH	stromelysin 1 (EC
4	133	51.6	476	1 JC6505	stromelysin 2 (EC
5	133	51.6	476	1 KCHUS2	stromelysin 2 (EC
6	133	51.6	476	1 KCRFS2	stromelysin 1 (EC
7	133	51.6	477	1 KCMSS1	stromelysin 1 (EC
8	121	46.9	472	2 S29243	interstitial colla
9	118	45.7	466	2 A23685	collagenase 3 (EC
10	117	45.3	471	2 A53711	matrilysin (EC 3.4
11	116	45.0	267	2 A57490	gelatinase A (EC 3.4
12	114	44.2	660	1 A28153	metalloelastase HM
13	113	43.8	470	2 A49499	interstitial colla
14	110	42.6	469	1 KCHUN	pro-matrix metallo
15	108	41.9	82	2 PW0052	matrix metalloprot
16	108	41.9	483	2 JC5743	matrix metalloprot
17	106	41.1	267	2 KCHUM	matrix metalloprot
18	104.5	40.5	582	2 I84471	matrix metalloprot
19	103	39.9	468	1 KCRBI	interstitial colla
20	100.5	39.0	582	2 I38028	matrix metalloprot
21	100	38.8	467	1 KCHUN	neutrophil collage
22	99	38.4	469	1 KCHUN	interstitial colla
23	98	38.0	469	1 KCB01	matrix metalloprot
24	97.5	37.8	582	2 I48573	probable matrix me
25	96	37.2	521	2 T37252	probable metallopro
26	92	35.7	364	2 E71433	macrophage elastase
27	92	35.7	422	2 A42401	matrix metalloprot
28	91	35.3	616	2 JC7776	probable metallopro
29	88	34.1	305	2 T08936	

30 85.5 33.1 341 2 T51957 metalloproteinase
31 85.5 33.1 342 2 G84885 probable metallopro
32 83.5 32.4 378 2 E96724 hypothetical prote
33 80 31.0 587 2 S12805 envlysin (EC 3.4.
34 79.5 30.8 508 2 JC5082 matrix metalloprot
35 75.5 29.3 384 2 I51267 collagenase (EC 3.
36 75 29.1 377 2 T00643 zinc metalloprotei
37 73 28.3 587 2 S41409 envlysin (EC 3.4.
38 67.5 26.2 478 2 T32825 hypothetical prote
39 60 23.3 136 1 TCR7 calcitonin precurs
40 59 22.9 579 2 T37248 probable matrix me
41 59 22.9 598 2 T32165 hypothetical prote
42 57 22.1 152 2 T03173 gelatinase homolog
43 57 22.1 351 2 F64880 ycs protein - bsc
44 57 22.1 351 2 C85753 probable dehydroge
45 57 22.1 351 2 F90865 probable dehydroge

ALIGNMENTS

RESULT 1

KCHUS1

stromelysin 1 (EC 3.4.24.17) precursor [validated] - human

N:Alternate names: angiotatin-converting enzyme; collagenase activating protein; matri

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1992 #sequence_revision 08-May-1998 #text_change 09-Jul-2004

C:Accession: A28156; C29157; A28399; A60964; S15427

R:Saus, J.; Quinones, S.; Otani, Y.; Nagase, H.; Harris Jr., E.D.; Kurkinen, M.

J. Biol. Chem. 263, 6742-6745, 1988

A:Title: The complete primary structure of human matrix metalloproteinase-3. Identity w

A:Reference number: A28156; MUID:88198243; PMID:3360803

A:Accession: A28156

A:Molecule type: mRNA

A:Residues: 1-44, 'E', '46-477 <SAU>

A:Cross-references: UNIPROT:P08254; GB:J03209; NID:G188618; PIDN:AAA36321.1; PID:G18861

R:Whitham, S.E.; Murphy, G.; Angel, P.; Rahmsdorf, H.J.; Smith, B.J.; Lyons, A.; Harris

Biochem. J. 240, 913-916, 1986

A:Title: Comparison of human stromelysin and collagenase by cloning and sequence analys

A:Reference number: A90336; MUID:87156645; PMID:3030290

A:Accession: C29157

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-477 <WHI>

A:Cross-references: ENBL:X05232; NID:G36632; PIDN:CAA28859.1; PID:G36633

R:Wilhelm, S.M.; Collier, I.E.; Kronberger, A.; Eisen, A.Z.; Marmer, B.L.; Grant, G.A.;

Proc. Natl. Acad. Sci. U.S.A. 84, 6725-6729, 1987

A:Title: Human skin fibroblast stromelysin: structure, glycosylation, substrate specifi

A:Reference number: A28399; MUID:88016164; PMID:3477804

A:Accession: A28399

A>Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-49, 'C', '51-419, 'L', '421-477 <WIL>

A:Cross-references: GB:U78045; NID:G1689257; PIDN:AAB36942.1; PID:G1689259

A>Note: part of the sequence, including the amino end of the proenzyme, was confirmed b

R:Lark, M.W.; Walakowits, L.A.; Shah, T.K.; Varmiddlesworth, J.; Cameron, P.M.; Lin, T.

Connect. Tissue Res. 25, 49-65, 1990

A:Title: Production and purification of prostromelysin and procollagenase from IL-1 bet

A:Reference number: A50964; MUID:91059606; PMID:2173990

A:Accession: A50964

A:Molecule type: protein

A:Residues: 18-29;100-108 <LAR>

R:Koklitis, P.A.; Murphy, G.; Sutton, C.; Angal, S.

Biochem. J. 276, 217-221, 1991

A:Title: Purification of recombinant human prostromelysin. Studies on heat activation t

A:Reference number: S15427; MUID:91248150; PMID:2039471

A:Accession: S15427

A>Status: preliminary

A:Molecule type: protein

A:Residues: 18-23 <BIO>

R:Linen, H.R.; Ugwu, F.; Bini, A.; Collen, D.

Biochemistry 37, 4699-4702, 1998

ed with collagenase. A:Reference number: A37306; MUID:88077214; PMID:2825726
A:Accession: A37306
A:Accession: A37306
A:Molecule type: mRNA
A:Residues: 1-478 <FN>
A:Cross-references: UNIPROT:P28863; GB:M35664; NID:G165709; PIDN:AAA31467.1; PID:G165710
R:W.H.Tham, S.E.; Murphy, G.; Angel, P.; Rahmsdorf, H.J.; Smith, B.J.; Lyons, A.; Harris, B.Schoem, J. 240, 913-916, 1986
A:Title: Comparison of human stromelysin and collagenase by cloning and sequence analysis
A:Reference number: A30336; MUID:87158645; PMID:3030290
A:Accession: A39157
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Residues: 1-82, '84-127, 'K', 129-167, 'GNS' <WHI>
A:Molecule type: mRNA
A:Residues: 1-82, '84-127, 'K', 129-167, 'GNS' <WHI>
A:Comment: This enzyme degrades various extracellular matrix proteins, including fibronectin, laminin, and basement membrane. Stromelysin 1 hydrolyzes peptide bonds in plasminogen to yield a fragment with a free amino group. Stromelysin 1 activates its proenzyme after cleavage(s) within the activation site. Stromelysin 1 is found in glycosylated and unglycosylated forms, both of which are active.
C:Function: endopeptidase preferentially hydrolyzing peptide bonds on the carboxyl si
A:Description: endopeptidase preferentially hydrolyzing peptide bonds on the carboxyl si
A:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotein
C:Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hyaluronase; metallo
F:1-17/Domain: signal sequence #status predicted <Sig>
F:18-478/Product: prostromelysin 1 #status predicted <PRO>
F:18-100/Domain: activation peptide #status predicted <ACT>
F:61-265/Domain: matrix metalloproteinase homology <MMP>
F:91-98/Region: autoinhibitory
F:103-478/Product: stromelysin 1 #status predicted <MAT>
F:288-478/Domain: hemopexin repeat homology <PXN>
F:93, 219, 223, 229/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status
F:121/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:219, 223, 229/Binding site: zinc, catalytic (His) (active) #status predicted
F:220/Active site: Glu #status predicted
F:291-478/Disulfide bonds: #status predicted

```

Query Match      53.5%; Score 138; DB 1; Length 478;
Best Local Similarity 60.5%; Pred.No. 1.6e-10;
Matches 26; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

QY   1 LQQLSLPETGELDSATLKAMRTPCRGVPDILGRFTQTFEGDLKW 43
      :|::|||::|::|::|::|::|::|::|::|::|::|::|::|
Db    68 MQKTLGLEVTGLKDSNTLEVRKPCRGVDPVGHFSTFGTPKW 110

RESULT 3
KKRIH
stromelysin 1 (EC 3.4.24.17) precursor - rat
NI:Alternate names: collagenase activating protein; matrix metalloproteinase 3 (MMP3); pr
C:Species: Rattus norvegicus (Norway rat)
C>Date: 13-Aug-1986 #sequence revision 13-Aug-1986 #text_change 09-Jul-2004
C:Accession: A00997; F80150; S22767
R:Mattisian, L.M.; Glaichenhaus, N.; Gesnel, M.C.; Breathnach, R.
EMBO J. 4, 1435-1440, 1985
A:Title: Epidermal growth factor and oncogenes induce transcription of the same cellular
A:Reference number: A00997; PMID:85284930; PMID:3875482
```

A.Reference number: A00997; MUID:85284930; PMID:3875482
A.Accession: A00997
A.Molecule type: mRNA
A.Residues: 1-475 <MAL>
A.Cross-references: UNIPROT:P03957; GB:X02601; NID:957460; PIDN:CAA26448.1; PID:957461
R.Umenishi, F.; Yasumatsu, H.; Ashida, Y.; Yamauti, J.; Umeda, M.; Miyazaki, K.
J. Biochem. 108, 537-543, 1990
A.Title: Purification and properties of extracellular matrix-degrading metallo-proteinases
A.Reference number: PQS150; MUID:91154156; PMID:1963430

A/Accession: F50150
A/Molecule type: protein
A/Residues: 19-20, 'X', 22-28; 110-112, 'X', 114-115, 'X', 117, 'X', 119; 309-325 <ME>
R/Breathnach, R.; Matrisian, L.M.; Gesnel, M.C.; Staub, A.; Leroy, P.
Nucleic Acids Res. 15, 1139-1151, 1987
A/Title: Sequences coding for part of oncogene-induced transin are highly conserved in a
A/Reference number: A56403; NUID:87146421; PMID:3547333
A/Contents: annotation; introns
A/Note: Intron positions were determined by comparison of the previously reported cDNA s
R/Sanchez-Lopez, R.; Nicholson, R.; Gesnel, M.C.; Matrisian, L.M.; Breathnach, R.

```

F:218,222,228/Binding site: zinc, catalytic (His) (active) #status predicted
F:219/Active site: Glu #status predicted
F:289-476/Disulfide bonds: #status predicted

Query Match 51.6%; Score 133; DB 1; Length 476;
Best Local Similarity 58.1%; Pred. No. 7.4e-10;
Matches 25; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

Qy 1 LQKLSLPETGELDSATLKAMRTPRCGVPDLGRFQTPEGDLKW 43
Db :|||:||||:|||||:|||||:|||||:|||||:|||||:
67 MQKFLGLEMTGKLDNTMELMHKPCGVPDVGGFSTFGSPKW 109

RESULT 5
KCHUS2
stromelysin 2 (EC 3.4.24.22) precursor [validated] - human
N:Alternate names: matrix metalloproteinase 10 (MMP10); transin-2
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
C:Accession: A28816; A47496
E:Muller, D.; Quantin, B.; Gesnel, M.C.; Millon-Collard, R.; Abecassis, J.; Breathnach,
Biochem. J. 253, 187-192, 1988
A:Title: The collagenase gene family in humans consists of at least four members.
A:Reference number: A90339; MUID:08339885; PMID:2844164
A:Accession: A28816
A:Molecule type: mRNA
A:Residues: 1-476 <MUL>
A:Cross-references: UNIPROT:P09238; ENMEL:X07820; NID:G36628; PIDN:CRAA30679.1; PID:G36628
A:Note: mRNA for this protein was detected in several human tumors
F:Windsor, L.J.; Grenett, H.; Birkedal-Hansen, B.; Bodden, M.K.; Engler, J.A.; Birkedal
J. Biol. Chem. 268, 17341-17347, 1993
A:Title: Cell type-specific regulation of SL-1 and SL-2 genes. Induction of the SL-2 gene
A:Reference number: A47496; MUID:93352520; PMID:8349617
A:Accession: A47496
A:Molecule type: protein
A:Residues: 17-33 <WIN>
C:Comment: This enzyme degrades various extracellular matrix proteins, including fibron
C:Genetics:
A:Gene: GDB:MMP10; STMY2
A:Cross-references: GDB:I120392; OMIM:185260
A:Map position: 11q22.3-11q23
C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprote
C:Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metal
F:1-16/Domain: signal sequence #status predicted <SIG>
F:17-476/Product: prostromelysin 2 #status experimental <PRO>
F:17-98/Domain: activation peptide #status predicted <ACT>
F:59-263/Domain: matrix metalloproteinase homology <MMP>
F:89-96/Region: autoinhibitory
F:99-476/Product: stromelysin 2 #status predicted <MAT>
F:283-476/Domain: hemopexin repeat homology <PXN>
F:91,217,221,227/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status
F:119/Binding site: carboxylate (Asn) (covalent) #status predicted
F:217,221,227/Binding site: zinc, catalytic (His) (active) #status predicted
F:219/Active site: Glu #status predicted
F:289-476/Disulfide bonds: #status predicted

Query Match 51.6%; Score 133; DB 1; Length 476;
Best Local Similarity 58.1%; Pred. No. 7.4e-10;
Matches 25; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

Qy 1 LQKLSLPETGELDSATLKAMRTPRCGVPDLGRFQTPEGDLKW 43
Db :|||:||||:|||||:|||||:|||||:|||||:|||||:
66 MQKFLGLEVTGKLDITLVEVNRKPCGVPDVGHFSSFFGMPKW 108

RESULT 6
KCHUS2
stromelysin 2 (EC 3.4.24.22) precursor - rat
N:Alternate names: matrix metalloproteinase 10 (MMP10); transin-2
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
C:Accession: B26403; A41775; S26498
R:Breathnach, R.; Marislian, L.M.; Gesnel, M.C.; Staub, A.; Leroy, P.

```

Nucleic Acids Res. 15, 1139-1151, 1987

A:Title: Sequences coding for part of oncogene-induced transin are highly conserved in a

A:Reference number: A26403; MUID:87146421; PMID:3547333

A:Accession: S26403

A:Molecule type: mRNA

A:Residues: 1-476 <BRE>

A:Cross-references: UNIPROT:P07152; EMBL:X05083; NID:G57388; PIDN:CAA28739.1; PID:G57389

A:Note: Intron positions were determined by comparison of the cDNA sequence to genomic

A:Note: mRNA for this protein was expressed in several transformed rat embryo fibroblast

P:Chan, J.C.; Scanlon, M.; Zhang, H.Z.; Jia, L.B.; Yu, D.H.; Hung, M.C.; French, M.; Eas

J. Biol. Chem. 267, 1099-1103, 1992

A:Title: Molecular cloning and characterization of v-mos-activated transformation-associ

A:Reference number: A41775; MUID:92112748; PMID:1370458

A:Accession: A41775

A:Molecule type: mRNA

A:Residues: 1-476 <CHA>

A:Cross-references: GB:M65253; NID:G207150; PIDN:AAA42202.1; PID:G207151

A:Note: Sequence extracted from NCBI backbone (NCBIP:76184)

R:de Voege, M.W.; Mukherjee, B.B.

Oncogene 7, 109-119, 1992

A:Title: Transformation of normal rat kidney cells by v-K-ras enhances expression of tra

A:Reference number: S26496; MUID:92158347; PMID:1741158

A:Accession: S26498

A:Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 31-103, 'L', 241-242, 'TQMEKPH', 251, 'L', 253-254, 'CE', 293-294, 'L', 296 <DEV>

A:Cross-references: EMBL:X64020

C:Genetics:

A:Introns: 35/3; 117/2; 167/1; 209/1; 264/1; 311/2; 356/1; 409/2; 444/1

C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprote

C:Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo

F:1-17/Domain: signal sequence #status predicted <SIG>

F:18-476/Product: prostromelysin 2 #status predicted <PRO>

F:18-99/Domain: activation peptide #status predicted <ACT>

F:60-264/Domain: matrix metalloproteinase homology <MMP>

F:90-97/Region: autoinhibitory

F:100-476/Domain: stromelysin 2 #status predicted <MAT>

F:283-476/Domain: hemopexin repeat homology <PXN>

F:92,218,222,228/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status

F:120/Binding site: carboxylate (Asn) (covalent) #status predicted

F:218,222,228/Binding site: zinc, catalytic (His) (active) #status predicted

F:219/Active site: Glu #status predicted

F:289-476/Disulfide bonds: #status predicted

Query Match 51.6%; Score 133; DB 1; Length 476;

Best Local Similarity 53.2%; Pred. No. 7.4e-10;

Matches 25; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

QY 1 LQKLSLPETGELDSATLKAMRPRCGVPLGRFOTFEGLKWHHN 47

DB 67 MQKFLGLEMTGKLDSTNEMHPRCGVDPVGGFSTFPGSPKRNH 113

RESULT 7

KCMSS1

stromelysin 1 (EC 3.4.24.17) precursor - mouse

N:Alternate names: collagenase activating protein; matrix metalloproteinase 3 (MMP3); pr

C:Species: Mus musculus (house mouse)

C>Date: 30-Sep-1992 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C:Accession: JCI476; S18867; S32963; S33139

R:Hammani, K.; Henriet, P.; Beckhout, Y.

Gene 120, 321-322, 1992

A:Title: Cloning and sequencing of a cDNA encoding mouse stromelysin 1.

A:Reference number: JCI476; MUID:93013057; PMID:1398148

A:Accession: JCI476

A:Molecule type: mRNA

A:Residues: 1-477 <HAM>

A:Cross-references: UNIPROT:P28862; EMBL:X66402; NID:G296167; PIDN:CAA47029.1; PID:G2961

A:Note: It is uncertain whether Met-1 is the initiator or whether translation is initiat

R:Li, F.; Strange, R.; Saurer, S.; Niemann, H.; Friis, R.R.

submitted to the EMBL Data Library, August 1991

A:Reference number: S18867

A:Accession: S18867

A:Molecule type: mRNA

A:Residues: 'MK', 1-477 <LIF>

A:Cross-references: EMBL:X63162; NID:G54871; PIDN:CAA44860.1; PID:G54872

R:Brenner, C.A.; Adler, R.R.; Rappolee, D.A.; Pedersen, R.A.; Werb, Z.

Genes Dev. 3, 848-859, 1989

A:Title: Genes for extracellular matrix-degrading metalloproteinases and their inhibitor

A:Reference number: A32963; MUID:89306621; PMID:2744464

A:Accession: B32963

A:Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 415-467, 'T', 469 <BRE>

A:Experimental source: Clone EWS-2

C:Comment: Stromelysin 1 activates its proenzyme after cleavage(s) within the activation

C:Comment: This enzyme degrades various extracellular matrix proteins, including fibron

C:Comment: Stromelysin 1 hydrolyzes peptide bonds in plasminogen to yield a fragment wit

C:Comment: Prostromelysin is found in glycosylated and unglycosylated forms, both of whi

C:Function: endopeptidase preferentially hydrolyzing peptide bonds on the carboxyl si

C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprote

C:Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo

F:1-17/Domain: signal sequence #status predicted <SIG>

F:18-477/Product: prostromelysin 1 #status predicted <PRO>

F:18-99/Domain: activation peptide #status predicted <ACT>

F:60-264/Domain: matrix metalloproteinase homology <MMP>

F:90-97/Region: autoinhibitory

F:100-477/Product: stromelysin 1 #status predicted <MAT>

F:284-477/Domain: hemopexin repeat homology <PXN>

F:92,218,222,228/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status

F:218,222,228/Binding site: zinc, catalytic (His) (active) #status predicted

F:219/Active site: Glu #status predicted

F:290-477/Disulfide bonds: #status predicted

Query Match 51.6%; Score 133; DB 1; Length 477;

Best Local Similarity 58.1%; Pred. No. 7.4e-10;

Matches 25; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

QY 1 LQKLSLPETGELDSATLKAMRPRCGVPLGRFOTFEGLKWH 43

DB 67 MQKFLGLEMTGKLDSTNEMHPRCGVDPVGGFSTFPGSPKW 109

RESULT 8

S29243

Interstitial collagenase (EC 3.4.24.7) precursor - mouse

N:Alternate names: matrix metalloproteinase 1 (MMP1)

C:Species: Mus musculus (house mouse)

C>Date: 22-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004

C:Accession: S29243

R:Henriet, P.; Rousseau, G.G.; Beckhout, Y.

FEBS Lett. 310, 175-178, 1992

A:Title: Cloning and sequencing of mouse collagenase cDNA. Divergence of mouse and rat c

A:Reference number: S29243; MUID:93011910; PMID:1383028

A:Accession: S29243

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-472 <HEN>

A:Cross-references: UNIPROT:P33435; EMBL:X66473; NID:G53603; PIDN:CAA47102.1; PID:G53604

C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprote

C:Keywords: hydrolase; metalloproteinase; zinc; zymogen

F:65-268/Domain: matrix metalloproteinase homology <MMP>

F:279-472/Domain: hemopexin repeat homology <PXN>

F:97,223,227,233/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status

F:223,227,233/Binding site: zinc, catalytic (His) (active) #status predicted

F:224/Active site: Glu #status predicted

Query Match 45.9%; Score 121; DB 2; Length 472;

Best Local Similarity 48.9%; Pred. No. 3e-08;

Matches 23; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

QY 1 LQKLSLPETGELDSATLKAMRPRCGVPLGRFOTFEGLKWHHN 47

DB 72 MQSPFGLVETGKLDPTLDIMRPRCGVDPVGGVNFPTLKWSQTN 118

RESULT 11
A57490

R;Okada, Y.; Morodomi, T.; Enghild, J.J.; Suzuki, K.; Yasui, A.; Nakanishi, I.; Saivesen Eur. J. Biochem. 194, 721-730, 1990

A;Title: Matrix metalloproteinase 2 from human rheumatoid synovial fibroblasts. Purification and characterization of the active site. PMID:2269296

A;Accession: S13858

A;Molecule type: protein

A;Residues: 30-45;110-124 <OKA>

R;Crabbe, T.; Ioannou, C.; Docherty, A.J.P.

Eur. J. Biochem. 218, 431-438, 1993

A;Title: Human progelatinase A can be activated by autocatalysis at a rate that is concentrated in the active site. PMID:8269931

A;Reference number: S39436; MUID:94094834; PMID:8269931

A;Accession: S39436

A;Molecule type: protein

A;Residues: 30-44;44-456 <CR2>

R;Stetler-Stevenson, W.G.; Krutzsch, H.C.; Wacher, M.F.; Margulies, I.M.K.; Liotta, L.A. J. Biol. Chem. 264, 1353-1356, 1989

A;Title: The activation of human type IV collagenase proenzyme. Sequence identification and characterization of the active site. PMID:2536363

A;Reference number: A31480; MUID:93109136; PMID:2536363

A;Accession: A31480

A;Molecule type: protein

A;Residues: 110-123 <STE>

R;Crabbe, T.; Smith, B.; O'Connell, J.; Docherty, A.

FEBS Lett. 345, 14-16, 1994

A;Title: Human progelatinase A can be activated by matrixlysin.

A;Reference number: S44432; MUID:94252395; PMID:8194591

A;Accession: S44432

A;Molecule type: protein

A;Residues: 110-115 <CRA>

R;Brown, D.; Chwa, M.; Escobar, M.; Kenney, M.C.

Exp. Eye Res. 52, 5-16, 1991

A;Title: Characterization of the major matrix degrading metalloproteinase of human cornea. PMID:1868885

A;Reference number: A61498; MUID:91330998; PMID:1868885

A;Accession: A61498

A;Molecule type: protein

A;Residues: 'X', '31', '33', '46', 'X', '48-50', 'Q' <BRO>

A;Experimental source: corneal stroma

R;Itch, Y.; Binner, S.; Nagase, H.

Biochem. J. 308, 645-651, 1995

A;Title: Steps involved in activation of the complex of pro-matrix metalloproteinase 2 and tissue inhibitor of metalloproteinase 1. PMID:7772054

A;Reference number: S55327; MUID:95250003; PMID:7772054

A;Accession: S55327

A;Molecule type: protein

A;Residues: 110-114 <ITO>

C;Genetics:

A;Gene: GDB:MMP2; CLQ4; CLG4A

A;Cross-references: GDB:120592; OMIM:120360

A;Map position: 16q31-16q13

A;Introns: 51/3; 127/2; 178/1; 220/1; 278/1; 336/1; 394/1; 446/1; 491/2; 537/1; 590/2; 600/1

C;Function:

A;Description: proteolytic cleavage of gelatin type I and collagen types IV, V, VII, and XVIII

C;Superfamily: gelatinase A; fibronectin type II repeat homology; hemopexin repeat homology

C;Keywords: extracellular matrix; fibroblast; glycoprotein; hydrolase; metalloproteinase

F;1-29/Domain: signal sequence #status predicted <SIG>

F;30-660/Product: progelatinase A #status predicted <PRO>

F;70-219,394-446/Domain: matrix metalloproteinase homology #status atypical <MMP>

F;110-660/Product: gelatinase A #status predicted <MAT>

F;233-390/Region: collagen binding #status predicted

F;233-374/Domain: fibronectin type II repeat homology <2F1>

F;291-332/Domain: fibronectin type II repeat homology <2F8>

F;349-390/Domain: fibronectin type II repeat homology <2F9>

F;463-660/Domain: hemopexin repeat homology <PXN>

F;402,403,407,413/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status predicted

F;403,407,413/Binding site: zinc, catalytic (His) (active) #status predicted

F;469-660/Disulfide bonds: #status predicted

F;573,642/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 44.2%; Score 114; DB 1; Length 660;

Best Local Similarity 46.5%; Pred. No. 3.8e-07;

Matches 20; Conservative 7; Mismatches 16; Indels 0; Gaps 0;

1 LQKLSLPTGELDSATLKAMRPRCGVDPDLGRFQTFEGDLKW 43

Db 77 MQKFFGLQTGDLQDQNTIETKRCGPNPDVANYNFFPRKPKW 119

RESULT 13

A49499

metalloelastase HME (EC 3.4.24.-) - human

C;Species: Homo sapiens (man)

C;Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

A;Accession: A49499

R;Shapiro, S.D.; Kobayashi, D.K.; Ley, T.J. J. Biol. Chem. 268, 23824-23829, 1993

A;Title: Cloning and characterization of a unique elastolytic metalloproteinase produced by a human fibroblast cell line. PMID:8226919

A;Reference number: A49499; MUID:94043200; PMID:8226919

A;Accession: A49499

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-470 <SHA>

A;Cross-references: UNIPROT:P39900; GB:L23808; NID:9435969

A;Experimental source: alveolar macrophage

A;Note: sequence extracted from NCBI backbone (NCBI:N:139457, NCBI:P:139458)

C;Genetics:

A;Gene: GDB:MMP12; HME

A;Cross-references: GDB:266582; OMIM:601046

A;Map position: 11q22.2-11q22.3

C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloproteinase

C;Keywords: hydrolase; metalloproteinase; zinc; zymogen

F;60-263/Domain: matrix metalloproteinase homology <MMP>

F;276-470/Domain: hemopexin repeat homology <PXN>

F;92,218,222,228/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status predicted

F;218,222,228/Binding site: zinc, catalytic (His) (active) #status predicted

F;219/Active site: Glu #status predicted

Query Match 43.8%; Score 113; DB 2; Length 470;

Best Local Similarity 45.7%; Pred. No. 3.5e-07;

Matches 21; Conservative 7; Mismatches 18; Indels 0; Gaps 0;

QY 1 LQKLSLPTGELDSATLKAMRPRCGVDPDLGRFQTFEGDLKW 46

Db 67 MQHFLGLKVTGDLTSTLEMMHAPRCGVPDVFHFRFMPGPGVWRKH 112

RESULT 14

KCHUI

interstitial collagenase (EC 3.4.24.7) precursor [validated] - human

N;Alternate names: fibroblast collagenase; matrix metalloproteinase 1 (MMP1); tissue collagenase

C;Species: Homo sapiens (man)

C;Date: 13-Aug-1986 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004

A;Accession: A37308; S22766; I57620; A00996; D29157; A44518; S06132; B60964; S10595; S53

R;Templation, N.S.; Brown, P.D.; Levy, A.T.; Margulies, I.M.K.; Liotta, L.A.; Stetler-Stetler, O. Cancer Res. 50, 5431-5437, 1990

A;Title: Cloning and characterization of human tumor cell interstitial collagenase.

A;Reference number: A37308; MUID:90325587; PMID:2167156

A;Accession: A37308

A;Molecule type: mRNA

A;Residues: 1-469 <TEM>

A;Cross-references: UNIPROT:P03956; GB:X54925; NID:G30125; PIDN:CAA38691.1; PID:G30126

R;Brinckerhoff, C.E.; Ruby, P.L.; Austin, S.D.; Fini, M.E.; White, H.D. J. Clin. Invest. 79, 542-546, 1987

A;Title: Molecular cloning of human synovial cell collagenase and selection of a single clone. PMID:3027129

A;Reference number: S22766; MUID:87109799; PMID:3027129

A;Accession: S22766

A;Molecule type: DNA

A;Residues: 1-63 65-70 <BRI>

A;Cross-references: EMBL:M15996; NID:G180666; PIDN:AAA35700.1; PID:G180667

R;Angel, P.; Baumann, I.; Stein, B.; Delius, H.; Ramsdorf, H.J.; Herrlich, P. Mol. Cell. Biol. 7, 2256-2266, 1987

A;Title: 12-O-tetradecanoyl-phorbol-13-acetate induction of the human collagenase gene. PMID:3037355

A;Reference number: I57620; MUID:87257941; PMID:3037355

A;Accession: I57620

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-35 <RES>

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A;Cross-references: GDB:119783; OMIM:120353
A;Map position: 11q22.2-11q22.3
C;Function:
C;Description: hydrolyzes collagens, in particular types I, II, III, and X, serpins, an C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotease C;Keywords: calcium; extracellular matrix; fibroblasts; glycoprotein; hydrolase; metallo F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-469/Product: procollagenase #status experimental <PRO>
F;20-59/Domain: activation peptide #status experimental <ACT>
F;60-261/Domain: matrix metalloproteinase homology <MMP>
F;90-97/Region: autoinhibitory
F;100-469/Product: interstitial collagenase #status experimental <MAT>
F;172-418/Domain: hemopexin repeat homology <PXN>
F;172-418,222,228/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status F;210,143/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;218,222,228/Binding site: zinc, catalytic (His) (active) #status predicted
F;219/Active site: Glu #status predicted
F;269-270/Cleavage site: Pro-Ile (autolytic) #status experimental
F;269-466/Disulfide bonds: #status experimental

Query Match          42.6%; Score 110; DB 1; Length 469;
Best Local Similarity 46.5%; Pred. No. 8.9e-07;
Matches 20; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

QY      1 LQKQLSPETGELDSATLKAMRTPRCGYPDLGRFQTFFGDLEW 43
         :|::||::||::||::||::||::||::||::||::||:
Db       67 MQEFLGLKVGTGPDAETLKWKPQRCGVDPVAQFVLTEGNPRW 109

RESULT 15
PW0052
pro-matrix metalloproteinase-3 - human (fragment)
N;Alternate names: proMMP-3
C;Species: Homo sapiens (man)
C;Date: 03-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 07-May-1999
C;Accession: PW0052
R;Towle, C.A.; Wright, M.; Hecht, A.C.; Kuong, S.J.; Papanicolas, L.E.; Totkovic, R.; M Biochem. Biophys. Res. Commun. 247, 324-331, 1998
A;Title: A matrix metalloproteinase proenzyme activator produced by articular cartilage A;Reference number: PW0052; PMID:98308115; PMID:9642125
A;Accession: PW0052
A;Molecule type: protein
A;Residues: 1-82 <ROW>
C;Comment: This matrix enzyme is involved in connective tissue turnover under physiologi. C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotease

Query Match          41.9%; Score 108; DB 2; Length 82;
Best Local Similarity 65.6%; Pred. No. 2.3e-07;
Matches 21; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY      1 LQKQLSPETGELDSATLKAMRTPRCGYPDLG 32
         :|::||::||::||::||::||::||::||::||::||:
Db       50 MQKFLGLEVTGKLDSDTLEVMRKKPCRGVPDVG 81

Search completed: November 15, 2004, 14:07:18
Job time : 11.5449 secs
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Job time : 11.5449 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 15, 2004, 14:01:34 ; Search time 43.3846 Seconds
(without alignments)
623.323 Million cell updates/sec

Title: US-10-032-376A-8

Perfect score: 258

Sequence: 1 LQQLSLPETGELDSATLKAA.....VPLGRFQTFEGDLKWHHN 47

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1606865

Minimum DB seq length: 47
Maximum DB seq length: 660

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 02: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	226	87.6	324	Q9N282	Q9N282 bos taurus
2	216	83.7	149	Q9TVB4	Q9TVB4 canis famil
3	141	54.7	477	MM03_HUMAN	P08254 homo sapien
4	141	54.7	477	AAH69676	AAH69676 homo sapi
5	141	54.7	477	AAH69716	AAH69716 homo sapi
6	138	53.5	478	MM03_RABIT	P28863 coryctolagus
7	135	52.3	145	Q9N283	Q9N283 bos taurus
8	134	51.9	475	MM03_RAT	P03957 rattus norv
9	133	51.6	139	Q9GM68	Q9GM68 sus scrofa
10	133	51.6	476	MM10_HUMAN	P09238 homo sapien
11	133	51.6	476	MM10_MOUSE	O55123 mus musculu
12	133	51.6	476	MM10_RAT	P07152 rattus norv
13	133	51.6	476	AAP36110	AAP36110 homo sapi
14	133	51.6	477	MM03_MOUSE	P28862 mus musculu
15	133	51.6	479	Q922M6	Q922M6 mus musculu
16	131	50.8	478	Q6Y4Q5	Q6Y4Q5 canis famil
17	131	50.8	478	AAO3580	AAO3580 canis fam
18	128	49.6	167	Q7ZWD0	Q7ZWD0 brachydanio
19	128	49.6	465	MM08_MOUSE	O70138 mus musculu
20	128	49.6	465	O8C209	O8C209 mus musculu
21	128	49.6	465	O8C230	O8C230 mus musculu
22	128	49.6	465	AAH42742	AAH42742 mus muscu
23	128	49.6	465	BAC40805	BAC40805 mus muscu
24	128	49.6	466	MM08_RAT	O88766 rattus norv
25	128	49.6	475	Q71G59	Q71G59 brachydanio
26	128	49.6	475	AAQ07962	AAQ07962 brachydan
27	127	49.2	393	O8M118	O8M118 felis silve
28	126	48.8	657	Q7SZM5	Q7SZM5 brachydanio
29	126	48.8	657	Q6DG10	Q6DG10 brachydanio
30	124	48.1	223	Q7T0K9	Q7T0K9 ambystoma m
31	124	48.1	252	Q6PWQ3	Q6PWQ3 xenopus lae

32	124	48.1	252	2	AAT00547	AAT00547 xenopus lae
33	124	48.1	259	2	O7ZTI9	O7ZTI9 xenopus lae
34	124	48.1	657	2	O9PTU7	O9PTU7 oryzias lat
35	123	47.7	477	1	MM03_HORSE	O28397 equus cabal
36	122	47.3	259	2	Q6DF35	O6df35 xenopus tro
37	121	46.9	471	2	Q98859	Q98859 cynops pyrr
38	121	46.9	472	1	MM13_MOUSE	P33435 mus musculu
39	120	46.5	126	2	Q9TT84	Q9TT84 sus scrofa
40	120	46.5	632	2	O9NIP6	O9NIP6 canis famil
41	119	46.1	655	2	O9W635	O9W635 oncorhynch
42	118	45.7	466	1	MM13_RAT	P23037 rattus norv
43	117	45.3	121	2	Q6LBE5	Q6LBE5 homo sapien
44	117	45.3	121	2	CAA57296	CAA57296 homo sapi
45	117	45.3	383	2	Q7Z5M0	Q7Z5M0 homo sapien

ALIGNMENTS

RESULT 1

Q9N282 ID Q9N282 PRELIMINARY; PRT; 324 AA.
AC Q9N282; 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE MXP-9 (Fragment).
GN Name=bmp-9;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
[1]
SEQUENCE FROM N.A.
RA Sato T., Hirata M., Ito A., Hashizume K.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB043996; BAA96389.1; -
DR GO; GO:0005578; C:extracellular matrix; IEA.
DR GO; GO:004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000562; FN Type II.
DR InterPro; IPR006026; Peptidase M.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR Pfam; PF00040; fn2; 2.
DR Pfam; PF00413; Peptidase M10; 1.
DR Pfam; PF03933; Peptidase M10_N; 1.
DR PRINTS; PR00013; FNTYPEII.
DR PRINTS; PR00138; MATRXIN.
DR ProDom; PD000995; FN Type II; 2.
DR SMART; SM00059; FN2_2.
DR SMART; SM00235; ZmMc; 1.
DR PROSITE; PS00546; CYSTEINE SWITCH; 1.
DR PROSITE; PS00023; FIBRONECTIN_2; 1.
FT NON TER 324 324
SQ SEQUENCE 324 AA; 36273 MW; 4137C9820C28E080 CRC64;

Query Match 87.6%; Score 226; DB 2; Length 324;

Best Local Similarity 84.8%; Pred. No. 2.8e-22; Indels 0; Gaps 0;
Matches 39; Conservative 4; Mismatches 3;

OY 2 QKQLSLPETGELDSATLKAMTPRCGVFDLGRFQTFEGDLKWHHN 47
Db 75 QRRSLRPETGELDTTLNAMPKRCGVFDVGRFQTFEGDLKWHHN 120

RESULT 2

Q9TVB4 ID Q9TVB4 PRELIMINARY; PRT; 149 AA.
AC Q9TVB4; 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2004 (TREMBLrel. 26, Last annotation update)

DE Type IV collagenase MMP-9 (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fibrosarcoma;
RA Paria B.C., Kitchell B.E.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF1471104; AAD31323.1;
DR GO; GO:0005578; C:extracellular matrix; IEA.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR005070; PGSD like.
DR Pfam; PF00413; Peptidase M10; 1.
DR Pfam; PF03933; Peptidase M10_N; 1.
DR PRINTS; PR00138; MATRXIN.
DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
KW Collagen.
FT NON_TER 149
SQ SEQUENCE 149 AA; 17025 MW; CAGA5062EFDCCBBF CRC64;
Query Match 83.7%; Score 216; DB 2; Length 149;
Best Local Similarity 78.7%; Pred. No. 2.7e-21;
Matches 37; Conservative 7; Mismatches 3; Indels 0; Gaps 0;
QY 1 LQKLSLPETGELDSATLKAMTPRCGVDPDLGRFQTFEGDLKWHHN 47
DB 74 LQRLALPETGELDKTLEAMRAPRCGVDPDLGKFTFEGDLKWHND 120
RESULT 3
MM03_HUMAN
ID MM03_HUMAN STANDARD; PRT; 477 AA.
AC P08254;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Stromelysin-1 precursor (EC 3.4.24.17) (Matrix metalloproteinase-3)
DE (MMP-3) (Transin-1) (SL-1).
GN Names=MMP3; Synonyms=STMY1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 18-24.
RX MEDLINE=88198243; PubMed=3360803;
RA Saus J., Quinones S., Orani Y., Nagase H., Harris E.D. Jr.,
RA Kurkinen M.;
RT "The complete primary structure of human matrix metalloproteinase-3.
RT Identity with stromelysin.";
RL J. Biol. Chem. 263:6742-6745(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Fibroblast;
RX MEDLINE=87156645; PubMed=3030290;
RA Whitham S.E., Murphy G., Angel P., Rahmsdorf H.J., Smith B., Lyons A.,
RA Harris T.J.R., Reynolds J.J., Herrlich P., Docherty A.J.P.;
RT "Comparison of human stromelysin and collagenase by cloning and
RT sequence analysis.";
RL Biochem. J. 240:913-916(1986).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=88016164; PubMed=3477804;
RA Wilhelm S.M., Collier I.E., Kronberger A., Eisen A.Z., Marmer B.L.,
RA Grant G.A., Bauer E.A., Goldberg G.I.;
RT "Human skin fibroblast stromelysin: structure, glycosylation, and
RT substrate specificity, and differential expression in normal and
RT tumorigenic cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:6725-6729(1987).
RN [12]
RN [4]
RP SEQUENCE FROM N.A.
RA Lin D., Duncan M., Allen E., Araujo R., Aparicio A., Chai A.,
RA Chung E., Davis K., Federspiel N., Hymen R., Kalman S., Komp C.,
RA Kurdi O., Lahekari D., Lew H., Namath A., Oefner P., Roberts D.,
RA Heller R., Davis R.W.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A., AND VARIANT GLU-45.
RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
RA Nickerson D.A.;
RT "SeattLeSNPs: NHLBI HL66682 program for genomic applications, UW-
RT FHCRC Seattle, WA (URL: <http://pga.gs.washington.edu>).";
RN Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [6]
RP ZYMOGEN ACTIVATION.
RX MEDLINE=90344802; PubMed=2383557;
RA Nagase H., Engild J.J., Suzuki K., Salvesen G.;
RT "Stepwise activation mechanisms of the precursor of matrix
RT metalloproteinase 3 (stromelysin) by proteinases and (4-
RT aminophenyl)mercuric acetate.";
RL Biochemistry 29:5783-5789(1990).
RN [7]
RP STRUCTURE BY NMR OF CATALYTIC DOMAIN.
RX MEDLINE=95384761; PubMed=7656014;
RA Gooley P.R., O'Connell J.F., Marcy A.I., Cuca G.C., Salowe S.P.,
RA Bush B.L., Hermes J.D., Esser C.K., Hagmann W.K., Springer J.P.,
RA Johnson B.A.;
RT "The NMR structure of the inhibited catalytic domain of human
RT stromelysin-1.";
RL Nat. Struct. Biol. 1:111-118(1994).
RN [8]
RP STRUCTURE BY NMR OF 100-267.
RX MEDLINE=99043696; PubMed=9827994;
RA Stockman B.J., Waldon D.J., Gates J.A., Scallill T.A.,
RA Kloosterman D.A., Mizeak S.A., Jacobsen E.J., Belonga K.L.,
RA Mitchell M.A., Mao B., Petke J.D., Goodman L., Powers E.A.,
RA Ledbetter S.R., Kaytes P.S., Vogeli G., Marshall V.P., Petzold G.L.,
RA Poorman R.A.;
RT "Solution structures of stromelysin complexed to thiadiazole
RT inhibitors.";
RL Protein Sci. 7:2281-2286(1998).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 18-272.
RX MEDLINE=96117647; PubMed=8535233;
RA Becker J.W., Marcy A.I., Rokosz L.L., Axel M.G., Burbaum J.J.,
RA Fitzgerald P.M.D., Cameron P.M., Esser C.K., Hagmann W.K.,
RA Hermes J.D., Springer J.P.;
RT "Stromelysin-1: three-dimensional structure of the inhibited catalytic
RT domain and of the C-truncated proenzyme.";
RL Protein Sci. 4:1966-1976(1995).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 100-266.
RX MEDLINE=96311273; PubMed=8740360;
RA Dhanraj V., Ye Q.-Z., Johnson L.L., Hupe D.J., Otwine D.F.,
RA Dunbar J.B. Jr., Rubin J.R., Pavlovsky A., Humblet C., Blundell T.L.;
RT "X-ray structure of a hydroxamate inhibitor complex of stromelysin
RT catalytic domain and its comparison with members of the zinc
RT metalloproteinase superfamily.";
RL Structure 4:375-386(1996).
RN [11]
RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 105-264.
RX MEDLINE=97236985; PubMed=9083493;
RA Esser C.K., Bugianesi R.D., Caldwell C.G., Chapman K.T., Durette P.L.,
RA Girotta N.N., Kopka I.E., Lanza T.J., Levorse D.A., Maccoss M.,
RA Owens K.A., Pompidom M.M., Simeone J.P., Harrison R.K.,
RA Niedzwiecki L., Becker J.W., Marcy A.I., Axel M.G., Christen A.J.,
RA McDonnell J., Moore V.L., Olszewski J.M., Saphos C., Visco D.M.,
RA Shen F., Colletti A., Krieter P.A., Hagmann W.K.;
RT "Inhibition of stromelysin-1 (MMP-3) by Fl'-biphenyl'ethyl
RT carboxylalkyl dipeptides.";
RL J. Med. Chem. 40:1026-1040(1997).
RN [12]

RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 100-267 IN COMPLEX WITH
TMPL.
RX MEDLINE=97433330; PubMed=9288970;
RA Gomis-Rueh F.-X., Maskos K., Betz M., Bergner A., Huber R.,
SUZUKI K., Yoshida N., Nagase H., Brew K., Bourenkov G.P.,
RA Bartunik H., Bode W.,
RT "Mechanism of inhibition of the human matrix metalloproteinase
stromelysin-1 by TIMP-1,"
RT Nature 389:77-81(1997).
RN [13]
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 100-264.
RX MEDLINE=99006562; PubMed=9792098;
RA Finzel B.C., Baldwin E.T., Bryant G.L. Jr., Hess G.F., Wilks J.W.,
RTepod C.M., Mott J.E., Marshall V.P., Petzold G.L., Poorman R.A.,
RA O'Sullivan T.J., Schostarez H.J., Mitchell M.A.,
RT "Structural characterizations of nonpeptidic thiazole inhibitors of
matrix metalloproteinases reveal the basis for stromelysin
selectivity,"
RT Protein Sci. 7:2118-2126(1998).
RN [14]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 100-272.
RX MEDLINE=20013087; PubMed=10543949;
RA Chen L., Rydel T.J., Gu F., Dunaway C.M., Pikul S., Dunham K.M.,
RA Barrett B.L.,
RT "Crystal structure of the stromelysin catalytic domain at 2.0-A
resolution: inhibitor-induced conformational changes,"
RT J. Mol. Biol. 293:545-557(1999).
RN [15]
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 100-267.
RX MEDLINE=99349695; PubMed=10422833;
RA Pavlovsky A.G., Williams M.G., Ye Q.-Z., Ortwein D.F.,
RA Purchase C.F. II, White A.D., Dhanraj V., Roth B.D., Johnson L.L.,
RA Hupe D., Humblet C., Blundell T.L.,
RT "X-ray structure of human stromelysin catalytic domain complexed with
nonpeptide inhibitors: implications for inhibitor selectivity,"
RT Protein Sci. 8:1455-1462(1999).
RN [16]
RP STRUCTURE BY NMR OF 100-272.
RX MEDLINE=98434377; PubMed=9760240;
RA Li Y.C., Zhang X., Melton R., Ganu V., Gonnella N.C.,
RT "Solution structure of the catalytic domain of human stromelysin-1
complexed to a potent, nonpeptidic inhibitor,"
RT Biochemistry 37:14048-14056(1998).
CC -!- FUNCTION: Can degrade fibronectin, laminin, gelatins of type I,
CC III, IV, and V; collagens III, IV, X, and IX, and cartilage
CC proteoglycans. Activates procollagenase.
CC -!- CATALYTIC ACTIVITY: Preferential cleavage where P1', P2' and P3'
CC are hydrophobic residues.
CC -!- COPACTOR: binds 2 zinc ions and 4 calcium ions per subunit.
CC -!- SIMILARITY: Belongs to peptidase family M10A.
CC -!- SIMILARITY: Contains 1 hemopexin-like domain.
CC -----
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CC or send an email to licenses@isb-sib.ch).
CC -----
DR ENBL; X05232; CAA28859.1; -
DR ENBL; J03209; AAA36321.1; -
DR ENBL; U78045; AAB36942.1; -
DR ENBL; AF405705; AAK95247.1; -
DR PIR; A28156; KCHU51.
DR PDB; 1B3D; X-ray; A/B=100-272.
DR PDB; 1B8Y; X-ray; A=100-266.
DR PDB; 1BIW; X-ray; A/B=100-272.
DR PDB; 1BM6; NMR; @=100-272.
DR PDB; 1BQ0; X-ray; A/B=100-272.
DR PDB; 1C31; X-ray; A/B=100-272.
DR PDB; 1C8T; X-ray; A/B=103-269.
DR PDB; 1CAQ; X-ray; A=100-267.

DR PDB; 1CIZ; X-ray; A=100-267.
DR PDB; 1CQR; X-ray; A/B=100-272.
DR PDB; 1D5J; X-ray; A/B=100-272.
DR PDB; 1D7X; X-ray; A/B=100-272.
DR PDB; 1D8F; X-ray; A/B=100-272.
DR PDB; 1D8M; X-ray; A/B=100-272.
DR PDB; 1G05; X-ray; A/B=100-272.
DR PDB; 1G49; X-ray; A/B=100-272.
DR PDB; 1G4K; X-ray; A/B/C=100-267.
DR PDB; 1HFS; X-ray; @=105-264.
DR PDB; 1HY7; X-ray; A/B=100-272.
DR PDB; 1M1W; Model; A=100-268.
DR PDB; 1O09; NMR; A=100-267.
DR PDB; 1Q1A; X-ray; A/B/C/D=106-267.
DR PDB; 1Q1C; X-ray; A/B/C/D=106-266.
DR PDB; 1SLM; X-ray; @=18-272.

Query Match 54.7%; Score 141; DB 1; Length 477;
Best Local Similarity 62.8%; Pred. No. 1.9e-10;
Matches 27; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 LOKLSLPETGELDSATLKAMRTPCGVDPDLGRFQTFEGDLKW 43
DB 67 MQKFLGLEVTGKLDSTLEVNKRPCGVDPVGHFRTPFGIPKW 109

RESULT 4
AAH69676 PRELIMINARY; PRT; 477 AA.
AC AAH69676;
DT 20-MAY-2004 (TrEMBLrel. 27, Created)
DT 20-MAY-2004 (TrEMBLrel. 27, Last sequence update)
DT 20-MAY-2004 (TrEMBLrel. 27, Last annotation update)
DE Matrix metalloproteinase 3, preproprotein.
CN MRP3.
OS Homo sapiens (Human).
OC Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PCR rescued clones;
RX MEDLINE=223825; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko K., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences,"
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=PCR rescued clones;
RA Strausberg R.;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR ENBL; BC069676; AAH69676.1; -
SQ SEQUENCE 477 AA; 53978 MW; 7497490A861DEEA9 CRC64;

Query Match 54.7%; Score 141; DB 2; Length 477;
Best Local Similarity 62.8%; Pred. No. 1.9e-10;

Matches 27; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 LQKQLSLPTGELDSATLKAMTPRCGVPDLGRFQTFEGDLKW 43
 Db 67 MQKFLGLEVTGKLDSTLEVMKPRCGVPDVGHFRTFPGIPKW 109

RESULT 5

AAH69716 PRELIMINARY; PRT; 477 AA.
 AC AAH69716;
 DT 20-MAY-2004 (TEMBLrel. 27, Created)
 DT 20-MAY-2004 (TEMBLrel. 27, Last sequence update)
 DT 20-MAY-2004 (TEMBLrel. 27, Last annotation update)
 DE Matrix metalloproteinase 3, preproprotein.
 GN MMP3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PCR rescued clones;
 RX MEDLINE=2238257; PubMedID=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PCR rescued clones;
 RA Strausberg R.;
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC069716; AAH69716.1; -
 SQ SEQUENCE 477 AA; 53978 MW; 7497490A861DEA9 CRC64;

Query Match 54.7%; Score 141; DB 2; Length 477;
 Best Local Similarity 62.8%; Pred. No. 1.9e-10;
 Matches 27; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 LQKQLSLPTGELDSATLKAMTPRCGVPDLGRFQTFEGDLKW 43
 Db 67 MQKFLGLEVTGKLDSTLEVMKPRCGVPDVGHFRTFPGIPKW 109

RESULT 6

MM03 RABIT STANDARD; PRT; 478 AA.
 AC P2863;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Stromelysin-1 precursor (EC 3.4.24.17) (Matrix metalloproteinase-3)
 DE (MMP-3) (Transin-1) (SL-1).
 GN Name=MMP3;
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88077214; PubMed=2825726;
 RA Fini M.E., Karmilowicz M.J., Ruby P.L., Beeman A.M., Borges K.A.,
 RA Brinckerhoff C.E.;
 RT "Cloning of a complementary DNA for rabbit proactivator. A
 RT metalloproteinase that activates synovial cell collagenase, shares
 RT homology with stromelysin and transin, and is coordinately regulated
 RT with collagenase";
 RL Arthritis Rheum. 30:1254-1264(1987).
 RN [2]
 RP SEQUENCE OF 1-167 FROM N.A.
 RX MEDLINE=87156645; PubMed=3030290;
 RA Whitham S.E., Murphy G., Angel P., Rahmsdorf H.J., Smith B., Lyons A.,
 RA Harris T.J.R., Reynolds J.J., Herrlich P., Docherty A.P.;
 RT "Comparison of human stromelysin and collagenase by cloning and
 RT sequence analysis";
 RL Biochem. J. 240:913-916(1986).
 CC -!- FUNCTION: Can degrade fibronectin, laminin, gelatins of type I,
 CC III, IV, and V; collagens III, IV, X, and IX, and cartilage
 CC proteoglycans. Activates procollagenase.
 CC -!- CATALYTIC ACTIVITY: Preferential cleavage where P1', P2' and P3'
 CC are hydrophobic residues.
 CC -!- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit (By
 CC similarity).
 CC -!- SIMILARITY: Belongs to peptidase family M10A.
 CC -!- SIMILARITY: Contains 1 hemopexin-like domain.
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 CC -----
 CC EMBL; M25664; AAA31467.1; -
 DR PIR; A37306; KCRBS1.
 DR HSPP; P08254; LG05.
 DR MEROPS; M10.005; -
 DR InterPro; IPR000585; Hemopexin.
 DR InterPro; IPR006026; Peptidase_M.
 DR InterPro; IPR001818; Pept_M10A_M12B.
 DR InterPro; IPR006025; Pept_M_Zn_BS.
 DR InterPro; IPR009070; PGBD_like.
 DR Pfam; PF00045; Hemopexin; 4.
 DR Pfam; PF00413; Peptidase_M10; 1.
 DR Pfam; PF03933; Peptidase_M10_N; 1.
 DR PRINTS; PR00138; MATRININ.
 DR SMART; SM00120; HX; 4.
 DR SMART; SM00235; ZnMc; 1.
 DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
 DR PROSITE; PS00024; HEMOPEXIN; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 KW Calcium-binding; Collagen degradation; Extracellular matrix;
 KW Glycoprotein; Hydrolase; Metal-binding; Metalloprotease; Signal; Zinc;
 KW Zymogen.
 FT SIGNAL 1 17 Probable.
 FT PROPEP 18 100 Activation peptide.
 FT CHAIN 101 478 Stromelysin-1.
 FT DOMAIN 288 478 Hemopexin-like.
 FT SITE 93 93 Cysteine switch (Potential).
 FT METAL 125 125 Calcium 1 (By similarity).
 FT METAL 159 159 Calcium 2 (By similarity).
 FT METAL 169 169 Zinc 1 (By similarity).
 FT METAL 171 171 Zinc 1 (By similarity).
 FT METAL 176 176 Calcium 3 (By similarity).
 FT METAL 177 177 Calcium 3 (via carbonyl oxygen) (By
 FT similarity).
 FT METAL 179 179 Calcium 3 (via carbonyl oxygen) (By
 FT similarity).

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CC EMBL; Y13185; CAA73641.1; -.

CC EMBL; AK020292; BAB32058.1; -.

CC PIR; JC6505; JG6505.

CC HSP; P08254; IG05.

CC MEROPS; M10.006; -.

CC MGI; 97007; Mmp10.

CC InterPro; IPR000585; Hemopexin.

CC InterPro; IPR006026; Peptidase M.

CC InterPro; IPR001843; Pept_M10A_M10C.

CC InterPro; IPR001818; Pept_M10A_M12B.

CC InterPro; IPR006025; Pept_M_Zn_BS.

CC InterPro; IPR009070; PCBD_like.

CC Pfam; PF02051; Fragilysin; 1.

CC Pfam; PF00045; Hemopexin; 4.

CC Pfam; PF00413; Peptidase M10; 1.

CC Pfam; PF03933; Peptidase M10_N; 1.

CC PRINTS; PR00138; MATRIXIN.

CC SMART; SM00120; HX; 4.

CC SMART; SM00235; ZnMc; 1.

CC PROSITE; PS00546; CYSTEINE SWITCH; 1.

CC PROSITE; PS00024; HEMOPEXIN; 1.

CC PROSITE; PS00142; ZINC_PROTEASE; 1.

CC Calcium; Collagen degradation; Extracellular matrix; Hydrolase;

CC Metalloprotease; Signal; Zinc; Zymogen.

FT SIGNAL 1 17 Probable

FT PROPEP 18 99 Activation peptide (By similarity).

FT CHAIN 100 476 Stromelysin-2.

FT DOMAIN 286 476 Hemopexin-like.

FT SITE 92 92 Cysteine switch (By similarity).

FT METAL 218 218 Zinc (catalytic) (By similarity).

FT ACT_SITE 219 219 By similarity.

FT METAL 222 222 Zinc (catalytic) (By similarity).

FT METAL 228 228 Zinc (catalytic) (By similarity).

FT DISULFID 289 476 By similarity.

CC SEQUENCE 476 AA; 53911 MW; 2EB1CC41468FOAC6 CRC64;

Query Match 51.6%; Score 133; DB 1; Length 476;

Best Local Similarity 58.1%; Pred. No. 2.4e-09;

Matches 25; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

QY 1 LQKQLSLPTGELDSATLKAMETPRCGVDPDLGRFOTFEGDLKW 43

DB 67 MQKFLGLEMTGKLDSTNWMHMKPRCGVDPVGVGFSTFGSPKRW 109

RESULT 12

MM10_RAT

ID MM10_RAT STANDARD; PRT; 476 AA.

AC P07152;

DT 01-APR-1988 (Rel. 07, Created)

DT 01-APR-1988 (Rel. 07, Last sequence update)

DE 05-JUL-2004 (Rel. 44, Last annotation update)

DE Stromelysin-2 precursor (EC 3.4.24.22) (Matrix metalloproteinase-10)

DE (MMP-10) (Traisin-2) (SL-2) (transformation-associated protein 34A).

GN Name=Mmp10;

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]_

RP SEQUENCE FROM N.A.

RX MEDLINE=87146421; PubMed=3547333;

RA Breathnach R., Matrisian L.M., Gesnel M.-C., Staub A., Leroy P.;

RT "Sequences coding for part of oncogene-induced transin are highly conserved in a related rat gene."

RL Nucleic Acids Res. 15:1139-1151 (1987).

RN [2]_

RP SEQUENCE FROM N.A.

RX MEDLINE=92112748; PubMed=1370458;

Chan J.C., Scanlon M., Zhang H.Z., Jia L.B., Yu D., Hung M.C., French M., Eastman E.M.;

RA "Molecular cloning and characterization of v-mos-activated transformation-associated proteins.";

RT J. Biol. Chem. 267:1099-1103 (1992).

RL -!- FUNCTION: Can degrade fibronectin. Gelatins of type I, III, IV, and V, weakly collagens III, IV, and V. Activates procollagenase.

CC -!- CATALYTIC ACTIVITY: Similar to stromelysin 1, but action on collagen types III, IV and V is weak.

CC -!- COFACTOR: Binds 2 zinc ions per subunit, calcium (By similarity).

CC -!- SIMILARITY: Belongs to peptidase family M10A.

CC -!- SIMILARITY: Contains 1 hemopexin-like domain.

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CC EMBL; X05083; CAA28739.1; -.

CC EMBL; M65253; AAA42202.1; -.

CC PIR; B26403; KCRTS2.

CC HSP; P08254; IHY7.

CC MEROPS; M10.006; -.

CC RGD; 620192; Mmp10.

CC InterPro; IPR000585; Hemopexin.

CC InterPro; IPR006026; Peptidase M.

CC InterPro; IPR001818; Pept_M10A_M12B.

CC InterPro; IPR006025; Pept_M_Zn_BS.

CC InterPro; IPR009070; PCBD_like.

CC Pfam; PF00045; Hemopexin; 4.

CC Pfam; PF00413; Peptidase M10; 1.

CC Pfam; PF03933; Peptidase M10_N; 1.

CC PRINTS; PR00138; MATRIXIN.

CC SMART; SM00120; HX; 4.

CC SMART; SM00235; ZnMc; 1.

CC PROSITE; PS00546; CYSTEINE SWITCH; 1.

CC PROSITE; PS00024; HEMOPEXIN; 1.

CC PROSITE; PS00142; ZINC_PROTEASE; 1.

CC Calcium; Collagen degradation; Extracellular matrix; Hydrolase;

CC Metalloprotease; Signal; Zinc; Zymogen.

FT SIGNAL 1 17 Probable

FT PROPEP 18 99 Activation peptide (By similarity).

FT CHAIN 100 476 Stromelysin-2.

FT DOMAIN 286 476 Hemopexin-like.

FT SITE 92 92 Cysteine switch (By similarity).

FT METAL 218 218 Zinc (catalytic) (By similarity).

FT ACT_SITE 219 219 By similarity.

FT METAL 222 222 Zinc (catalytic) (By similarity).

FT METAL 228 228 Zinc (catalytic) (By similarity).

FT DISULFID 289 476 By similarity.

CC SEQUENCE 476 AA; 54221 MW; B556B6FB1D8BA7EE CRC64;

Query Match 51.6%; Score 133; DB 1; Length 476;

Best Local Similarity 53.2%; Pred. No. 2.4e-09;

Matches 25; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

QY 1 LQKQLSLPTGELDSATLKAMETPRCGVDPDLGRFOTFEGDLKWHHN 47

DB 67 MQKFLGLEMTGKLDSTNWMHMKPRCGVDPVGVGFSTFGSPKRW 113

RESULT 13

AAP36110

ID AAP36110 PRELIMINARY; PRT; 476 AA.

AC AAP36110;

DT 02-MAR-2004 (TrEMBLrel. 27, Created)

DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)

DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)

DE Matrix metalloproteinase 10 (Stromelysin 2).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_SEQUENCE FROM N.A.
RP Kalline N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
RA Phelan M., Farmer A.;
RT "Cloning of human full-length cDNAs in BD Creator(TM) System Donor
RT vector";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BF007442; AAP36110.1; -- 516CDDFFP92A0D6 CRC64;
SQ SEQUENCE 476 AA; 54151 MW; 516CDDFFP92A0D6 CRC64;

Query Match 51.6%; Score 133; DB 2; Length 476;
Best Local Similarity 58.1%; Pred. No. 2.4e-09;
Matches 25; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

OY 1 LQKQSLPTGELDSATLKAMTPRCGVDPDLGRFOTFSGDLKW 43
DB 66 MQKFLGLEVTGKLDITDLEVMRKPRCGVDPVGHFSFGMPKWK 108

RESULT 14
MM03 MOUSE
ID MM03 MOUSE STANDARD; PRT; 477 AA.
AC P28862;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Stromelysin-1 precursor (EC 3.4.24.17) (Matrix metalloproteinase-3)
DE (MMP-3) (Transin-1) (SL-1) (EMS-2).
GN Name=Mmp3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_SEQUENCE FROM N.A.
RP STRAIN=NMRI; TISSUE=Calvaria;
RC MEDLINE=93013057; PubMed=1398148;
RA Hammani K., Henriot P., Beckhout Y.;
RT "Cloning and sequencing of a cDNA encoding mouse Stromelysin 1.";
RL Gene 120:321-322(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss;
RA Li F., Strange R., Saurer S., Niemann H., Friis R.R.;
RL Submitted (AUG-1991) to the EMBL/GenBank/DBSJ databases.
RN [3]
RP SEQUENCE OF 415-469 FROM N.A., AND DEVELOPMENTAL STAGE.
RX PubMed=2744464;
RA Brenner C.A., Adler R.R., Rappolee D.A., Pedersen R.A., Werb Z.;
RT "Genes for extracellular-matrix-degrading metalloproteinases and their
inhibitor, TIMP, are expressed during early mammalian development.";
RL Genes Dev. 3:848-859(1989).
CC CC -1- FUNCTION: Can degrade fibronectin, laminin, gelatins of type I,
III, IV, and V; collagens III, IV, X, and IX, and cartilage
proteoglycans. Activates procollagenase.
CC CC -1- CATALYTIC ACTIVITY: Preferential cleavage where P1', P2' and P3'
are hydrophobic residues.
CC CC -1- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit (By
similarity).
CC CC -1- DEVELOPMENTAL STAGE: Present in unfertilized eggs and at the
zygote and cleavage stages. Levels increase at the blastocyst
stages and with endoderm differentiation.
CC CC -1- SIMILARITY: Belongs to peptidase family M10A.
CC CC -1- SIMILARITY: Contains 1 hemopexin-like domain.

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between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way

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CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X66402; CAA47029.1; --
DR EMBL; X63162; CAA44860.1; ALT_INIT.
DR PIR; JC1476; KCMSS1.
DR HSSP; P08254; IG05.
DR MEROPS; M10.005; --
DR MGD; MGI:97010; Mmp3.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR006026; Peptidase_M.
DR InterPro; IPR001843; Pept_M10A_M10C.
DR InterPro; IPR001813; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR009070; PCBD_like.
DR Pfam; PF02051; Fragilysin; 1.
DR Pfam; PF00453; Hemopexin; 4.
DR Pfam; PF00413; Peptidase_M10; 1.
DR Pfam; PF03933; Peptidase_M10_N; 1.
DR PRINTS; PRO0138; MATRIXIN.
DR SMART; SMO0120; HX; 4.
DR SMART; SMO0235; ZnMc; 1.
DR PROSITE; PS00546; CYSTEINE SWITCH; 1.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC PROTEASE; 1.
DR Calcium-binding; Collagen degradation; Extracellular matrix;
KW Glycoprotein; Hydrolase; Metal-binding; Metalloprotease; Signal; Zinc;
KW Zymogen.
FT SIGNAL 1 17 Probable.
FT PROPEP 18 99 Activation peptide.
FT CHAIN 100 477 Stromelysin-1.
FT DOMAIN 287 477 Hemopexin-like.
FT SITE 92 92 Cysteine switch (Potential).
FT METAL 124 124 Calcium 1 (By similarity).
FT METAL 158 158 Calcium 2 (By similarity).
FT METAL 168 168 Zinc 1 (By similarity).
FT METAL 170 170 Zinc 1 (By similarity).
FT METAL 175 175 Calcium 3 (By similarity).
FT METAL 176 176 Calcium 3 (via carbonyl oxygen) (By
similarity).
FT METAL 178 178 Calcium 3 (via carbonyl oxygen) (By
similarity).
FT METAL 180 180 Calcium 3 (via carbonyl oxygen) (By
similarity).
FT METAL 183 183 Zinc 1 (By similarity).
FT METAL 190 190 Calcium 2 (via carbonyl oxygen) (By
similarity).
FT METAL 192 192 Calcium 2 (via carbonyl oxygen) (By
similarity).
FT METAL 194 194 Calcium 2 (By similarity).
FT METAL 196 196 Zinc 1 (By similarity).
FT METAL 198 198 Calcium 3 (By similarity).
FT METAL 199 199 Calcium 1 (By similarity).
FT METAL 201 201 Calcium 1 and 3 (By similarity).
FT METAL 218 218 Zinc 2 (Catalytic) (By similarity).
FT ACT_SITE 219 219 By similarity.
FT METAL 222 222 Zinc 2 (Catalytic) (By similarity).
FT METAL 228 228 Zinc 2 (Catalytic) (By similarity).
FT METAL 297 297 Calcium 4 (via carbonyl oxygen) (By
similarity).
FT METAL 389 389 Calcium 4 (via carbonyl oxygen) (By
similarity).
FT METAL 438 438 Calcium 4 (via carbonyl oxygen) (By
similarity).
FT CARBOHYD 120 120 N-linked (GlcNAc...) (Potential).
FT DISULFID 290 477 By similarity.
FT CONFLICT 468 468 I -> T (in Ref. 3).
SQ SEQUENCE 477 AA; 53845 MW; 9C15594F45262D37 CRC64;

Query Match 51.6%; Score 133; DB 1; Length 477;
Best Local Similarity 58.1%; Pred. No. 2.4e-09;
Matches 25; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

```

Oy 1 LQKQLSPETGELDSATLKAMRTPRCGVPDLGRFQTFEGDLKW 43
Db 67 MQKFLGLEMTGKLDSTNMTLMHKPRCGVPDVGGFSTFFGSPKW 109

RESULT 15
Q922W6 PRELIMINARY; PRT; 479 AA.
AC Q922W6;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-OCT-2004 (T-EMBLrel. 28, Last annotation update)
DE Matrix metalloproteinase 3.
GN Name=Mmp3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N;
RC TISSUE=Mammary tumor. Metallothionien-TGF alpha model. 10 month old
RC virgin mouse. Taken by biopsy.;
RX MEDLINE=22368257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalios D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N;
RC TISSUE=Mammary tumor. Metallothionien-TGF alpha model. 10 month old
RC virgin mouse. Taken by biopsy.;
RA Strausberg R.;
RN Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RA Brathwaite M., Waeltz P., Nagaraja R.;
RN Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006725; AAH06725.1; -
DR EMBL; AY211543; AAO37583.1; -
DR HSSP; P08254; IG05.
DR MGD; MGI:97010; Mmp3.
DR GO; GO:0005578; C:extracellular matrix; IEA.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR006026; Peptidase M.
DR InterPro; IPR001843; Pept_M10A_M10C.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR009070; PGSD_like.
DR Pfam; PF02051; Fragilysin; 1.
DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF00413; Peptidase_M10; 1.

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Pfam; PF03933; Peptidase_M10_N; 1.
DR PRINTS; PR00138; MATRIKIN.
DR SMART; SMO0120; HX; 4.
DR SMART; SMO0235; ZmMc; 1.
DR PROSITE; PS00546; CYSTEINE SWITCH; 1.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC PROTEASE; UNKNOWN 1.
SQ SEQUENCE 479 AA; 54104 MW; 1FA89D6CF8FE5841 CRC64;

Query Match 51.68; Score 133; DB 2; Length 479;
Best Local Similarity 58.1%; Pred. No. 2.4e-09;
Matches 25; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

Oy 1 LQKQLSPETGELDSATLKAMRTPRCGVPDLGRFQTFEGDLKW 43
Db 69 MQKFLGLEMTGKLDSTNMTLMHKPRCGVPDVGGFSTFFGSPKW 111

Search completed: November 15, 2004, 14:06:37
Job time : 45.3846 secs

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OM protein - protein search, using sw model

Run on: November 15, 2004, 14:01:34 ; Search time 49.5 Seconds
(without alignments)
.391.341 Million cell updates/sec

Title: US-10-032-376A-9

Perfect score: 292

Sequence: 1 MQEFGGLKVTGKPDATLKV.....VLTEGNPRWEQTHLYRIEN 54

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 1022821

Minimum DB seq length: 47

Maximum DB seq length: 660

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	292	100.0	54	6	ABP97131 Human mat
2	292	100.0	54	6	ABG76317 Human mat
3	292	100.0	54	8	ADQ17032 Human mat
4	292	100.0	454	7	ADE16002 G-coupled
5	292	100.0	454	7	ADE16004 G-coupled
6	292	100.0	454	7	ADE16008 G-coupled
7	292	100.0	454	7	ADE16006 G-coupled
8	292	100.0	454	8	ADL93945 Human G-c
9	292	100.0	454	8	ADL93943 Human G-c
10	292	100.0	455	8	ADL93941 Human G-c
11	292	100.0	469	4	AAB84606 Amino aci
12	292	100.0	469	4	AAE10415 Human mat
13	292	100.0	469	6	ABU03466 Angiogene
14	292	100.0	469	6	ABR58543 Human can
15	292	100.0	469	6	ABR58542 Human can
16	292	100.0	469	6	ABR48148 Human bla
17	292	100.0	469	6	ABU56536 Lung canc
18	292	100.0	469	6	ABU56537 Lung canc
19	292	100.0	469	6	ABU07454 Protein d
20	292	100.0	469	6	ABP54454 Matrix me
21	292	100.0	469	7	ADB79176 Matrix me
22	292	100.0	469	7	ADB34550 Human ski
23	292	100.0	469	7	ADE16000 G-coupled
24	292	100.0	469	7	ADE16010 G-coupled
25	292	100.0	469	7	ADN39849 Cancer/an

26	292	100.0	469	7	ADN38694	Adn38694	Cancer/an
27	292	100.0	469	7	ADN38696	Adn38696	Cancer/an
28	292	100.0	469	7	ADN39850	Adn39850	Cancer/an
29	292	100.0	469	7	ADN95538	Adn95538	Human BEC
30	292	100.0	469	8	ADL93949	Adl93949	Human G-c
31	292	100.0	469	8	ADL93939	Adl93939	Human G-c
32	292	100.0	470	8	ADN07695	Adn07695	Human mat
33	292	100.0	490	7	ADE07892	Ado7892	Novel pro
34	292	100.0	496	4	AAG75509	Agg75509	Human col
35	286	97.9	457	1	AAP93628	Ap93628	Sequence
36	286	97.9	469	1	RAP70611	Rap70611	Sequence
37	286	97.9	469	8	ADQ18359	Adq18359	Human sof
38	285	97.6	454	8	ADL93947	Adl93947	Human G-c
39	214	73.3	55	6	ABP97132	Abp97132	Human mat
40	214	73.3	55	6	ABG76318	Abg76318	Human mat
41	214	73.3	55	8	ADQ17093	Adq17093	Human mat
42	214	73.3	444	4	RAG65357	Rag65357	Human MMP
43	214	73.3	467	4	RAB84610	Rab84610	Amino aci
44	214	73.3	467	4	AAE10416	Aae10416	Human mat
45	214	73.3	467	4	AAG65358	Agg65358	Human neu

ALIGNMENTS

RESULT 1

ABP97131

ID ABP97131 standard; peptide; 54 AA.

AC ABP97131;

XX

DT 24-JUN-2003 (first entry)

XX

DE Human matrix metalloproteinase 1 cleavage region peptide SEQ ID NO:9.

XX

KW Human; matrix metalloproteinase; MMP; anticancer; wound healing;
KW matrix metalloproteinase inhibitor; antitumor; antiangiogenic; cardiant;
KW vascular endothelial growth factor inhibitor; VEGF inhibitor; cytostatic;
KW vulnary; cerebroprotective; antidiabetic; ophthalmological; tumour;
KW dermatological; metastatic; non-metastatic; vascularised; heart disease;
KW non-vascularised; surgical incision; chronic wound; stroke; angiogenesis;
KW macular degeneration; diabetic retinopathy; cleavage region.

OS Homo sapiens.

XX WO2003018748-A2.

PN 06-MAR-2003.

PD 15-AUG-2002; 2002WO-US026319.

XX 16-AUG-2001; 2001US-0312726P.

XX 21-DEC-2001; 2001US-00032376.

XX 21-MAY-2002; 2002US-00153185.

XX (KIMB) KIMBERLY-CLARK WORLDWIDE INC.

XX Quirk S, Weart IF;

XX WPI; 2003-381408/36.

XX Anti-angiogenic composition comprising peptide inhibitor of matrix

XX metalloproteinase, useful for decreasing the expression of vascular

XX endothelial growth factor and treating cancers and tissue injuries.

XX Claim 17; Page 16; 103pp; English.

XX The present invention describes an anti-angiogenic composition (I) for

XX inhibiting expression of vascular endothelial growth factor (VEGF). (I)

XX comprises an effective amount of a peptide inhibitor of matrix

XX metalloproteinase (MMP), where the peptide can inhibit the expression of

XX VEGF. (I) has cytostatic, vulnerary, cardiant, cerebroprotective,

XX antidiabetic, ophthalmological and dermatological activities. (I) can be

CC used for inhibiting expression of VEGF, and so can be used for inhibiting
 CC growth of tumours and diminishing tumours size. The tumour can be
 CC metastatic, non-metastatic, vascularised, non-vascularised, hard or soft.
 CC (I) is also useful for treating injuries including wounds, surgical
 CC incisions, chronic wounds, heart diseases and stroke. (I) is also useful
 CC for treating disorders characterised by excessive angiogenesis e.g.
 CC macular degeneration and diabetic retinopathy. The present sequence
 CC represents a human MMP cleavage region peptide, which is used in the
 CC exemplification of the present invention
 XX
 XX Sequence 54 AA;

Query Match 100.0%; Score 292; DB 6; Length 54;
 Best Local Similarity 100.0%; Pred. No. 1.4e-32;
 Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 54
 |||||
 Db 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 54

RESULT 2
 ABG76317
 ID ABG76317 standard; protein; 54 AA.

AC ABG76317;
 XX
 DT 10-MAY-2003 (first entry)

DE Human matrix metalloproteinase (MMP) peptide inhibitor #9.

XX Human; peptide inhibitor; matrix metalloproteinase-1; MMP-1;
 XX cleavage region; proenzyme form; cellular proliferation; fibroblast;
 KW keratinocyte; healthy skin development; wound healing; scarring;
 KW skin tone; wrinkle; anti-aging; vulnerary.

XX Homo sapiens.

XX WO2003016520-A1.

XX 27-FEB-2003.

XX 15-AUG-2002; 2002WO-US026198.

XX 16-AUG-2001; 2001US-0312726P.

XX 21-DEC-2001; 2001US-00032376.

XX 21-MAY-2002; 2002US-00153185.

XX (KIMB) KIMBERLY-CLARK WORLDWIDE INC.

XX Quirk S, Malik S, Villanueva JM;

XX WPI; 2003-289980/28.

XX Novel peptide inhibitor of proteinase activity of matrix

XX metalloproteinases, e.g. matrix metalloproteinase-2, useful for

XX stimulating cellular proliferation of fibroblasts or keratinocytes.

XX Claim 1; Page 16; 120pp; English.

XX The present invention relates to peptide inhibitors of metalloproteinases
 CC (MMPs), particularly metalloproteinase-2 (MMP-2). The inhibitors have
 CC peptide sequences related to the cleavage regions of the proenzyme forms
 CC of the MMPs. The peptide inhibitors are useful for stimulating cellular
 CC proliferation of fibroblasts or keratinocytes, promoting healthy skin
 CC development, treating wounds, preventing scarring, improving skin tone,
 CC reducing wrinkling and for simulating the development of smooth, healthy
 CC skin. The peptide inhibitors are useful as anti-aging and wound healing
 CC compounds. ABG76309-ABG76321 represent peptide inhibitors of MMPs

XX Sequence 54 AA;

Query Match 100.0%; Score 292; DB 6; Length 54;

Best Local Similarity 100.0%; Pred. No. 1.4e-32;
 Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 54
 |||||
 Db 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 54

RESULT 3

ADQ17092

ID ADQ17092 standard; peptide; 54 AA.

XX ADQ17092;

XX 23-SEP-2004 (first entry)

XX Human matrix metalloproteinase-1 (MMP1) cleavage region peptide.

XX Fibronection; healthy skin; wrinkle; wound; vulnerary; dermatological;

XX human; matrix metalloproteinase; MMP.

XX Homo sapiens.

XX US2004127421-A1.

XX 01-JUL-2004.

XX 30-DEC-2002; 2002US-00335207.

XX 30-DEC-2002; 2002US-00335207.

XX (MALI/) MALIK S.

XX (QUIR/) QUIRK S.

XX Malik S, Quirk S;

XX WPI; 2004-506456/48.

XX Composition used for preventing and treating wrinkles and treating wounds
 PT comprises peptide having sequence related to matrix metalloproteinase
 PT proenzyme.

XX Example 1; SEQ ID NO 9; 60pp; English.

XX The present invention provides peptides and compositions containing such
 CC peptides that are useful as agents to maintain healthy skin and to
 CC promote the condition of the skin. The invention is useful for increasing
 CC the amount of fibronectin in tissue. The invention is also useful for
 CC encouraging the maintenance and development of healthy skin, preventing
 CC and treating wrinkles and for treating wounds. The invention acts as
 CC vulnerary and dermatological agents. The present sequence is human matrix
 CC metalloproteinase (MMP) cleavage region peptide. This sequence is used in
 CC the exemplification of the invention.

XX Sequence 54 AA;

Query Match 100.0%; Score 292; DB 8; Length 54;

Best Local Similarity 100.0%; Pred. No. 1.4e-32;
 Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 54
 |||||
 Db 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 54

RESULT 4

ADE16002

ID ADE16002 standard; protein; 454 AA.

XX ADE16002;

XX 29-JAN-2004 (first entry)

PA (CURA-) CURAGEN CORP.
 XX Li L, Gerlach V, Liu X, Miller CE, Spytek KA, Zethusen BD;
 PI Pena CEA, Shenoy SG, Zhong H, Smithson G, Casman SJ, Boldog FL;
 PI Voss EZ, Vernet CAM, Macdougall JR, Rastelli L, Anderson DW;
 PI Zhong M, Mezes PD, Furtak K, Patturajan M, Burgess CE, Malyankar UM;
 PI Shimkets RA, Taupier RJ, Edinger SR, Mazur A;
 XX WPI: 2003-067574/06.
 DR N-PSDB; ADE16003.
 XX New isolated NOVX polypeptides and polynucleotides, useful for
 PT preventing, diagnosing or treating NOVX-associated disorders e.g.
 PT diabetes, obesity, dyslipidaemias, cancer, Parkinson's disease,
 PT Alzheimer's disease, infections.
 XX Claim 1; SEQ ID NO 34; 320pp; English.
 PS The invention relates to a novel isolated G-coupled protein receptor
 XX related polypeptides. The novel polypeptide comprises any of the 22 fully
 CC defined sequences of 87-1780 amino acids, given in the specification;
 CC their mature forms; and possible variants. The novel polypeptides have
 CC the following activities: antidiabetic, anorectic, antibacterial,
 CC virucide, fungicide, cytostatic, nootropic, neuroprotective,
 CC antiparkinsonian, haemostatic, and antilipaeamic. The G-coupled protein
 CC receptor related polypeptides are useful in a method of treating or
 CC preventing in a human, a pathology associated with the G-coupled protein
 CC receptor related polypeptides. The polypeptides are useful in the
 CC manufacture of a medicament for treating a syndrome associated with a
 CC human disease, preferably a NOVX-associated disorder. The novel
 CC polypeptides are useful for treating, preventing or diagnosing diseases,
 CC such as metabolic disorders, diabetes, obesity, infectious diseases,
 CC anorexia, cancer-associated diseases, neurodegenerative disorders,
 CC Alzheimer's disease, Parkinson's disease, immune disorders, hematopoietic
 CC disorders, and various dyslipidaemias, metabolic disturbances associated
 CC with obesity, metabolic X syndrome and wasting disorders associated with
 CC chronic diseases and various cancers. The nucleic acids and polypeptides
 CC may also be used as targets for the identification of small molecules
 CC that modulate or inhibit e.g. neurogenesis, cell differentiation, cell
 CC proliferation, hematopoiesis, wound healing and angiogenesis, in gene
 CC therapy, in generation of antibodies that bind immunospecifically to NOVX
 CC substances for use in therapeutic or diagnostic methods. The nucleic
 CC acids are further used as hybridization probes, in chromosome mapping,
 CC tissue typing, preventive medicine, and pharmacogenomics. This sequence
 CC represents one of the novel G-coupled protein receptor related
 CC polypeptides of the invention.
 XX Sequence 454 AA;
 SQ

Query Match 100.0%; Score 292; DB 7; Length 454;
 Best Local Similarity 100.0%; Pred. No. 2e-31;
 Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MOEFGLKVTGPDATLTKVMKQPCGVPDVAQFVLTEGNRWEOHTLTYRIEN 54
 DB 50 MOEFGLKVTGPDATLTKVMKQPCGVPDVAQFVLTEGNRWEOHTLTYRIEN 103

RESULT 6
 ADE16008
 ID ADE16008 standard; protein; 454 AA.
 XX ADE16008;
 AC ADE16008;
 XX 29-JAN-2004 (first entry)
 DT G-coupled protein receptor related polypeptide, SEQ ID NO 38.
 DE G-coupled protein receptor; antidiabetic; anorectic; antibacterial;
 XX virucide; fungicide; cytostatic; nootropic; neuroprotective;
 KW antiparkinsonian; haemostatic; antilipaeamic; neurogenesis;
 KW cell differentiation; cell proliferation; hematopoiesis; wound healing;
 KW angiogenesis; gene therapy; chromosome mapping; tissue typing;

preventive medicine; pharmacogenomics; human.
 Homo sapiens.
 WO200283841-A2.
 24-OCT-2002.
 03-APR-2002; 2002WO-US010713.
 03-APR-2001; 2001US-0281136P.
 05-APR-2001; 2001US-0281863P.
 05-APR-2001; 2001US-0281906P.
 10-APR-2001; 2001US-0282934P.
 13-APR-2001; 2001US-0283657P.
 13-APR-2001; 2001US-0283678P.
 13-APR-2001; 2001US-0283687P.
 13-APR-2001; 2001US-0283710P.
 17-APR-2001; 2001US-0284234P.
 19-APR-2001; 2001US-0285325P.
 20-APR-2001; 2001US-0285609P.
 23-APR-2001; 2001US-0285748P.
 23-APR-2001; 2001US-0285890P.
 24-APR-2001; 2001US-0286068P.
 27-APR-2001; 2001US-0287213P.
 30-MAY-2001; 2001US-0288509P.
 30-MAY-2001; 2001US-0294495P.
 31-MAY-2001; 2001US-0294801P.
 31-JUL-2001; 2001US-0309216P.
 25-SEP-2001; 2001US-0324775P.
 28-NOV-2001; 2001US-0333900P.
 02-APR-2002; 2002US-00115479.
 (CURA-) CURAGEN CORP.
 Li L, Gerlach V, Liu X, Miller CE, Spytek KA, Zethusen BD;
 PI Pena CEA, Shenoy SG, Zhong H, Smithson G, Casman SJ, Boldog FL;
 PI Voss EZ, Vernet CAM, Macdougall JR, Rastelli L, Anderson DW;
 PI Zhong M, Mezes PD, Furtak K, Patturajan M, Burgess CE, Malyankar UM;
 PI Shimkets RA, Taupier RJ, Edinger SR, Mazur A;
 XX WPI: 2003-067574/06.
 DR N-PSDB; ADE16007.
 XX New isolated NOVX polypeptides and polynucleotides, useful for
 PT preventing, diagnosing or treating NOVX-associated disorders e.g.
 PT diabetes, obesity, dyslipidaemias, cancer, Parkinson's disease,
 PT Alzheimer's disease, infections.
 XX Claim 1; SEQ ID NO 38; 320pp; English.
 PS The invention relates to a novel isolated G-coupled protein receptor
 XX related polypeptides. The novel polypeptide comprises any of the 22 fully
 CC defined sequences of 87-1780 amino acids, given in the specification;
 CC their mature forms; and possible variants. The novel polypeptides have
 CC the following activities: antidiabetic, anorectic, antibacterial,
 CC virucide, fungicide, cytostatic, nootropic, neuroprotective,
 CC antiparkinsonian, haemostatic, and antilipaeamic. The G-coupled protein
 CC receptor related polypeptides are useful in a method of treating or
 CC preventing in a human, a pathology associated with the G-coupled protein
 CC receptor related polypeptides. The polypeptides are useful in the
 CC manufacture of a medicament for treating a syndrome associated with a
 CC human disease, preferably a NOVX-associated disorder. The novel
 CC polypeptides are useful for treating, preventing or diagnosing diseases,
 CC such as metabolic disorders, diabetes, obesity, infectious diseases,
 CC anorexia, cancer-associated diseases, neurodegenerative disorders,
 CC Alzheimer's disease, Parkinson's disease, immune disorders, hematopoietic
 CC disorders, and various dyslipidaemias, metabolic disturbances associated
 CC with obesity, metabolic X syndrome and wasting disorders associated with
 CC chronic diseases and various cancers. The nucleic acids and polypeptides
 CC may also be used as targets for the identification of small molecules
 CC that modulate or inhibit e.g. neurogenesis, cell differentiation, cell
 CC proliferation, hematopoiesis, wound healing and angiogenesis, in gene
 CC therapy, in generation of antibodies that bind immunospecifically to NOVX
 CC substances for use in therapeutic or diagnostic methods. The nucleic
 CC acids are further used as hybridization probes, in chromosome mapping,
 CC tissue typing, preventive medicine, and pharmacogenomics. This sequence
 CC represents one of the novel G-coupled protein receptor related
 CC polypeptides of the invention.
 XX Sequence 454 AA;
 SQ

CC therapy, in generation of antibodies that bind immunospecifically to NOVX
CC substances for use in therapeutic or diagnostic methods. The nucleic
CC acids are further used as hybridization probes, in chromosome mapping,
CC tissue typing, preventive medicine, and pharmacogenomics. This sequence
CC represents one of the novel G-coupled protein receptor related
CC polypeptides of the invention.
XX
SQ Sequence 454 AA;

Query Match 100.0%; Score 292; DB 7; Length 454;
Best Local Similarity 100.0%; Pred. No. 2e-31;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQEFGKLVTKGPDATLKVWKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 54
DB 50 MQEFGKLVTKGPDATLKVWKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 103

RESULT 7
AD216006
ID ADE16006 standard; protein; 454 AA.

AC ADE16006;

XX 29-JAN-2004 (first entry)

DE G-coupled protein receptor related polypeptide, SEQ ID No. 36.

XX G-coupled protein receptor; antidiabetic; anorectic; antibacterial;
XX virucide; fungicide; cytostatic; neurotropic; neuroprotective;
XX antiparkinsonian; haemostatic; antilipaeamic; neurogenesis;
XX cell differentiation; cell proliferation; hematopoiesis; wound healing;
XX angiogenesis; gene therapy; chromosome mapping; tissue typing;
XX preventive medicine; pharmacogenomics; human.

OS Homo sapiens.

XX WO200283841-A2.

XX 24-OCT-2002.

XX 03-APR-2002; 2002WO-US010713.

XX 03-APR-2001; 2001US-0281136P.

XX 05-APR-2001; 2001US-0281863P.

XX 10-APR-2001; 2001US-0282934P.

XX 13-APR-2001; 2001US-0283657P.

XX 13-APR-2001; 2001US-0283678P.

XX 13-APR-2001; 2001US-0283687P.

XX 13-APR-2001; 2001US-0283710P.

XX 17-APR-2001; 2001US-0284234P.

XX 19-APR-2001; 2001US-0285325P.

XX 20-APR-2001; 2001US-0285609P.

XX 23-APR-2001; 2001US-0285748P.

XX 24-APR-2001; 2001US-0286068P.

XX 27-APR-2001; 2001US-0287213P.

XX 03-MAY-2001; 2001US-0288509P.

XX 30-MAY-2001; 2001US-0294495P.

XX 31-MAY-2001; 2001US-0294801P.

XX 31-JUL-2001; 2001US-0309216P.

XX 25-SEP-2001; 2001US-0324775P.

XX 28-NOV-2001; 2001US-0333900P.

XX 02-APR-2002; 2002US-00115479.

XX (CURA-) CURAGEN CORP.

XX Li L, Gerlach V, Liu X, Miller CB, Spytek KA, Zerhusen BD;

XX Pena CEA, Shenoy SG, Zhong H, Smithson G, Casman SJ, Boldog FL;

XX Voss EZ, Vernet CAM, MacDougall JR, Rastelli L, Anderson DW;

XX Zhong W, Mezes PD, Furtak K, Patturajan M, Burgess CE, Malyankar UM;

XX Shimkets RA, Taupier RJ, Edinger SR, Mazur A;

XX

DR WPI; 2003-067574/06.

XX N-PSDB; ADE16005.

XX

PT New isolated NOVX polypeptides and polynucleotides, useful for

PT preventing, diagnosing or treating NOVX-associated disorders e.g.

PT diabetes, obesity, dyslipidemias, cancer, Parkinson's disease,

PT Alzheimer's disease, infections.

XX

PS Claim 1; SEQ ID NO 36; 320pp; English.

XX

CC The invention relates to a novel isolated G-coupled protein receptor

CC related polypeptides. The novel polypeptide comprises any of the 22 fully

CC defined sequences of 87-1780 amino acids, given in the specification,

CC their mature forms; and possible variants. The novel polypeptides have

CC the following activities: antidiabetic, anorectic, antibacterial,

CC virucide, fungicide, cytostatic, neurotropic, neuroprotective,

CC antiparkinsonian, haemostatic, and antilipaeamic. The G-coupled protein

CC receptor related polypeptides are useful in a method of treating or

CC preventing in a human, a pathology associated with the G-coupled protein

CC receptor related polypeptides. The polypeptides are useful in the

CC manufacture of a medicament for treating a syndrome associated with a

CC human disease, preferably a NOVX-associated disorder. The novel

CC polypeptides are useful for treating, preventing or diagnosing diseases,

CC such as metabolic disorders, diabetes, obesity, infectious diseases,

CC anorexia, cancer-associated diseases, neurodegenerative disorders,

CC Alzheimer's disease, Parkinson's disease, immune disorders, hematopoietic

CC disorders, and various dyslipidaemias, metabolic disturbances associated

CC with obesity, metabolic X syndrome and wasting disorders associated with

CC chronic diseases and various cancers. The nucleic acids and polypeptides

CC may also be used as targets for the identification of small molecules

CC that modulate or inhibit e.g. neurogenesis, cell differentiation, cell

CC proliferation, hematopoiesis, wound healing and angiogenesis, in gene

CC therapy, in generation of antibodies that bind immunospecifically to NOVX

CC substances for use in therapeutic or diagnostic methods. The nucleic

CC acids are further used as hybridization probes, in chromosome mapping,

CC tissue typing, preventive medicine, and pharmacogenomics. This sequence

CC represents one of the novel G-coupled protein receptor related

CC polypeptides of the invention.

XX

SQ Sequence 454 AA;

Query Match 100.0%; Score 292; DB 7; Length 454;

Best Local Similarity 100.0%; Pred. No. 2e-31;

Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQEFGKLVTKGPDATLKVWKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 54

DB 50 MQEFGKLVTKGPDATLKVWKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 103

RESULT 8

ADL93945

ID ADL93945 standard; protein; 454 AA.

XX ADL93945;

XX 20-MAY-2004 (first entry)

DE Human G-coupled protein receptor-related protein #18.

XX human; transgenic; Gene Therapy; Protein Therapy; cardiomyopathy;
XX atherosclerosis; hypertension; congenital heart defect; aortic stenosis;
XX atrial septal defect; atrioventricular canal defect; ductus arteriosus;
XX pulmonary stenosis; subaortic stenosis; ventricular septal defect;
XX valve disease; tuberculous sclerosis; scleroderma; obesity; transplantation;
XX adrenoleukodystrophy; congenital adrenal hyperplasia; prostate cancer;
XX neoplasm; adenocarcinoma; lymphoma; uterus cancer; fertility;
XX haemophilia; hypercoagulation; idiopathic thrombocytopenic purpura;
XX immunodeficiency; graft versus host disease; AIDS; bronchial asthma;
XX Crohn's disease; G-coupled protein receptor; metabolic disorder;
XX neurodegenerative disorder; receptor.

OS Homo sapiens.
 XX US2004006205-A1.
 XX 08-JAN-2004.
 XX 02-APR-2002; 2002US-00115479.
 XX 03-APR-2001; 2001US-0281136P.
 XX 05-APR-2001; 2001US-0281863P.
 XX 05-APR-2001; 2001US-0281906P.
 XX 10-APR-2001; 2001US-0282934P.
 XX 13-APR-2001; 2001US-0283657P.
 XX 13-APR-2001; 2001US-0283787P.
 XX 13-APR-2001; 2001US-0283867P.
 XX 13-APR-2001; 2001US-0283710P.
 XX 17-APR-2001; 2001US-0284234P.
 XX 19-APR-2001; 2001US-0285325P.
 XX 20-APR-2001; 2001US-0285609P.
 XX 23-APR-2001; 2001US-0285748P.
 XX 24-APR-2001; 2001US-0285890P.
 XX 24-APR-2001; 2001US-0286068P.
 XX 27-APR-2001; 2001US-0287213P.
 XX 03-MAY-2001; 2001US-0288509P.
 XX 30-MAY-2001; 2001US-0294495P.
 XX 31-MAY-2001; 2001US-0294801P.
 XX 31-JUL-2001; 2001US-0309216P.
 XX 25-SEP-2001; 2001US-0324775P.
 XX 28-NOV-2001; 2001US-0333900P.
 XX (LILL/) LI L.
 XX (GERL/) GERLACH V.
 XX (LIUX/) LIU X.
 XX (MILL/) MILLER C E.
 XX (SPVT/) SPYTEK K A.
 XX (ZERH/) ZERHUSEN B D.
 XX (PENR/) PENA C E A.
 XX (SHEN/) SHENOY S G.
 XX (ZHON/) ZHONG H.
 XX (SMIT/) SMITHSON G.
 XX (CASM/) CASMAN S J.
 XX (BOLD/) BOLDOG F L.
 XX (VOSS/) VOSS E Z.
 XX (VERN/) VERNET C A.
 XX (MACD/) MACDOUGALL J R.
 XX (RASI/) RASTELLI L.
 XX (ANDE/) ANDERSON D W.
 XX (ZHON/) ZHONG M.
 XX (MEZE/) MEZES P S.
 XX (FURI/) FURIAK K.
 XX (PATT/) PATTURAJAN M.
 XX (BURG/) BURGESS C E.
 XX (MALY/) MALYANKAR U M.
 XX (SHIM/) SHIMKETS R A.
 XX (TAUP/) TAUPIER R J.
 XX (EDIN/) EDINGER S.
 XX (MAZU/) MAZUR A.
 XX Li L, Gerlach V, Liu X, Miller CE, Spytek KA, Zerhusen BD;
 XX Pena CE, Shenoy SG, Zhong H, Smithson G, Casman SJ, Boldog FL;
 XX Voss EZ, Vernet CA, MacDougall JR, Rastelli L, Anderson DW, Zhong M;
 XX Mezes PS, Furtak K, Patturajan M, Burgess CE, Malyankar UM;
 XX Shinkets RA, Taupier RJ, Edinger S, Mazur A;
 XX WPI; 2004-224146/21.
 XX N-PSDB; ADL93944.
 XX New G-coupled protein-receptor related polypeptides, for preventing
 XX treating or ameliorating, e.g. acquired immunodeficiency syndrome,
 XX bronchial asthma, Crohn's disease, prostate cancer, hemophilia,
 XX scleroderma or obesity.
 XX Claim 1; Page 66; 220pp; English.

XX The invention relates to isolated human G-coupled protein receptor-
 CC related polypeptides and polynucleotides. The proteins are useful for
 CC preventing, treating or ameliorating medical disorders by protein or gene
 CC therapy. Disorders include cardiomyopathy, atherosclerosis, hypertension,
 CC congenital heart defects, aortic stenosis, atrial septal defect,
 CC atrioventricular canal defect, ductus arteriosus, pulmonary stenosis,
 CC subaortic stenosis, ventricular septal defect, valve diseases, tubercous
 CC sclerosis, scleroderma, obesity, transplantation, adrenoleukodystrophy,
 CC congenital adrenal hyperplasia, prostate cancer, neoplasm,
 CC adenocarcinoma, lymphoma, uterus cancer, fertility, haemophilia,
 CC hypercoagulation, idiopathic thrombocytopenic purpura,
 CC immunodeficiencies, graft versus host disease, AIDS, bronchial asthma,
 CC metabolic disorders, neurodegenerative disorders or Crohn's disease. They
 CC are also useful as diagnostic or research tools. The present sequence
 CC represents a human G-coupled protein receptor-related protein of the
 CC invention.
 XX Sequence 454 AA;
 XX SQ

Query Match 100.0%; Score 292; DB 8; Length 454;
 Best Local Similarity 100.0%; Pred. No. 2e-31;
 Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MQEFFGLKVTGKPDATLTKVMKQPRCGVDPDAQFVLTGPNRWEQTHLYRIEN 54
 Db 50 MQEFFGLKVTGKPDATLTKVMKQPRCGVDPDAQFVLTGPNRWEQTHLYRIEN 103

RESULT 9
 ADL93943
 ID ADL93943 standard; protein; 454 AA.
 XX
 AC ADL93943;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Human G-coupled protein receptor-related protein #17.
 XX
 KW human; transgenic; Gene Therapy; Protein Therapy; cardiomyopathy;
 KW atherosclerosis; hypertension; congenital heart defect; aortic stenosis;
 KW atrial septal defect; atrioventricular canal defect; ductus arteriosus;
 KW pulmonary stenosis; subaortic stenosis; scleroderma; obesity; transplantation;
 KW valve disease; tubercous sclerosis; adenoleukodystrophy; congenital adrenal hyperplasia; prostate cancer;
 KW neoplasm; adenocarcinoma; lymphoma; uterus cancer; fertility;
 KW haemophilia; hypercoagulation; idiopathic thrombocytopenic purpura;
 KW immunodeficiency; graft versus host disease; AIDS; bronchial asthma;
 KW Crohn's disease; G-coupled protein receptor; metabolic disorder;
 KW neurodegenerative disorder; receptor.
 XX
 OS Homo sapiens.
 XX
 DN US2004006205-A1.
 XX
 PD 08-JAN-2004.
 XX
 XX 02-APR-2002; 2002US-00115479.
 XX
 XX 03-APR-2001; 2001US-0281136P.
 XX 05-APR-2001; 2001US-0281863P.
 XX 05-APR-2001; 2001US-0281906P.
 XX 10-APR-2001; 2001US-0282934P.
 XX 13-APR-2001; 2001US-0283657P.
 XX 13-APR-2001; 2001US-0283787P.
 XX 13-APR-2001; 2001US-0283867P.
 XX 13-APR-2001; 2001US-0283710P.
 XX 17-APR-2001; 2001US-0284234P.
 XX 19-APR-2001; 2001US-0285325P.
 XX 20-APR-2001; 2001US-0285609P.
 XX 23-APR-2001; 2001US-0285748P.
 XX 24-APR-2001; 2001US-0285890P.
 XX 24-APR-2001; 2001US-0286068P.

PR 27-APR-2001; 2001US-0287213P.
PR 03-MAY-2001; 2001US-0288509P.
PR 30-MAY-2001; 2001US-0294495P.
PR 31-MAY-2001; 2001US-0294801P.
PR 31-JUL-2001; 2001US-0309216P.
PR 25-SEP-2001; 2001US-0324775P.
PR 28-NOV-2001; 2001US-0333900P.
XX
PA (LILL/) LI L.
PA (GERL/) GERLACH V.
PA (LIUX/) LIU X.
PA (MILL/) MILLER C E.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PENA/) PENNA C E A.
PA (SHEN/) SHENOY S G.
PA (ZHON/) ZHONG H.
PA (SMIT/) SMITHSON G.
PA (CASM/) CASMAN S J.
PA (BOLD/) BOLDOGF L.
PA (VOSS/) VOSS E Z.
PA (VERN/) VERNET C A.
PA (MACD/) MACDOUGALL J R.
PA (RAST/) RASTELLI L.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (MEZE/) MEZES P S.
PA (FURT/) FURTAK K.
PA (PATI/) PATURAJAN M.
PA (BURG/) BURGESS C E.
PA (MALY/) MALYANKAR U M.
PA (SHIM/) SHIMKETS R A.
PA (TAUP/) TAUPIER R J.
PA (EDIN/) EDINGER S.
PA (MAZU/) MAZUR A.
XX
PI Li L, Gerlach V, Liu X, Miller CE, Spytek KA, Zehrusen BD;
PI Pena CE, Shenoy SG, Smithson G, Casman SJ, Boldog FL;
PI Voss EZ, Vernet CA, Macdougall JR, Rastelli L, Anderson DW, Zhong M;
PI Mezes PS, Furtak K, Patturajan M, Burgess CE, Malyankar UM;
PI Shinkets RA, Taupier RJ, Edinger S, Mazur A;
XX
XX WPI; 2004-224146/21.
DR N-PSDB; ADL93942.
XX
XX
XX New G-coupled protein-receptor related polypeptides, for preventing
PT treating or ameliorating, e.g. acquired immunodeficiency syndrome,
PT bronchial asthma, Crohn's disease, prostate cancer, hemophilia,
PT scleroderma or obesity.
XX
XX
XX Claim 1; Page 67; 220pp; English.
XX
XX The invention relates to isolated human G-coupled protein receptor-
CC related polypeptides and polynucleotides. The proteins are useful for
CC preventing, treating or ameliorating medical disorders by protein or gene
CC therapy. Disorders include cardiomyopathy, atherosclerosis, hypertension,
CC congenital heart defects, aortic stenosis, ductus arteriosus, septal defect,
CC atrioventricular canal defect, ductus arteriosus, pulmonary stenosis,
CC subaortic stenosis, ventricular septal defect, valve diseases, tuberos
CC sclerosis, scleroderma, obesity, transplacental, adrenoleukodystrophy,
CC congenital adrenal hyperplasia, prostate cancer, neoplasm,
CC adenocarcinoma, lymphoma, uterus cancer, fertility haemophilia,
CC hypercoagulation, idiopathic thrombocytopenic purpura,
CC immunodeficiencies, graft versus host disease, AIDS, bronchial asthma,
CC metabolic disorders, neurodegenerative disorders or Crohn's disease. They
CC are also useful as diagnostic or research tools. The present sequence
CC represents a human G-coupled protein receptor-related protein of the
CC invention.
XX
SQ Sequence 454 AA;

Query Match 100.0%; Score 292; DB 8; Length 454;
Best Local Similarity 100.0%; Pred. No. 2e-31;

Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQEFGGLKVTGKPDAAETLKVMPKQRCGVDPVDAQFVLTEGPRWEQTHLYRIEN 54
DB 50 MQEFGGLKVTGKPDAAETLKVMPKQRCGVDPVDAQFVLTEGPRWEQTHLYRIEN 103
RESULT 10
ADL93941
ID ADL93941 standard; protein; 455 AA.
XX
AC ADL93941;
XX
XX 20-MAY-2004 (first entry)
XX
DE Human G-coupled protein receptor-related protein #16.
XX
XX human; transgenic; Gene Therapy; Protein Therapy; cardiomyopathy;
KW atherosclerosis; hypertension; congenital heart defect; aortic stenosis;
KW atrial septal defect; atrioventricular canal defect; ductus arteriosus;
KW pulmonary stenosis; subaortic stenosis; ventricular septal defect;
KW valve disease; tuberos sclerosis; scleroderma; obesity; transplacental;
KW adrenoleukodystrophy; congenital adrenal hyperplasia; prostate cancer;
KW neoplasm; adenocarcinoma; lymphoma; uterus cancer; fertility;
KW hemophilia; hypercoagulation; idiopathic thrombocytopenic purpura;
KW immunodeficiency; graft versus host disease; AIDS; bronchial asthma;
KW Crohn's disease; G-coupled protein receptor; metabolic disorder;
KW neurodegenerative disorder; receptor.
XX
OS Homo sapiens.
XX
XX US2004006205-A1.
XX
XX 08-JAN-2004.
XX
XX 02-APR-2002; 2002US-00115479.
XX
XX 03-APR-2001; 2001US-0281136P.
PR 05-APR-2001; 2001US-0281863P.
PR 05-APR-2001; 2001US-0281906P.
PR 10-APR-2001; 2001US-0282934P.
PR 13-APR-2001; 2001US-0283657P.
PR 13-APR-2001; 2001US-0283678P.
PR 13-APR-2001; 2001US-0283687P.
PR 13-APR-2001; 2001US-0283710P.
PR 17-APR-2001; 2001US-0284234P.
PR 19-APR-2001; 2001US-0285325P.
PR 20-APR-2001; 2001US-0285609P.
PR 23-APR-2001; 2001US-0285748P.
PR 23-APR-2001; 2001US-0285890P.
PR 24-APR-2001; 2001US-0286068P.
PR 27-APR-2001; 2001US-0287213P.
PR 03-MAY-2001; 2001US-0288509P.
PR 30-MAY-2001; 2001US-0294495P.
PR 31-MAY-2001; 2001US-0294801P.
PR 31-JUL-2001; 2001US-0309216P.
PR 25-SEP-2001; 2001US-0324775P.
PR 28-NOV-2001; 2001US-0333900P.
XX
XX (LILL/) LI L.
PA (GERL/) GERLACH V.
PA (LIUX/) LIU X.
PA (MILL/) MILLER C E.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PENA/) PENNA C E A.
PA (SHEN/) SHENOY S G.
PA (ZHON/) ZHONG H.
PA (SMIT/) SMITHSON G.
PA (CASM/) CASMAN S J.
PA (BOLD/) BOLDOGF L.
PA (VOSS/) VOSS E Z.
PA (VERN/) VERNET C A.


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FT Protein /label= Signal_peptide
FT 20..469
FT /label= Mature_MMP_1_protein
FT 90..96
FT Domain /label= Cysteine_switch_domain
FT 161..171
FT Domain /note= "Zinc and calcium binding domain"
FT 161..171
XX WO200166766-A2.
XX PN
XX PD
XX 13-SEP-2001.
XX PD
XX 06-MAR-2001; 2001WO-US007167.
XX PF
XX 06-MAR-2000; 2000US-0187196P.
XX PR
XX (DARW-) DARWIN MOLECULAR CORP.
XX PA
XX (SCHA/) SCHATZMAN R.
XX PA
XX Fajardo M, Wang K, Smith R, Moss P;
XX PI
XX WPI; 2001-592276/65.
XX DR
XX Novel isolated matrix metalloproteinase-25 nucleic acid molecule and
XX PT proteins encoded by them whose inhibition is useful for modulation of
XX PT hair growth in mammals.
XX PT
XX Example 2; Fig 3; 119pp; English.
XX PS
XX The present sequence is human matrix metalloproteinase (MMP)-1 protein
XX CC used in the exemplification of the invention. MMP-25 DNA is located on
XX CC chromosome 11q22. Matrix metalloproteinases are a family of zinc
XX CC dependent endopeptidases that function extracellularly to degrade
XX CC proteins typically found in the extracellular matrix. MMP-25 is expressed
XX CC in skin cells of mammals, particularly in breast cells and hair
XX CC follicles. MMP-25 DNA is useful for identifying a nucleic acid molecule
XX CC encoding all or part of MMP by hybridising MMP-25 to a nucleic acid
XX CC sample and identifying a sequence that hybridises in the nucleic acid
XX CC sample. The identification step involves performing polymerase chain
XX CC reaction (PCR) to amplify the hybridising sequence. MMP-25 antibody is
XX CC useful for identifying type 25 MMP. MMP-25 protein inhibitors may be used
XX CC to modulate hair growth and breast cancer in a mammal
XX SQ Sequence 469 AA;
XX Query Match 100.0%; Score 292; DB 4; Length 469;
XX Best Local Similarity 100.0%; Pred. NO. 2.1e-31;
XX Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX SQ
XX 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLTTRYEN 54
XX 67 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLTTRYEN 120
XX Db
XX RESULT 13
XX ABU03466
XX ID ABU03466 standard; protein; 469 AA.
XX AC ABU03466;
XX XX
XX 21-JAN-2003 (first entry)
XX DT
XX Angiogenesis-associated human protein sequence #11.
XX DE
XX Human; angiogenesis-associated transcript; angiogenesis;
XX KW angiogenesis-associated disease; cancer; cytostatic.
XX KW
XX Homo sapiens.
XX OS
XX WO200279492-A2.
XX PN
XX 10-OCT-2002.
XX PD
XX XX
```

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PF 14-FEB-2002; 2002WO-US004915.
XX 14-FEB-2001; 2001US-00784356.
XX 22-FEB-2001; 2001US-00791390.
XX 19-APR-2001; 2001US-0285475P.
XX 03-AUG-2001; 2001US-0310025P.
XX 13-NOV-2001; 2001US-0350666P.
XX 29-NOV-2001; 2001US-0334244P.
XX PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX XX
XX Murray R, Glynn R, Watson SR, Aziz N;
XX PI
XX WPI; 2003-040681/03.
XX DR
XX N-PSDB; ABX08749.
XX DR
XX Detecting angiogenesis-associated transcript in a cell for diagnosing and
XX PT treating cancer by contacting a sample with a polynucleotide that
XX PT exhibits changes in expression level as a function of time in tissue
XX PT undergoing angiogenesis.
XX PT
XX Example 2; Page 189; 291pp; English.
XX PS
XX The present invention relates to methods and compositions for detecting
XX CC an angiogenesis-associated transcript in a cell in a patient. The method
XX CC involves contacting a biological sample from the patient with a
XX CC polynucleotide that selectively hybridises to a sequence at least 80%
XX CC identical to any of the angiogenesis-associated human polynucleotide
XX CC sequences given in the specification. These angiogenesis-associated
XX CC polynucleotide sequences comprise genes that exhibit changes in
XX CC expression levels as a function of time in tissue undergoing
XX CC angiogenesis. The method and the polynucleotide sequences of the
XX CC invention are useful for diagnosing and treating angiogenesis and
XX CC angiogenesis-associated diseases e.g. cancer. The polynucleotide
XX CC sequences are also useful in the gene therapy of such disorders. The
XX CC angiogenesis-associated proteins encoded by the polynucleotide sequences
XX CC are useful as a vaccine for therapeutic and prophylactic immunisation.
XX CC ABU03456-ABU03569 represent angiogenesis-associated protein sequences
XX SQ Sequence 469 AA;
XX Query Match 100.0%; Score 292; DB 6; Length 469;
XX Best Local Similarity 100.0%; Pred. NO. 2.1e-31;
XX Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX SQ
XX 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLTTRYEN 54
XX 67 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLTTRYEN 120
XX Db
XX RESULT 14
XX ABR58543
XX ID ABR58543 standard; protein; 469 AA.
XX XX
XX AC ABR58543;
XX XX
XX 09-JUL-2003 (first entry)
XX DT
XX Human cancer related protein SEQ ID NO:200.
XX DE
XX Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;
XX KW heart disease; atherosclerosis; endometriosis.
XX KW
XX Homo sapiens.
XX OS
XX WO2003025138-A2.
XX PN
XX 27-MAR-2003.
XX PD
XX 17-SEP-2002; 2002WO-US029560.
XX PF
XX 17-SEP-2001; 2001US-0323459P.
XX PR
XX 20-SEP-2001; 2001US-0323887P.
XX PR
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PR 13-NOV-2001; 2001US-0350666P.
PR 08-FEB-2002; 2002US-0355145P.
PR 08-FEB-2002; 2002US-0355257P.
PR 12-APR-2002; 2002US-0372246P.
XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX
XX Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;
XX Zlotnik A;
XX
XX WPI: 2003-354600/33.
XX N-PSDB; ACC72663.
XX
XX New genes that are up-regulated or down-regulated in cancers, useful as
XX PT markers for diagnosing e.g. cancer, ischemia or heart diseases, or as
XX PT therapeutic targets for screening drugs for treating these diseases.
XX
XX Claim 12; Page 735; 767pp; English.
XX
XX The present invention describes an isolated nucleic acid molecule, which
XX CC comprises the sequence of any of the genes that are up-regulated or down-
XX CC regulated in specific cancers (e.g. about 1031 genes up-regulated in
XX CC acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer
XX CC related gene nucleotide sequences which encode the proteins given in
XX CC ABR58521 to ABR58709. Also described: (1) determining the presence or
XX CC absence of a pathological cell in a patient; (2) an expression vector
XX CC comprising a nucleic acid molecule described above; (3) a host cell
XX CC comprising the vector; (4) an isolated polypeptide, which is encoded by
XX CC the nucleic acid; (5) an antibody that specifically binds the polypeptide
XX CC of (4); (6) specifically targeting a compound to a pathological cell in a
XX CC patient by administering to the patient the antibody above; and (7) a
XX CC drug screening assay. The nucleic acid is useful as diagnostic markers or
XX CC therapeutic targets. In particular, the nucleic acid is useful for
XX CC diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,
XX CC bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,
XX CC pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases,
XX CC atherosclerosis and endometriosis. The nucleic acid is also useful in
XX CC drug screening, particularly for identifying agents for treating these
XX CC pathologies
XX SQ Sequence 469 AA;
XX
XX Query Match 100.0%; Score 292; DB 6; Length 469;
XX Best Local Similarity 100.0%; Pred. No. 2.1e-31;
XX Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 54
XX DB 67 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 120
XX
XX RESULT 15
XX ABR58542
XX ID ABR58542 standard; protein; 469 AA.
XX AC ABR58542;
XX
XX DT 09-JUL-2003 (first entry)
XX
XX DE Human cancer related protein SEQ ID NO:199.
XX
XX KW Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;
XX KW heart disease; atherosclerosis; endometriosis.
XX OS Homo sapiens.
XX
XX PN WO2003025138-A2.
XX
XX PD 27-MAR-2003.
XX
XX PF 17-SEP-2002; 2002WO-US029560.
XX
XX PR 17-SEP-2001; 2001US-0323469P.
XX
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PR 20-SEP-2001; 2001US-0323887P.
PR 13-NOV-2001; 2001US-0350666P.
PR 08-FEB-2002; 2002US-0355145P.
PR 08-FEB-2002; 2002US-0355257P.
PR 12-APR-2002; 2002US-0372246P.
XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX
XX Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;
XX Zlotnik A;
XX
XX WPI: 2003-354600/33.
XX N-PSDB; ACC72662.
XX
XX New genes that are up-regulated or down-regulated in cancers, useful as
XX PT markers for diagnosing e.g. cancer, ischemia or heart diseases, or as
XX PT therapeutic targets for screening drugs for treating these diseases.
XX
XX Claim 12; Page 735; 767pp; English.
XX
XX The present invention describes an isolated nucleic acid molecule, which
XX CC comprises the sequence of any of the genes that are up-regulated or down-
XX CC regulated in specific cancers (e.g. about 1031 genes up-regulated in
XX CC acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer
XX CC related gene nucleotide sequences which encode the proteins given in
XX CC ABR58521 to ABR58709. Also described: (1) determining the presence or
XX CC absence of a pathological cell in a patient; (2) an expression vector
XX CC comprising a nucleic acid molecule described above; (3) a host cell
XX CC comprising the vector; (4) an isolated polypeptide, which is encoded by
XX CC the nucleic acid; (5) an antibody that specifically binds the polypeptide
XX CC of (4); (6) specifically targeting a compound to a pathological cell in a
XX CC patient by administering to the patient the antibody above; and (7) a
XX CC drug screening assay. The nucleic acid is useful as diagnostic markers or
XX CC therapeutic targets. In particular, the nucleic acid is useful for
XX CC diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,
XX CC bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,
XX CC pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases,
XX CC atherosclerosis and endometriosis. The nucleic acid is also useful in
XX CC drug screening, particularly for identifying agents for treating these
XX CC pathologies
XX SQ Sequence 469 AA;
XX
XX Query Match 100.0%; Score 292; DB 6; Length 469;
XX Best Local Similarity 100.0%; Pred. No. 2.1e-31;
XX Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 54
XX DB 67 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 120
XX
XX Search completed: November 15, 2004, 14:04:09
XX Job time : 51.5 secs
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OM protein - protein search, using sw model

Run on: November 15, 2004, 14:01:35 ; Search time 14.5385 Seconds
(without alignments)
246.324 Million cell updates/sec

Title: US-10-032-376A-9

Perfect score: 292

Sequence: 1 MQEFFGLKVTGKPDATLKV.....VLTEGNPRWEQTHLYRIEN 54

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 205538

Minimum DB seq length: 47

Maximum DB seq length: 660

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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- 2: /cgn2_6/prodata/1/iaa/5B COMB.pep:*
- 3: /cgn2_6/prodata/1/iaa/6A COMB.pep:*
- 4: /cgn2_6/prodata/1/iaa/6B COMB.pep:*
- 5: /cgn2_6/prodata/1/iaa/6C COMB.pep:*
- 6: /cgn2_6/prodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	292	100.0	469	3 US-08-704-711A-16	Sequence 16, Appl
2	292	100.0	469	3 US-08-448-489-12	Sequence 12, Appl
3	292	100.0	469	3 US-09-521-220-16	Sequence 16, Appl
4	292	100.0	469	3 US-09-391-104-23	Sequence 23, Appl
5	214	73.3	444	1 US-09-178-002-2	Sequence 2, Appl
6	214	73.3	466	3 US-08-704-711A-17	Sequence 17, Appl
7	214	73.3	466	3 US-09-521-220-17	Sequence 17, Appl
8	214	73.3	467	1 US-09-178-002-4	Sequence 4, Appl
9	214	73.3	467	3 US-09-391-104-24	Sequence 24, Appl
10	214	73.3	468	3 US-08-448-489-13	Sequence 13, Appl
11	189	64.7	476	3 US-08-704-711A-21	Sequence 21, Appl
12	189	64.7	476	3 US-08-448-489-14	Sequence 14, Appl
13	189	64.7	476	3 US-09-521-220-21	Sequence 21, Appl
14	189	64.7	476	3 US-09-391-104-22	Sequence 22, Appl
15	189	64.7	477	3 US-08-704-711A-20	Sequence 20, Appl
16	189	64.7	477	3 US-08-448-489-15	Sequence 15, Appl
17	189	64.7	477	3 US-08-281-313-1	Sequence 9, Appl
18	189	64.7	477	3 US-09-521-220-20	Sequence 20, Appl
19	189	64.7	477	3 US-09-391-104-21	Sequence 21, Appl
20	163	55.8	471	3 US-09-391-104-25	Sequence 25, Appl
21	163	55.8	513	4 US-10-140-002-192	Sequence 192, App
22	163	55.8	513	4 US-08-662-631-4	Sequence 4, Appl
23	159	54.5	470	3 US-08-862-392-2	Sequence 2, Appl
24	159	54.5	470	3 US-08-396-988-2	Sequence 2, Appl
25	159	54.5	470	3 US-09-391-104-26	Sequence 26, Appl
26	134	52.7	471	4 US-08-394-689C-1	Sequence 1, Appl
27	151	51.7	264	3 US-09-009-156-6	Sequence 6, Appl

28	151	51.7	264	3 US-09-372-154-6	Sequence 6, Appl
29	151	51.7	267	3 US-08-448-489-18	Sequence 18, Appl
30	151	51.7	267	3 US-08-391-104-27	Sequence 27, Appl
31	151	51.7	271	3 US-08-896-062-2	Sequence 2, Appl
32	150	51.4	135	4 US-09-513-999C-4163	Sequence 21, Appl
33	147	50.3	471	4 US-08-994-689C-21	Sequence 21, Appl
34	144	49.3	462	3 US-08-068-392-3	Sequence 3, Appl
35	144	49.3	462	3 US-08-396-988-3	Sequence 3, Appl
36	144	49.3	631	3 US-08-448-489-17	Sequence 17, Appl
37	144	49.3	660	3 US-08-704-711A-18	Sequence 18, Appl
38	144	49.3	660	3 US-09-521-220-18	Sequence 18, Appl
39	144	49.3	660	3 US-09-391-104-19	Sequence 19, Appl
40	144	49.3	660	4 US-09-917-254-89	Sequence 89, Appl
41	136.5	46.7	604	3 US-09-391-104-30	Sequence 30, Appl
42	136.5	46.7	607	3 US-09-000-041A-2	Sequence 2, Appl
43	136.5	46.7	607	3 US-09-211-704A-10	Sequence 10, Appl
44	136.5	46.7	607	4 US-09-734-002-2	Sequence 2, Appl
45	134.5	46.1	582	3 US-08-704-711A-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-08-704-711A-16
; Sequence 16, Application US/08704711A
; Patent No. 6114159
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; APPLICANT: HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,711A
; FILING DATE: 20-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/DE95/00357
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 469 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-704-711A-16

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Best Local Similarity 100.0%; Pred. No. 3.8e-31;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 54
Db 67 MOEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 120

RESULT 2
US-08-448-489-12
; Sequence 12, Application US/08448489
; Patent No. 6184022
; GENERAL INFORMATION:
; APPLICANT: SEIKI, Motoharu
; APPLICANT: SATO, Hiroshi
; APPLICANT: SHINAGAWA, Akira
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
; FILE REFERENCE: 55-290P
; CURRENT APPLICATION NUMBER: US/08/448,489
; CURRENT FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 12
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Known Member of
; OTHER INFORMATION: Matrix Metalloproteinase Family
US-08-448-489-12

Query Match      100.0%; Score 292; DB 3; Length 469;
Best Local Similarity 100.0%; Pred. No. 3.8e-31;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 54
Db 67 MOEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 120

RESULT 3
US-09-521-220-16
; Sequence 16, Application US/09521220
; Patent No. 6399348
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/521,220
; FILING DATE: 08-Mar-2000
; CLASSIFICATION: <Unknown>
; 21-OCT-1994
; 17-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/704,711
; FILING DATE: <Unknown>
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```
APPLICATION NUMBER: DE 4438838.1
FILING DATE: 21-OCT-1994
APPLICATION NUMBER: DE 4409663.1
FILING DATE: 17-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 26083/124
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 469 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-521-220-16

Query Match      100.0%; Score 292; DB 3; Length 469;
Best Local Similarity 100.0%; Pred. No. 3.8e-31;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 54
Db 67 MOEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 120

RESULT 4
US-09-391-104-23
; Sequence 23, Application US/09391104
; Patent No. 6399371
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Falduto, Michael T.
; APPLICANT: Magnuson, Scott R.
; APPLICANT: Morgan, Douglas W.
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEINASE GENE,
; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
; TITLE OF INVENTION: OF USING SAME
; FILE REFERENCE: 6073.US.P1
; CURRENT APPLICATION NUMBER: US/09/391,104
; CURRENT FILING DATE: 1999-09-07
; PRIOR APPLICATION NUMBER: US 08/814,394
; PRIOR FILING DATE: 1997-03-11
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-391-104-23

Query Match      100.0%; Score 292; DB 3; Length 469;
Best Local Similarity 100.0%; Pred. No. 3.8e-31;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 54
Db 67 MOEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 120

RESULT 5
US-09-178-002-2
; Sequence 2, Application US/09178002
; Patent No. H001973
; GENERAL INFORMATION:
; APPLICANT: Hu, Shou-Ih
; TITLE OF INVENTION: Human Neutrophil Collagenase Splice Variant
; FILE REFERENCE: CGC 2048
; CURRENT APPLICATION NUMBER: US/09/178,002
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1 MOEFFGLKVTGKPDATLTKVMKPCRGVDPDVAQFVLTEGPNRWEQTHLTYYRIEN 54
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RESULT 7
US-09-521-220-17
; Sequence 17, Application US/09521220
; Patent No. 6393448
; GENERAL INFORMATION:
; APPLICANT: WILLI, Horst
; HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/521,220
; FILING DATE: 08-Mar-2000
; CLASSIFICATION: <Unknown>
; 21-OCT-1994
; 17-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/704,711
; FILING DATE: <Unknown>
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 466 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-521-220-17
Query Match 73.3%; Score 214; DB 3; Length 466;
Best Local Similarity 70.4%; Pred. No. 1.3e-20;
Matches 38; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
CY 1 MQEFFGLKVTGKPDATLTKVMKPCRGVDPDVAQFVLTEGPNRWEQTHLTYYRIEN 54
DB 66 MORFFGLNVTGRNPEETLDMMKKPCRGVDPDGGFMLTTPGNPKWERTNLTYYRIEN 119

RESULT 8
US-09-178-002-4
; Sequence 4, Application US/09178002
; Patent No. H001973
; GENERAL INFORMATION:
; APPLICANT: Hu, Shou-Ih


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RESULT 12
US-08-448-489-14
; Sequence 14, Application US/08448489
; Patent No. 6184022
; GENERAL INFORMATION:
; APPLICANT: SEIKI, Motoharu
; APPLICANT: SATO, Hiroshi
; APPLICANT: SHINAGAWA, Akira
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
; FILE REFERENCE: 55-290P
; CURRENT APPLICATION NUMBER: US/08/448,489
; CURRENT FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Known Member of
; OTHER INFORMATION: Matrix Metalloproteinase Family
US-08-448-489-14

Query Match          64.7%; Score 189; DB 3; Length 476;
Best Local Similarity 63.0%; Pred. No. 3.2e-17;
Matches 34; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

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Db 66 MQKFLGLEVTGKLDTDLEVMRKPCGVDPDVGHFSSFGMPKWKTKHLYRIYN 119

RESULT 13
US-09-521-220-21
; Sequence 21, Application US/09521220
; Patent No. 6399348
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/521,220
; FILING DATE: 08-Mar-2000
; CLASSIFICATION: <Unknown>
; 21-OCT-1994
; 17-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/704,711
; FILING DATE: <Unknown>
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124

US-08-448-489-14
; Sequence 14, Application US/08448489
; Patent No. 6184022
; GENERAL INFORMATION:
; APPLICANT: SEIKI, Motoharu
; APPLICANT: SATO, Hiroshi
; APPLICANT: SHINAGAWA, Akira
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
; FILE REFERENCE: 55-290P
; CURRENT APPLICATION NUMBER: US/08/448,489
; CURRENT FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Known Member of
; OTHER INFORMATION: Matrix Metalloproteinase Family
US-08-448-489-14

Query Match          64.7%; Score 189; DB 3; Length 476;
Best Local Similarity 63.0%; Pred. No. 3.2e-17;
Matches 34; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

Qy 1 MQEFFGLKVTGKPDATLTKVMKQPCGVDPDVAQFVLTGPNRWEQTHLYRIEN 54
|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db 66 MQKFLGLEVTGKLDTDLEVMRKPCGVDPDVGHFSSFGMPKWKTKHLYRIYN 119

RESULT 14
US-09-391-104-22
; Sequence 22, Application US/09391104
; Patent No. 6399371
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Falduto, Michael T.
; APPLICANT: Magnuson, Scott R.
; APPLICANT: Morgan, Douglas W.
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEINASE GENE,
; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
; TITLE OF INVENTION: OF USING SAME
; FILE REFERENCE: 6073 US.P1
; CURRENT APPLICATION NUMBER: US/09/391,104
; CURRENT FILING DATE: 1999-09-07
; PRIOR APPLICATION NUMBER: US 08/814,394
; PRIOR FILING DATE: 1997-03-11
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-391-104-22

Query Match          64.7%; Score 189; DB 3; Length 476;
Best Local Similarity 63.0%; Pred. No. 3.2e-17;
Matches 34; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

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RESULT 15
US-08-704-711A-20
; Sequence 20, Application US/08704711A
; Patent No. 6114159
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; APPLICANT: HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
```

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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-521-220-21

Query Match          64.7%; Score 189; DB 3; Length 476;
Best Local Similarity 63.0%; Pred. No. 3.2e-17;
Matches 34; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

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RESULT 14
US-09-391-104-22
; Sequence 22, Application US/09391104
; Patent No. 6399371
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Falduto, Michael T.
; APPLICANT: Magnuson, Scott R.
; APPLICANT: Morgan, Douglas W.
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEINASE GENE,
; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
; TITLE OF INVENTION: OF USING SAME
; FILE REFERENCE: 6073 US.P1
; CURRENT APPLICATION NUMBER: US/09/391,104
; CURRENT FILING DATE: 1999-09-07
; PRIOR APPLICATION NUMBER: US 08/814,394
; PRIOR FILING DATE: 1997-03-11
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-391-104-22

Query Match          64.7%; Score 189; DB 3; Length 476;
Best Local Similarity 63.0%; Pred. No. 3.2e-17;
Matches 34; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

Qy 1 MQEFFGLKVTGKPDATLTKVMKQPCGVDPDVAQFVLTGPNRWEQTHLYRIEN 54
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Db 66 MQKFLGLEVTGKLDTDLEVMRKPCGVDPDVGHFSSFGMPKWKTKHLYRIYN 119

RESULT 15
US-08-704-711A-20
; Sequence 20, Application US/08704711A
; Patent No. 6114159
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; APPLICANT: HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/704,711A
FILING DATE: 20-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/DE95/00357
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4438838.1
FILING DATE: 21-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4409663.1
FILING DATE: 17-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 26083/124
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 477 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-704-711A-20

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Query Match      64.7%; Score 189; DB 3; Length 477;
Best Local Similarity 63.0%; Pred. No. 3.2e-17;
Matches 34; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

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QY      1 MQEFTGLKVTGKPDATLTKVMKQPCRCGVDPVDAQFVLTEGNPRWEOHTLTYPRIEN 54
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Search completed: November 15, 2004, 14:08:07
Job time : 14.5385 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 15, 2004, 14:06:45 ; Search time 139.846 Seconds
(without alignments)
136.623 Million cell updates/sec

Title: US-10-032-376A-9

Perfect score: 292
Sequence: 1 MQEFFGLKVTGKPDATLKV.VLTEGNPRWEQTHLTYRIEN 54

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1568699 seqs, 353819137 residues

Total number of hits satisfying chosen parameters: 1077212

Minimum DB seq length: 47

Maximum DB seq length: 660

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 su

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query #		DB	ID	Description
		Match	Length			
1	292	100.0	54	14	US-10-219-329-9	Sequence 9, Appli
2	292	100.0	54	14	US-10-153-185-9	Sequence 9, Appli
3	292	100.0	54	14	US-10-219-561-9	Sequence 9, Appli
4	292	100.0	54	16	US-10-032-376A-9	Sequence 9, Appli
5	292	100.0	54	16	US-10-335-207-9	Sequence 9, Appli
6	292	100.0	454	15	US-10-115-479-32	Sequence 32, Appl
7	292	100.0	454	15	US-10-115-479-34	Sequence 34, Appl
8	292	100.0	454	15	US-10-115-479-36	Sequence 36, Appl
9	292	100.0	454	15	US-10-115-479-38	Sequence 38, Appl
10	292	100.0	469	9	US-09-391-104-23	Sequence 23, Appl
11	292	100.0	469	9	US-09-801-196-19	Sequence 19, Appl
12	292	100.0	469	9	US-09-853-386-100	Sequence 100, App
13	292	100.0	469	14	US-10-301-822-119	Sequence 119, App

14	292	100.0	469	14	US-10-021-560-76	Sequence 76, Appl
15	292	100.0	469	14	US-10-308-279-34	Sequence 34, Appl
16	292	100.0	469	14	US-10-131-985-23	Sequence 23, Appl
17	292	100.0	469	14	US-10-295-027-12	Sequence 12, Appl
18	292	100.0	469	14	US-10-295-027-14	Sequence 14, Appl
19	292	100.0	469	14	US-10-295-027-1167	Sequence 1167, Ap
20	292	100.0	469	14	US-10-295-027-1168	Sequence 1168, Ap
21	292	100.0	469	15	US-10-115-479-30	Sequence 30, Appl
22	292	100.0	469	15	US-10-115-479-40	Sequence 40, Appl
23	292	100.0	469	15	US-10-211-462-22	Sequence 22, Appl
24	292	100.0	469	15	US-10-188-832-6	Sequence 6, Appl
25	292	100.0	469	16	US-10-734-564-109	Sequence 109, App
26	292	100.0	470	15	US-10-447-315-1	Sequence 1, Appl
27	292	100.0	496	14	US-10-106-698-6283	Sequence 6283, Ap
28	214	73.3	55	14	US-10-219-329-10	Sequence 10, Appl
29	214	73.3	55	14	US-10-153-185-10	Sequence 10, Appl
30	214	73.3	55	14	US-10-219-561-10	Sequence 10, Appl
31	214	73.3	55	16	US-10-032-376A-10	Sequence 10, Appl
32	214	73.3	55	16	US-10-335-207-10	Sequence 10, Appl
33	214	73.3	467	9	US-09-391-104-24	Sequence 24, Appl
34	214	73.3	467	9	US-09-801-196-20	Sequence 20, Appl
35	214	73.3	467	10	US-09-759-1308-176	Sequence 176, App
36	214	73.3	467	14	US-10-131-985-31	Sequence 31, Appl
37	214	73.3	467	16	US-10-741-790-176	Sequence 176, App
38	200.5	68.7	267	14	US-10-133-797-73	Sequence 73, Appl
39	191	55.4	173	15	US-10-115-479-48	Sequence 48, Appl
40	190.5	65.2	325	15	US-10-115-479-78	Sequence 78, Appl
41	189	64.7	54	14	US-10-219-329-5	Sequence 5, Appl
42	189	64.7	54	14	US-10-153-185-5	Sequence 5, Appl
43	189	64.7	54	14	US-10-219-561-5	Sequence 5, Appl
44	189	64.7	54	16	US-10-032-376A-5	Sequence 5, Appl
45	189	64.7	54	16	US-10-335-207-5	Sequence 5, Appl

ALIGNMENTS

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RESULT 1
US-10-219-329-9
; Sequence 9, Application US/10219329
; Publication No. US20030096757A1
; GENERAL INFORMATION:
; APPLICANT: Quirk, Stephen
; APPLICANT: Weart, Ilona f.
; TITLE OF INVENTION: Anti-Cancer and Wound Healing Compounds
; FILE REFERENCE: 1443.035WO1
; CURRENT APPLICATION NUMBER: US/10/219,329
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-219-329-9

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; GENERAL INFORMATION:
; APPLICANT: Quirk, Stephen
; APPLICANT: Malik, Sohail
; TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds
; FILE REFERENCE: 1443.034US1
; CURRENT APPLICATION NUMBER: US/10/153,185
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-185-9

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; Sequence 9, Application US/10219561
; Publication No. US20030166567A1
; GENERAL INFORMATION:
; APPLICANT: Quirk, Stephen
; APPLICANT: Malik, Sohail
; TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds
; FILE REFERENCE: 1443.008US2
; CURRENT APPLICATION NUMBER: US/10/219,561
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 10/153,185
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-219-561-9

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Best Local Similarity 100.0%; Pred. No. 4.4e-30;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MOEFFGLKVTGKPDATLTKVMKQPRCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54

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; Sequence 9, Application US/10032376A
; Publication No. US20040127420A1
; GENERAL INFORMATION:
; APPLICANT: Quirk, Steven
; TITLE OF INVENTION: Metalloproteinase Inhibitors for Wound Healing
; FILE REFERENCE: 1443.008US1
; CURRENT APPLICATION NUMBER: US/10/032,376A
; CURRENT FILING DATE: 2001-12-21
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; PRIOR APPLICATION NUMBER: 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-376A-9

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; Publication No. US20040127421A1
; GENERAL INFORMATION:
; APPLICANT: Malik, Sohail
; APPLICANT: Quirk, Stephen
; TITLE OF INVENTION: Method to Increase Fibronectin
; FILE REFERENCE: 1443.047US1
; CURRENT APPLICATION NUMBER: US/10/335,207
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-335-207-9

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RESULT 6
US-10-115-479-32
; Sequence 32, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glenda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera
```


APPLICANT: Burgess, Catherine E.
APPLICANT: Malyanker, Uriel M.
APPLICANT: Shimkets, Richard A.
APPLICANT: Taupier, Raymond J.
APPLICANT: Edinger, Shlomit R.
APPLICANT: Mazur, Ann
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REFERENCE: 21402-322 B (Cura 622 PT)
CURRENT APPLICATION NUMBER: US/10/115,479
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: 60/281,136
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/281,863
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/281,906
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/282,934
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: 60/283,657
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/283,678
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/283,687
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/283,710
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PRIOR APPLICATION NUMBER: 60/284,234
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PRIOR APPLICATION NUMBER: 60/285,325
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LENGTH: 454
TYPE: PRT
ORGANISM: Homo sapiens
US-10-115-479-32

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US-10-115-479-34
Sequence 34, Application US/10115479
Publication No. US2004006205A1
GENERAL INFORMATION:
APPLICANT: Li, Li
APPLICANT: Gerlach, Valerie L.
APPLICANT: Liu, Xiaohong
APPLICANT: Miller, Charles E.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Zerhusen, Bryan D.
APPLICANT: Pena, Carol E.A.
APPLICANT: Zhong, Haihong
APPLICANT: Smithson, Glendda
APPLICANT: Casman, Stacie J.
APPLICANT: Boldog, Ferenc L.;
APPLICANT: Voss, Edward
APPLICANT: Vernet, Corine
APPLICANT: MacDougall, John A.
APPLICANT: Rastelli, Luca
APPLICANT: Anderson, David W.
APPLICANT: Zhong, Mei
APPLICANT: Mezes, Peter S.
APPLICANT: Furtak, Katarzyna
APPLICANT: Patturajan, Meera

APPLICANT: Burgess, Catherine E.
APPLICANT: Malyanker, Uriel M.
APPLICANT: Shimkets, Richard A.
APPLICANT: Taupier, Raymond J.
APPLICANT: Edinger, Shlomit R.
APPLICANT: Mazur, Ann
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REFERENCE: 21402-322 B (Cura 622 PT)
CURRENT APPLICATION NUMBER: US/10/115,479
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: 60/281,136
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/281,863
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/281,906
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/282,934
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: 60/283,657
PRIOR FILING DATE: 2001-04-13
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PRIOR APPLICATION NUMBER: 60/283,687
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/283,710
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/284,234
PRIOR FILING DATE: 2001-04-17
PRIOR APPLICATION NUMBER: 60/285,325
PRIOR FILING DATE: 2001-04-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 198
SEQ ID NO 34
LENGTH: 454
TYPE: PRT
ORGANISM: Homo sapiens
US-10-115-479-34

Query Match 100.0%; Score 292; DB 15; Length 454;
Best Local Similarity 100.0%; Pred. No. 5e-29;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 50 MQEFFGLKVTGKPDASTLKVWKQRCGVPDVAQFVLTEGNPRWEQHLTYRIEN 103

RESULT 8
US-10-115-479-36
Sequence 36, Application US/10115479
Publication No. US2004006205A1
GENERAL INFORMATION:
APPLICANT: Li, Li
APPLICANT: Gerlach, Valerie L.
APPLICANT: Liu, Xiaohong
APPLICANT: Miller, Charles E.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Zerhusen, Bryan D.
APPLICANT: Pena, Carol E.A.
APPLICANT: Zhong, Haihong
APPLICANT: Smithson, Glendda
APPLICANT: Casman, Stacie J.
APPLICANT: Boldog, Ferenc L.;
APPLICANT: Voss, Edward
APPLICANT: Vernet, Corine
APPLICANT: MacDougall, John A.
APPLICANT: Rastelli, Luca
APPLICANT: Anderson, David W.
APPLICANT: Zhong, Mei
APPLICANT: Mezes, Peter S.
APPLICANT: Furtak, Katarzyna
APPLICANT: Patturajan, Meera

APPLICANT: Burgess, Catherine E.
APPLICANT: Malyanker, Uriel M.
APPLICANT: Shimkets, Richard A.
APPLICANT: Taupier, Raymond J.
APPLICANT: Edinger, Shlomit R.
APPLICANT: Mazur, Ann

TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REFERENCE: 21402-322 B (Cura 622 PT)
CURRENT APPLICATION NUMBER: US/10/115,479
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: 60/281,136
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/281,863
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/281,906
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/282,934
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: 60/283,657
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/283,678
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/283,687
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/283,710
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/284,234
PRIOR FILING DATE: 2001-04-17
PRIOR APPLICATION NUMBER: 60/285,325
PRIOR FILING DATE: 2001-04-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 198
SEQ ID NO 36
LENGTH: 454
TYPE: PRT
ORGANISM: Homo sapiens
US-10-115-479-36

Query Match 100.0%; Score 292; DB 15; Length 454;
Best Local Similarity 100.0%; Pred. No. 5e-29;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQEFFGLKVTGKPDATLTKMKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 54
DB 50 MQEFFGLKVTGKPDATLTKMKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 103

RESULT 9

US-10-115-479-38
Sequence 38, Application US/10115479
Publication No. US2004006205A1
GENERAL INFORMATION:
APPLICANT: Li, Li
APPLICANT: Gerlach, Valerie L.
APPLICANT: Liu, Xiaohong
APPLICANT: Miller, Charles E.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Zerhusen, Bryan D.
APPLICANT: Pena, Carol E.A.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Zhong, Haihong
APPLICANT: Smithson, Glenda
APPLICANT: Casman, Stacie J.
APPLICANT: Boldog, Ferenc L.;
APPLICANT: Voss, Edward
APPLICANT: Vernet, Corine
APPLICANT: MacDougall, John A.
APPLICANT: Rastelli, Luca
APPLICANT: Anderson, David W.
APPLICANT: Zhong, Mei
APPLICANT: Mezes, Peter S.
APPLICANT: Furtak, Katarzyna
APPLICANT: Patturajan, Meera

APPLICANT: Burgess, Catherine E.
APPLICANT: Malyanker, Uriel M.
APPLICANT: Shimkets, Richard A.
APPLICANT: Taupier, Raymond J.
APPLICANT: Edinger, Shlomit R.
APPLICANT: Mazur, Ann

TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REFERENCE: 21402-322 B (Cura 622 PT)
CURRENT APPLICATION NUMBER: US/10/115,479
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: 60/281,136
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/281,863
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/281,906
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/282,934
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: 60/283,657
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/283,678
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/283,687
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/283,710
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/284,234
PRIOR FILING DATE: 2001-04-17
PRIOR APPLICATION NUMBER: 60/285,325
PRIOR FILING DATE: 2001-04-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 198
SEQ ID NO 38
LENGTH: 454
TYPE: PRT
ORGANISM: Homo sapiens
US-10-115-479-38

Query Match 100.0%; Score 292; DB 15; Length 454;
Best Local Similarity 100.0%; Pred. No. 5e-29;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQEFFGLKVTGKPDATLTKMKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 54
DB 50 MQEFFGLKVTGKPDATLTKMKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 103

RESULT 10

US-09-391-104-23
Sequence 23, Application US/09391104
Publication No. US20020031817A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Falduto, Michael T.
APPLICANT: Magnuson, Scott R.
APPLICANT: Morgan, Douglas W.
TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,
TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
FILE REFERENCE: 6073.US.P1
CURRENT APPLICATION NUMBER: US/09/391,104
CURRENT FILING DATE: 1999-09-07
PRIOR APPLICATION NUMBER: US 08/814,394
PRIOR FILING DATE: 1997-03-11
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 23
LENGTH: 469
TYPE: PRT
ORGANISM: Homo sapiens
US-09-391-104-23

Query Match 100.0%; Score 292; DB 9; Length 469;

Best Local Similarity 100.0%; Pred. No. 5.2e-29;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOEFFGLKVTGKPDATLKVWKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54
|||||
Db 67 MOEFFGLKVTGKPDATLKVWKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 120
|||||

RESULT 11
US-09-801-196-19
; Sequence 19, Application US/09801196
; Patent No. US20020037827A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Kai
; APPLICANT: Smith, Ryan
; APPLICANT: Fajardo, Mark
; APPLICANT: Moss, Patrick
; TITLE OF INVENTION: A NOVEL MATRIX METALLOPROTEINASE (MMP-25)
; FILE REFERENCE: 240083.509
; CURRENT APPLICATION NUMBER: US/09/801,196
; PRIOR FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-801-196-19

Query Match 100.0%; Score 292; DB 9; Length 469;
Best Local Similarity 100.0%; Pred. No. 5.2e-29;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOEFFGLKVTGKPDATLKVWKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54
|||||
Db 67 MOEFFGLKVTGKPDATLKVWKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 120
|||||

RESULT 12
US-09-853-386-100
; Sequence 100, Application US/09853386
; Patent No. US20020049151A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Evelyn
; APPLICANT: Bresnahan, Barry
; APPLICANT: Conneely, Orla
; APPLICANT: Fitzgerald, Oliver
; TITLE OF INVENTION: Therapeutic Approaches to Diseases by Suppression of the NURR
; FILE REFERENCE: P01972US1
; CURRENT APPLICATION NUMBER: US/09/853,386
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/203645
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 100
; LENGTH: 469
; TYPE: PRT
; ORGANISM: HUMAN
US-09-853-386-100

Query Match 100.0%; Score 292; DB 9; Length 469;
Best Local Similarity 100.0%; Pred. No. 5.2e-29;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOEFFGLKVTGKPDATLKVWKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54
|||||
Db 67 MOEFFGLKVTGKPDATLKVWKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 120
|||||

RESULT 13

US-10-301-822-119
; Sequence 119, Application US/10301822
; Publication No. US20030148410A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MEM01-029P2RNM
; CURRENT APPLICATION NUMBER: US/10/301,822
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/351,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 119
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-301-822-119

Query Match 100.0%; Score 292; DB 14; Length 469;
Best Local Similarity 100.0%; Pred. No. 5.2e-29;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOEFFGLKVTGKPDATLKVWKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54
|||||
Db 67 MOEFFGLKVTGKPDATLKVWKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 120
|||||

RESULT 14
US-10-021-660-76
; Sequence 76, Application US/10021660
; Publication No. US20030152926A1
; GENERAL INFORMATION:
; APPLICANT: Murray, Richard
; APPLICANT: Glynn, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: EOS Biotechnology, Inc.
; TITLE OF INVENTION: No. US20030152926A1el Methods of Diagnosis of Angiogenesis,
; TITLE OF INVENTION: Compositions and Methods of Screening for Angiogenesis
; TITLE OF INVENTION: Modulators
; FILE REFERENCE: 018501-000710US
; CURRENT APPLICATION NUMBER: US/10/021,660
; CURRENT FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US/09/784,356
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/637,977
; PRIOR FILING DATE: 2000-08-11
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 76
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-021-660-76

Query Match 100.0%; Score 292; DB 14; Length 469;
Best Local Similarity 100.0%; Pred. No. 5.2e-29;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOEFFGLKVTGKPDATLKVWKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54
|||||

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Db      67 MQEFFGLKVTGKPDATLTKVMKQPRCGVPDVAQFVLTEGNPRWEQTHLTYYRIEN 120
|||||
RESULT 15
US-10-308-279-34
; Sequence 34, Application US/10308279
; Publication No. US20030170742A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE DEVELOPMENT
; FILE OF INVENTION: RHEUMATOID ARTHRITIS
; FILE REFERENCE: D0190 NP
; CURRENT APPLICATION NUMBER: US/10/308,279
; CURRENT FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: 60/337,429
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 469
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-308-279-34

Query Match      100.0%; Score 292; DB 14; Length 469;
Best Local Similarity 100.0%; Pred No. 5.2e-29;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MQEFFGLKVTGKPDATLTKVMKQPRCGVPDVAQFVLTEGNPRWEQTHLTYYRIEN 54
|||||
Db      67 MQEFFGLKVTGKPDATLTKVMKQPRCGVPDVAQFVLTEGNPRWEQTHLTYYRIEN 120
|||||

Search completed: November 15, 2004, 14:22:34
Job time : 139.846 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 15, 2004, 14:01:35 ; Search time 12.1154 Seconds
(without alignments)
428.852 Million cell updates/sec

Title: US-10-032-376A-9
Perfect score: 292
Sequence: 1 MQEPFGLKVTGKPAETLKV.....VLTEGNRWEOHTLTYRIEN 54

Scoring table: BLOSUM62
Gapcp 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 246014

Minimum DB seq length: 47
Maximum DB seq length: 660

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:.*
1: Pir1:.*
2: Pir2:.*
3: Pir3:.*
4: Pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	292	100.0	469	1 KCHUI	interstitial colla
2	283	96.9	469	1 KCRBI	interstitial colla
3	270	92.5	469	1 KCPGI	interstitial colla
4	234	80.1	469	1 KCBPI	interstitial colla
5	231.5	79.3	384	2 I51267	collagenase [EC 3.1.1.1]
6	214	73.3	467	1 KCHUN	neutrophil collage
7	189	64.7	476	1 KCHUS2	stromelysin 2 (EC 3.4.21.2)
8	189	64.7	476	1 KCRBS1	stromelysin 1 (EC 3.4.21.2)
9	186	63.7	478	1 KCRBS1	stromelysin 1 (EC 3.4.21.2)
10	173	59.2	476	1 JC6505	stromelysin 2 (EC 3.4.21.2)
11	173	59.2	477	1 KCMSS1	stromelysin 1 (EC 3.4.21.2)
12	172	58.9	475	1 KCRTH	stromelysin 1 (EC 3.4.21.2)
13	172	58.9	483	2 JC5743	matrix metallopro
14	168	57.5	472	2 S23243	interstitial colla
15	167	57.2	476	1 KCRTS2	collagenase 3 (EC 3.4.21.2)
16	163	55.8	471	2 A53711	collagenase 3 (EC 3.4.21.2)
17	152	55.5	466	2 A23685	interstitial colla
18	153	54.5	470	2 A43499	matrix metallopro
19	155	53.1	267	2 A57490	macrophage elast
20	151	51.7	267	1 KCHUM	gelatinase A (EC 3.4.21.2)
21	144	49.3	462	2 A42401	gelatinase A (EC 3.4.21.2)
22	144	49.3	660	1 A28153	matrix metallopro
23	134.5	46.1	582	2 I38028	matrix metallopro
24	126.5	43.3	582	2 I84471	matrix metallopro
25	124	42.5	82	2 PW0052	matrix metallopro
26	118.5	40.6	582	2 I48673	matrix metallopro
27	111	38.0	364	2 E71433	probable metallopro
28	108	37.0	341	2 T51957	metalloproteinase
29	108	37.0	342	2 G84885	probable metallopro

RESULT 1

KCHUI

interstitial collagenase (EC 3.4.24.7) precursor [validated] - human
N:Alternate names: fibroblast collagenase; matrix metalloproteinase 1 (MMP1); tissue col
C:Species: Homo sapiens (man)
C:Date: 13-Aug-1986 #sequence revision 30-Sep-1992 #text change 09-Jul-2004
C:Accession: A37308, S22766; I57620; A00996; D29157; A44518; S06130; B60964; S10595; S5:
R:Templeton, N.S.; Brown, P.D.; Levy, A.T.; Margulies, I.M.K.; Liotta, L.A.; Stetler-St
Cancer Res. 50, 5431-5437, 1990
A:Title: Cloning and characterization of human tumor cell interstitial collagenase.
A:Reference number: A37308; MUID:90352587; PMID:2167156
A:Accession: A37308
A:Molecule type: mRNA
A:Residues: 1-469 <TEM>
A:Cross-references: UNIPROT:P03956; GB:X54925; NID:G30125; PIDN:CAA38691.1; PID:G30126
R:Brinckerhoff, C.E.; Ruby, P.L.; Austin, S.D.; Fini, M.E.; White, H.D.
J. Clin. Invest. 79, 543-546, 1987
A:Title: Molecular cloning of human synovial cell collagenase and selection of a single
A:Reference number: S22766; MUID:87109799; PMID:3027129
A:Accession: S22766
A:Molecule type: DNA
A:Residues: 1-63,65-70 <BRI>
A:Cross-references: EMBL:M15996; NID:G180666; PIDN:AAA35700.1; PID:G180667
R:Angel, P.; Baumann, I.; Stein, B.; Dellus, H.; Rahmsdorf, H.J.; Herrlich, P.
Mol. Cell. Biol. 7, 2256-2266, 1987
A:Title: 12-O-tetradecanoyl-phorbol-13-acetate induction of the human collagenase gene
A:Reference number: I57620; MUID:87257941; PMID:3037355
A:Accession: I57620
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-35 <RES>
A:Cross-references: GB:M16567; NID:G180668; PIDN:AAA52033.1; PID:G180669
R:Goldberg, G.I.; Wilhelm, S.M.; Kronberger, A.; Bauer, E.A.; Grant, G.A.; Eisen, A.Z.
J. Biol. Chem. 261, 6600-6605, 1986
A:Title: Human fibroblast collagenase. Complete primary structure and homology to an on
A:Reference number: A00996; MUID:86196089; PMID:3009463
A:Accession: A00996
A:Molecule type: mRNA
A:Residues: 1-114, 'R', 116-409, 'S', 411-469 <GOL>
A:Cross-references: GB:M13509; NID:G180664; PIDN:AAA35699.1; PID:G180665
A:Note: part of this sequence was confirmed by protein sequencing of the proenzyme
R:Whitham, S.E.; Murphy, G.; Angel, P.; Rahmsdorf, H.J.; Smith, B.J.; Lyons, A.; Harris
Biochem. J. 240, 913-916, 1986
A:Title: Comparison of human stromelysin and collagenase by cloning and sequence analysis
A:Reference number: A90336; MUID:87156645; PMID:3030290
A:Accession: D29157
A:Molecule type: mRNA
A:Residues: 1-199, 'H', 201-207, 'T', 209-469 <WHI>
A:Cross-references: EMBL:X05231; NID:G38266; PIDN:CAA38858.1; PID:G38267
A:Note: parts of this sequence, including the amino end of the proenzyme and of the mat
R:Birkedal-Hansen, B.; Moore, W.G.I.; Taylor, R.E.; Brown, A.S.; Birkedal-Hansen, H.
Biochemistry 27, 6751-6758, 1988

ALIGNMENTS

30	106.5	36.5	305	2	T08836
31	103.5	35.4	579	2	T32448
32	103.5	35.4	598	2	T32166
33	100	34.2	521	2	T37252
34	92.5	31.7	587	2	S12805
35	92	31.5	508	2	JCS082
36	91	31.2	488	2	S13423
37	89.5	30.7	378	2	E96724
38	85.5	29.3	477	1	I51645
39	85.5	29.3	587	2	S41409
40	83	28.4	616	2	JC7776
41	82	28.1	492	2	A44399
42	80	27.4	377	2	T00643
43	79	27.1	491	2	JC6197
44	69.5	23.8	170	2	T17286
45	61	20.9	478	2	T32825

C:Species: Sus scrofa domestica (domestic pig)
C>Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
C:Accession: S15986; S15997
R:Richards, C.D.; Rafferty, J.A.; Reynolds, J.J.; Saklatvala, J.
Matrix 11, 161-167, 1991
A:Title: Porcine collagenase from synovial fibroblasts: cDNA sequence and modulation of
A:Reference number: S15986; MUID:91333421; PMID:1651440
A:Accession: S15986
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-469 <NC>
A:Cross-references: UNIPROT:P21692
A>Note: Part of the sequence, including the amino end of the proenzyme, was confirmed by
R:Clarke, N.J.; O'Hare, M.C.; Cawston, T.E.; Harper, G.P.
Nucleic Acids Res. 18, 6703, 1990
A:Title: Nucleotide sequence of a cDNA for porcine type I collagenase, obtained by PCR.
A:Reference number: S15997; MUID:91067477; PMID:2174547
A:Accession: S15997
A:Molecule type: mRNA
A:Residues: 25-469 <CLA>
A:Cross-references: EMBL:X54724; NID:g2016; PIDN:CAA38526.1; PID:g930269
submitted to the Brookhaven Protein Data Bank, April 1995
A:Reference number: A65568; PDB:1FBL
R:Li, J.; Brick, P.; Blow, D.M.
A:Contents: annotation; X-ray crystallography, 2.5 angstroms, residues 100-466
C:Comment: Procollagenase can be activated without removal of the activation peptide. S
tion peptide by other proteinases.
C:Comment: Procollagenase is found in glycosylated and unglycosylated forms, both of whi
C:Function:
A:Description: hydrolyzes collagens, in particular types I, II, III, and X, serpins, and
A>Note: also hydrolyzes type X collagen, serpins, and alpha-macroglobulins
C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprote
C:Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-469/Product: procollagenase #status predicted <PRO>
F:60-261/Domain: activation peptide #status experimental <ACT>
F:100-469/Product: matrix metalloproteinase homology <MMP>
F:100-469/Product: interstitial collagenase #status predicted <MAT>
F:272-466/Domain: hemopexin repeat homology <PXN>
F:92,218,222,228/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
F:120,143/Binding site: carboxylate (Asn) (covalent) #status predicted
F:218,222,228/Binding site: zinc, catalytic (His) (active) #status experimental
F:219/Active site: Glu #status predicted
F:278-466/Disulfide bonds: #status experimental

Query Match 92.5%; Score 270; DB 1; Length 469;
Best Local Similarity 90.7%; Pred. No. 1.5e-25;
Matches 49; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MQEFFGLKVTGKPDATLTKVMKQRCGVPDVAQFVLTEGPRWEQTHLYRIEN 54
DB 67 MQOFFGLKVTGKPDATLTKVMKQRCGVPDVAQFVLTEGPRWEQTHLYRIEN 120

RESULT 4
KCBOI
Interstitial collagenase (EC 3.4.24.7) precursor - bovine
N/Alternate names: fibroblast collagenase; matrix metalloproteinase 1 (MMP1); tissue col
C:Species: Bos primigenius taurus (cattle)
C>Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
C:Accession: S14654; S20336; S14655
R:Tamura, M.; Shimokawa, H.; Sasaki, S.
submitted to the EMBL Data Library, March 1991
A:Reference number: S14654
A:Accession: S14654
A:Molecule type: mRNA
A:Residues: 1-469 <TAM>
A:Cross-references: UNIPROT:P28053; EMBL:X58256; NID:g259; PIDN:CAA41210.1; PID:g260
R:Sudbeck, B.D.; Jeffrey, J.J.; Welgus, H.G.; Mecham, R.P.; McCourt, D.; Parks, W.C.
Arch. Biochem. Biophys. 293, 370-376, 1992
A:Title: Purification and characterization of bovine interstitial collagenase and tissue
A:Reference number: S20336; MUID:92161820; PMID:1311165
A:Accession: S20336

A:Molecule type: protein
A:Residues: 19-21, 'PP', 24-29, 'L', 31-34, 'LL', 37-39, 'F', 86-105, 'NPR', 109-112, 'D', 114-125
C:Comment: This enzyme cleaves collagens of types I, II, and III at a Gly-Ile site in the
C:Comment: Procollagenase can be activated without removal of the activation peptide. S
tion peptide by other proteinases.
C:Comment: Procollagenase is found in glycosylated and unglycosylated forms, both of wh
C:Function:
A:Description: hydrolyzes collagens, in particular types I, II, III, and X, serpins, and
C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprote
C:Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-469/Product: procollagenase #status predicted <PRO>
F:19-99/Domain: activation peptide #status predicted <ACT>
F:60-261/Domain: matrix metalloproteinase homology <MMP>
F:90-97/Region: autoinhibitory
F:100-469/Product: interstitial collagenase #status predicted <MAT>
F:272-466/Domain: hemopexin repeat homology <PXN>
F:92,218,222,228/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
F:120,143/Binding site: carboxylate (Asn) (covalent) #status predicted
F:218,222,228/Binding site: zinc, catalytic (His) (active) #status predicted
F:219/Active site: Glu #status predicted
F:278-466/Disulfide bonds: #status predicted

Query Match 80.1%; Score 234; DB 1; Length 469;
Best Local Similarity 81.5%; Pred. No. 4.2e-21;
Matches 44; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 MQEFFGLKVTGKPDATLTKVMKQRCGVPDVAQFVLTEGPRWEQTHLYRIEN 54
DB 67 MQOFFGLKVTGKPDATLTKVMKQRCGVPDVAQFVLTEGPRWEQTHLYRIEN 120

RESULT 5
151267
collagenase (EC 3.4.24.-) - bullfrog
C:Species: Rana catesbeiana (bullfrog)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: 151267
R:Oofusa, K.; Yomori, S.; Yoshizato, K.
Int. J. Dev. Biol. 38, 345-350, 1994
A:Title: Regionally and hormonally regulated expression of genes of collagen and collag
A:Reference number: 151267; MUID:95071832; PMID:7991043
A:Accession: 151267
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-384 <OOF>
A:Cross-references: UNIPROT:Q11133; GB:S75623; NID:g913070; PIDN:AAB32661.1; PID:g91307
C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprote
C:Keywords: hydrolase; metalloproteinase; zinc; zymogen
F:53-231/Domain: matrix metalloproteinase homology <MMP>
F:236-381/Domain: hemopexin repeat homology <PXN>
F:181,189,193,199/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
F:189,193,199/Binding site: zinc, catalytic (His) (active) #status predicted
F:190/Active site: Glu #status predicted

Query Match 79.3%; Score 231.5; DB 2; Length 384;
Best Local Similarity 79.6%; Pred. No. 6.9e-21;
Matches 43; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

QY 1 MQEFFGLKVTGKPDATLTKVMKQRCGVPDVAQFVLTEGPRWEQTHLYRIEN 54
DB 57 LKQFFGLKVTGKPDATLTKVMKQRCGVPDVAQFVLTEGPRWEQTHLYRIEN 109

RESULT 6
KCHUN
Neutrophil collagenase (EC 3.4.24.34) precursor [validated] - human
N/Alternate names: matrix metalloproteinase 8
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
C:Accession: A37073; A61175; A36230; S09680; S11026; S19576; S27225; S32527; S6
R:Hasty, K.A.; Pourmotabbed, T.F.; Goldberg, G.I.; Thompson, J.P.; Spinella, D.G.; Stev
J. Biol. Chem. 265, 11421-11424, 1990

R;Stams, T.; Spurlino, J.C.; Smith, D.L.; Wahl, R.C.; Ho, T.F.; Qoronfleh, M.W.; Banks, Nat. Struct. Biol. 1, 119-123, 1994

A:Title: Structure of human neutrophil collagenase reveals large S1' specificity pocket.

A:Reference number: A58274; MUID:95384762; PMID:7656015

A:Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 'G',106-149,'G',111-149.

C:Comment: This protein is more highly glycosylated than interstitial collagenase and is C:Genetics:

A:Gene: GDS:WMP8; CLIG1

A:Cross-references: GDB:128173; OMIM:120355

A:Map position: 11q22.2-11q22.3

C:Function:

A:Description: hydrolyzes collagen types I, II, and III at Gly-Ile sites in collagenous A:Note: cleaves type I collagen most rapidly

C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloproteinase; C:Keywords: calcium; extracellular matrix; glycoprotein; hydrolase; metalloproteinase; n F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-467/Product: procollagenase #status predicted <SIG>

F:21-100/Domain: activation peptide #status experimental <ACT>

F:59-262/Domain: matrix metalloproteinase homology <WMP>

F:89-96/Region: autoinhibitory

F:101-467/Product: neutrophil collagenase #status predicted <MAT>

F:173-464/Domain: hemopexin repeat homology <PXN>

F:54,73,112,119,204,246/Binding site: carbohydrate (Asn) #status predicted

F:73-74/Cleavage site: Asn-Val (autolytic) #status experimental

F:84-85/Cleavage site: Asp-Met (autolytic) #status experimental

F:91,217,221,227/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status F:99-100/Cleavage site: Phe-Met (autolytic) #status experimental

F:167,169,177,182,185/Binding site: zinc, noncatalytic (His, Asp, His, His) #status experime F:174,175,177,179,197,200/Binding site: calcium (Asp, Gly, Asn, Ile, Asp, Glu) #status e F:217,221,227/Binding site: zinc, catalytic (His) (active) #status experimental

F:218/Active site: Glu #status predicted

F:262-263/Cleavage site: Gly-Leu (autolytic) #status experimental

F:279-464/Disulfide bonds: #status predicted

Query Match 73.3%; Score 214; DB 1; Length 467;
Best Local Similarity 70.4%; Pred. No. 1.2e-18;
Matches 38; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 MOEFFGLKVTGKPDAAETLLKWKMGPCGVPDVAQFVLTEGNPRWEOTHLTYRIEN 54
DB 66 MORFFGLNVTGAPNSETLDMKKKPGVDPDSGGFMLTGPNGKWTNLTYYRN 119

RESULT 7

KCHUS2

stromelysin 2 (EC 3.4.24.22) precursor [validated] - human

N:Alternate names: matrix metalloproteinase 10 (MMP10); transin-2

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004

C:Accession: A28816; A47496

R:Biochem. J. 253, 187-192, 1988

A:Title: The collagenase gene family in humans consists of at least four members.

A:Reference number: A30339; MUID:86339885; PMID:2844164

A:Accession: A28816

A:Molecule type: mRNA

A:Residues: 1-476 <MUL>

A:Cross-references: UNIPROT:P09238; EMBL:X07820; NID:g36628; PID:g36629

A:Note: mRNA for this protein was detected in several human tumors

R:Windsor, L.J.; Grenett, H.; Birkedal-Hansen, B.; Bodden, M.K.; Engler, J.A.; Birkedal-J Biol. Chem. 268, 17341-17347, 1993

A:Title: Cell type-specific regulation of SL-1 and SL-2 genes. Induction of the SL-2 gene A:Reference number: A47496; MUID:93352520; PMID:8349617

A:Accession: A47496

A:Molecule type: protein

A:Residues: 17-33 <WIN>

C:Comment: This enzyme degrades various extracellular matrix proteins, including fibronectin

C:Genetics:

A:Gene: GDB:MMP10; STMY2

A:Cross-references: GDB:120392; OMIM:185260

A:Map position: 11q22.3-11q23

C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloproteinase; C:Keywords: calcium; extracellular matrix; fibroblast; hydrolase; metalloproteinase

F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-476/Product: prostromelysin 2 #status experimental <PRO>
F;17-98/Domain: activation peptide #status predicted <ACT>
F;59-263/Domain: matrix metalloproteinase homology <MMP>
F;89-96/Region: autoinhibitory
F;99-476/Product: stromelysin 2 #status predicted <MAT>
F;283-476/Domain: hemopexin repeat homology <PXN>
F;91-217,221,227/Banding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
F;91/Binding site: carboxylate (Asn) (covalent) #status predicted
F;217,221,227/Banding site: zinc, catalytic (His) (active) #status predicted
F;218/Active site: Glu #status predicted
F;289-476/Disulfide bonds: #status predicted

Query Match 64.7%; Score 189; DB 1; Length 476;
Best Local Similarity 63.0%; Pred. No. 1.6e-15;
Matches 34; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 MQEFLGKLVTPDAETLKVMPKQRCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54
DB 66 MQKFLGLEVTGKLDTDTELVMPKRCGVPDVGHFSFGMPKWKTHLYRIVN 119

RESULT 8
KCHUS1
stromelysin 1 (EC 3.4.24.17) precursor [validated] - human
A;Alternate names: angiotensin-converting enzyme; collagenase activating protein; matrix
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1992 #sequence revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: A28156; C29157; A28399; A60964; S15427
R;Saue, J.; Quinones, S.; Otani, Y.; Nagase, H.; Harris Jr., E.D.; Kurkinen, M.
J. Biol. Chem. 263, 6742-6745, 1988
A;Title: The complete primary structure of human matrix metalloproteinase-3. Identity wi
A;Reference number: A28156; MUID:88198243; PMID:3360803
A;Accession: A28156
A;Molecule type: mRNA
A;Residues: 1-44, 'E', '46-477 <SAU>
A;Cross-references: UNIPROT:P08254; GB:J03209; NID:G18618; PIDN:AAA36321.1; PID:G18619
R;Whitham, S.E.; Murphy, G.; Angel, P.; Rahmsdorf, H.J.; Smith, B.J.; Lyons, A.; Harris,
Biochem. J. 240, 913-916, 1986
A;Title: Comparison of human stromelysin and collagenase by cloning and sequence analysis
A;Reference number: A90336; MUID:87156645; PMID:3030290
A;Accession: C29157
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-477 <WHI>
A;Cross-references: EMBL:X05232; NID:G36632; PIDN:CAA28859.1; PID:G36633
R;Wilhelm, S.M.; Collier, I.E.; Kronberger, A.; Eisen, A.Z.; Marmer, B.L.; Grant, G.A.;
Proc. Natl. Acad. Sci. U.S.A. 84, 6725-6729, 1987
A;Title: Human skin fibroblast stromelysin: structure, glycosylation, substrate specific
A;Reference number: A28399; MUID:98016164; PMID:3477804
A;Accession: A28399
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-49, 'G', '51-419, 'L', '421-477 <WIL>
A;Cross-references: GB:U78045; NID:G1688257; PIDN:AA836942.1; PID:G1688259
R;Mark, M.W.; Walakowitz, L.A.; Shah, T.K.; Vamiedlesworth, J.; Cameron, P.M.; Lin, T.Y.
Connect. Tissue Res. 25, 49-65, 1990
A;Title: Production and purification of prostromelysin and procollagenase from IL-1 beta
A;Reference number: A60964; MUID:91059606; PMID:2173990
A;Accession: A60964
A;Molecule type: protein
A;Residues: 18-29;100-108 <LAR>
R;Koklitis, P.A.; Murphy, G.; Sutton, C.; Angal, S.
Biochem. J. 276, 217-221, 1991
A;Title: Purification of recombinant human prostromelysin. Studies on heat activation to
A;Reference number: S15427; MUID:91248150; PMID:2039471
A;Accession: S15427
A;Status: preliminary
A;Molecule type: protein
A;Residues: 18-23 <BIO>
R;Jinjen, H.R.; Ugwu, F.; Bini, A.; Collen, D.


```

Query Match      57.2%; Score 167; DB 1; Length 476;
Best Local Similarity 51.9%; Pred. No. 8.4e-13;
Matches 28; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY      1  MOEFGFLKVTGKDAETLKVMPGRCVGPVDAQFVLTEGPNRWEQHTLTYYRIEN 54
      ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB      67  MOKFLEGMTKGLDNTVEMMHKPRCGVPDVGGEFTFPFGPKVRKHHSYRIYVN 120

```

Search completed: November 15, 2004, 14:07:19
Job time : 13.1154 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 15, 2004, 14:01:34 ; Search time 49.8462 Seconds
(without alignments)
623.323 Million cell updates/sec

Title: US-10-032-376A-9

Perfect score: 292

Sequence: 1 MQEFFGLKVTGKPAETLKV.....VLTEGNPRWEQTHLYRIEN 54

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1606865

Minimum DB seq length: 47

Maximum DB seq length: 660

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 02:*

1: uniprot_prot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	292	100.0	469	1	MM01_HUMAN	P03956 homo sapien
2	292	100.0	469	2	AAP3520	Aap3520 homo sapi
3	293	96.9	468	1	MM01_RABIT	P13943 oryctolagus
4	279	95.5	469	1	MM01_HORSE	Q9X825 equus caball
5	270	92.5	469	1	MM01_PIG	P21692 sus scrofa
6	234	80.1	469	1	MM01_BOVIN	P28053 bos taurus
7	231.5	79.3	384	1	MM01_RANCA	Q11133 rana catesb
8	214	73.3	467	1	MM08_HUMAN	P22894 homo sapien
9	204	69.9	205	2	O810Z2	Q81022 mus musculu
10	204	69.9	463	2	Q9EPL6	Q9EPL6 mus musculu
11	204	69.9	464	2	Q9EPL5	Q9EPL5 mus musculu
12	196	67.1	466	1	MM08_RAT	O88766 rattus norv
13	189	64.7	476	1	MM10_HUMAN	P09238 homo sapien
14	189	64.7	476	2	AAP36110	Aap36110 homo sapi
15	189	64.7	477	1	MM03_HUMAN	P08254 homo sapien
16	189	64.7	477	2	AAP65676	Aap65676 homo sapi
17	189	64.7	477	2	AAP69716	Aap69716 homo sapi
18	189	64.7	478	2	Q6Y4Q5	Q6Y4Q5 canis faml
19	189	64.7	478	2	AAO63580	AAO63580 canis fam
20	186	63.7	145	2	Q9N283	Q9N283 bos taurus
21	186	63.7	393	2	Q8MI18	Q8MI18 felis silve
22	186	63.7	478	1	MM03_RABIT	P28863 oryctolagus
23	184	63.0	252	2	Q6PWQ3	Q6PWQ3 xenopus lae
24	184	63.0	252	2	AAT00547	Aat00547 xenopus l
25	184	63.0	259	2	Q7ZTI9	Q7ZTI9 xenopus lae
26	183	62.7	472	2	O93342	O93342 gallus gall
27	183	62.7	477	1	MM03_HORSE	Q28397 equus caball
28	181	62.0	466	2	Q7SYX1	Q7SYX1 xenopus lae
29	180	61.6	259	2	Q7SXT5	Q7SXT5 xenopus lae
30	179	61.3	458	2	Q6DCN8	Q6DCN8 xenopus lae
31	178	61.0	258	2	Q7S2S8	Q7S2S8 xenopus lae

RESULT 1

ID	MM01_HUMAN	STANDARD;	PRT;	469 AA.
AC	P03956; P08156;			
DT	23-OCT-1986 (Rel. 02, Created)			
DT	01-DEC-1992 (Rel. 24, Last sequence update)			
DT	01-OCT-2004 (Rel. 45, Last annotation update)			
DE	Interstitial collagenase precursor (EC 3.4.24.7) (Matrix			
DE	metalloproteinase-1) (MMP-1) (Fibroblast collagenase).			
GN	Name=MPPI; Synonyms=CLG;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
FX	MEDLINE=90352587; PubMed=2167156;			
RA	Templeton N.S., Brown P.D., Levy A.T., Margulies I.M.K., Liotta L.A.,			
RA	Stetler-Stevenson W.G.;			
RT	"Cloning and characterization of human tumor cell interstitial			
RT	collagenase.";			
RL	Cancer Res. 50:5431-5437(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
FX	MEDLINE=87156645; PubMed=3030290;			
RA	Whitham S.E., Murphy G., Angel P., Rahmsdorf H.J., Smith B., Lyons A.,			
RA	Harris T.J.R., Reynolds J.J., Herrlich P., Docherty A.J.P.;			
RT	"Comparison of human stromelysin and collagenase by cloning and			
RT	sequence analysis.";			
RL	Biochem. J. 240:913-916(1986).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
FX	MEDLINE=86196089; PubMed=3009463;			
RA	Goldberg G.I., Wilhelm S.M., Kronberger A., Bauer E.A., Grant G.A.,			
RA	Eisen A.Z.;			
RT	"Human fibroblast collagenase. Complete primary structure and homology			
RT	to an oncogene transformation-induced rat protein.";			
RL	J. Biol. Chem. 261:6600-6605(1986).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RA	Lin D., Duncan M., Allen E., Araujo R., Aparicio A., Chai A.,			
RA	Chung E., Davis K., Federspiel N., Hyman R., Kalman S., Komp C.,			
RA	Kurdi O., Lashkari D., Lew H., Namath A., Oefner P., Roberts D.,			
RA	Heller R., Davis R.W.;			
RL	Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE FROM N.A.			
FX	MEDLINE=23386257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			

32	178	61.0	259	2	Q6DF35	Q6df35 xenopus tro
33	178	61.0	481	1	MM20_BOVIN	O18767 bos taurus
34	176	60.3	465	2	Q8C209	Q8c209 mus musculu
35	176	60.3	465	2	Q8C230	Q8c230 mus musculu
36	176	60.3	465	2	AAH42742	Aah42742 mus muscu
37	176	60.3	465	2	BAC40805	Bac40805 mus muscu
38	176	60.3	471	1	MM13_RABIT	O62806 oryctolagus
39	174	59.6	167	2	Q7ZWD0	Q7zwd0 brachydanic
40	174	59.6	482	1	MM20_MOUSE	P57748 mus musculu
41	173	59.2	476	1	MM10_MOUSE	O55123 mus musculu
42	173	59.2	477	1	MM03_MOUSE	P28862 mus musculu
43	173	59.2	479	2	Q922W6	Q922w6 mus musculu
44	172	58.9	475	1	MM03_RAT	P03957 rattus norv
45	172	58.9	483	1	MM20_HUMAN	O60882 homo sapien

ALIGNMENTS

RA Stapleton M., Soares M.B., Bernaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RP SEQUENCE OF 1-35 FROM N.A.
RX MEDLINE=87257941; PubMed=3037355;
RA Angel P., Baumann I., Stein B., Delius H., Rahmsdorf H.J.,
RA Herrlich P.,
RT "12-O-tetradecanoyl-phorbol-13-acetate induction of the human
RT collagenase gene is mediated by an inducible enhancer element located
RT in the 5'-flanking region.";
RL Mol. Cell. Biol. 7:2256-2266(1987).
RN [7]
RP SEQUENCE OF 1-70 FROM N.A.
RC TISSUE-Synovial cell;
RX MEDLINE=87109799; PubMed=3027129;
RA Brinckerhoff C.E., Ruby P.L., Austin S.D., Fini M.E., White H.D.,
RT "Molecular cloning of human synovial cell collagenase and selection of
RT a single gene from genomic DNA.";
RL J. Clin. Invest. 79:542-546(1987).
RN [8]
RP SEQUENCE OF 100-112 AND 270-287.
RC TISSUE=Fibroblast;
RX MEDLINE=90104231; PubMed=2557822;
RA Clark I.M., Cawston T.E.,
RT "Fragments of human fibroblast collagenase. Purification and
RT characterization.";
RL Biochem. J. 263:201-206(1989).
RN [9]
RP SIMILARITY TO THERMOLYSIN TYPE PROTEASES.
RX MEDLINE=87194799; PubMed=3032950;
RA McKerrow J.H.,
RT "Human fibroblast collagenase contains an amino acid sequence
RT homologous to the zinc-binding site of Serratia protease.";
RL J. Biol. Chem. 262:5943-5943(1987).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 100-269.
RX MEDLINE=95384760; PubMed=7656013;
RA Borakoti N., Winkler F.K., Williams D.H., D'Arcy A., Broadhurst M.J.,
RA Brown P.A., Johnson W.H., Murray E.J.,
RT "Structure of the catalytic domain of human fibroblast collagenase
RT complexed with an inhibitor.";
RL Nat. Struct. Biol. 1:106-110(1994).
RN [11]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 102-269.
RX MEDLINE=94304829; PubMed=8031754;
RA Lovejoy B., Hassell A.M., Luther M.A., Weigl D., Jordan S.R.,
RT "Crystal structures of recombinant 19-kDa human fibroblast collagenase
RT complexed to itself.";
RL Biochemistry 33:8207-8217(1994).
RN [12]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 102-269.
RX MEDLINE=94105765; PubMed=8278810;
RA Lovejoy B., Cleasby A., Hassell A.M., Longley K., Luther M.A.,
RA Weigl D., McGeehan G., McElroy A.B., Drewry D., Lambert M.H.,
RA Jordan S.R.,
RT "Structure of the catalytic domain of fibroblast collagenase complexed
RT with an inhibitor.";
RL Science 263:375-377(1994).
RN [13]
RP X-RAY CRYSTALLOGRAPHY (1.56 ANGSTROMS) OF 101-269.

RX MEDLINE=94377426; PubMed=8090713;
RA Spurlino J.C., Smallwood A.M., Carlton D.D., Banks T.M., Vavra K.J.,
RA Johnson J.S., Cook E.R., Falvo J., Wahl R.C., Pulvino T.A., Et A.L.,
RT "1.56-A structure of mature truncated human fibroblast collagenase.";
RL Proteins 19:98-109(1994).
RN [14]
RP STRUCTURE BY NMR OF 101-269.
RX MEDLINE=98145213; PubMed=9484219;
RA Moy F.J., Chanda P.K., Cosmi S., Pisano M.R., Urbano C., Wilhelm J.,
RA Powers R.,
RT "High-resolution solution structure of the inhibitor-free catalytic
RT fragment of human fibroblast collagenase determined by
RL multidimensional NMR.";
RL Biochemistry 37:1495-1504(1998).
CC -!- FUNCTION: Cleaves collagens of types I, II, and III at one site in
CC the helical domain. Also cleaves collagens of types VII and X.
CC -!- CATALYTIC ACTIVITY: Cleaves preferentially one bond in native
CC collagen. Cleavage of the triple helix of collagen at about three-
CC quarters of the length of the molecule from the N-terminus, at
CC 775-Gly-|-Ile-776 in the alpha-1(I) chain. Cleaves synthetic
CC substrates and alpha-macroglobulins at bonds where P1' is a
CC hydrophobic residue.
CC -!- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit.
CC -!- ENZYME REGULATION: Can be activated without removal of the
CC activation peptide.
CC -!- DOMAIN: There are two distinct domains in this protein; the
CC catalytic N-terminal, and the C-terminal which is involved in
CC substrate specificity and in binding TIMP (tissue inhibitor of
CC metalloproteinases).
CC -!- PM: Undergoes autocatalytic cleavage to two major forms (22 kDa and
CC 27 kDa). A minor form (25 kDa) is the glycosylated form of the 22
CC kDa form. The 27 kDa form has no activity while the 22/25 kDa form
CC can act as activator for collagenase.
CC -!- SIMILARITY: Belongs to peptidase family M10A.
CC -!- SIMILARITY: Contains 1 hemopexin-like domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X05231; CAA28858.1; -
DR EMBL; M13509; AAA35699.1; -
DR EMBL; M16567; AAA32033.1; -
DR EMBL; U78045; AAB36941.1; -
DR EMBL; BC013875; AAH13875.1; -
DR EMBL; M15996; AAA35700.1; -
DR EMBL; X54925; CAA38691.1; -
DR PIR; A37308; KCHUI
DR PDB; 1AYK; NMR; @=101-269.
DR PDB; 1CGE; X-ray; @=102-269.
DR PDB; 1CGF; X-ray; A/B=102-263.
DR PDB; 1CGL; X-ray; A/B=101-269.
DR PDB; 1HFC; X-ray; @=101-269.
DR PDB; 2AYK; NMR; @=101-269.
DR PDB; 2TCL; X-ray; @=101-269.
DR PDB; 3AYK; NMR; A=101-269.
DR PDB; 4AYK; NMR; A=101-269.
DR MEROPS; M10.001; -
DR GlycoSuiteDB; P03956; -
DR Genew; HGNC:7155; MMP1.
DR MTM; 120353; -
DR GO; GO:0008133; F:collagenase activity; TAS.
DR GO; GO:0008270; F:zinc ion binding; TAS.
DR GO; GO:0006508; P:proteolysis and peptidolysis; TAS.
DR InterPro; IPR00585; Hemopexin.
DR InterPro; IPR006026; Peptidase M.
DR InterPro; IPR001818; Pept M10A_M12B.
DR InterPro; IPR006025; Pept M_Zn_BS.
DR InterPro; IPR009070; PGSD_Like.

DR Pfam; PF00045; Hemopexin; 4.
 DR Pfam; PF00413; Peptidase_M10; 1.

Query Match 100.0%; Score 292; DB 1; Length 469;
 Best Local Similarity 100.0%; Pred. No. 8.2e-29;
 Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQEFFGLKVTGKPDAAETLKVMKPRCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54
 |||||
 Db 67 MQEFFGLKVTGKPDAAETLKVMKPRCGVPDVAQFVLTEGNPRWEQTHLYRIEN 120

RESULT 2
 AAP35520
 ID AAP35520 PRELIMINARY; PRT; 469 AA.
 AC AAP35520;
 DT 02-MAR-2004 (T-EMBLrel. 27, Created)
 DT 02-MAR-2004 (T-EMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (T-EMBLrel. 27, Last annotation update)
 DE Matrix metalloproteinase 1 (interstitial collagenase).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kainine N., Chen X., Rolfes A., Halleck A., Hines L., Eisenstein S.,
 RA Koundinya M., Raphael J., Moreira D., Kelley T., Labaer J., Lin Y.,
 RA Phelan M., Farmer A.;
 RT "Cloning of human full-length cDNAs in BD Creator(TM) System Donor
 RT vector";
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BT006874; AAP35520.1; -;
 KW Collagen.
 SQ SEQUENCE 469 AA; 54007 MW; 4B1361DCF4C54B20 CRC64;

Query Match 100.0%; Score 292; DB 2; Length 469;
 Best Local Similarity 100.0%; Pred. No. 8.2e-29;
 Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQEFFGLKVTGKPDAAETLKVMKPRCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54
 |||||
 Db 67 MQEFFGLKVTGKPDAAETLKVMKPRCGVPDVAQFVLTEGNPRWEQTHLYRIEN 120

RESULT 3
 XM01_RABIT
 ID XM01_RABIT STANDARD; PRT; 468 AA.
 AC P13943;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Interstitial collagenase precursor (EC 3.4.24.7) (Matrix
 DE metalloproteinase-1) (MMP-1).
 GN Name=MMP1;
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Synovial cell;
 RX MEDLINE=88077876; PubMed=2825772;
 RA Fini M.E., Plucinska I.M., Mayer A.S., Gross R.H., Brinckerhoff C.E.;
 RT "A gene for rabbit synovial cell collagenase: member of a family of
 RT metalloproteinases that degrade the connective tissue matrix.";
 RL Biochemistry 26:6156-6165 (1987).
 RN [2]
 RP SEQUENCE OF 449-468 FROM N.A.
 RC STRAIN=New Zealand white;
 RX MEDLINE=87029174; PubMed=3021384;
 RA Fini M.E., Austin S.D., Holt P.T., Ruby P.L., Gross R.H., White H.D.,
 RA Brinckerhoff C.E.;

"Homology between exon-containing portions of rabbit genomic clones
 for synovial cell collagenase and human foreskin and synovial cell
 mRNAs.";
 Coll. Relat. Res. 6:239-248 (1986).
 CC -!- FUNCTION: Cleaves collagens of types I, II, and III at one site in
 the helical domain. Also cleaves collagens of types VII and X.
 CC -!- CATALYTIC ACTIVITY: Cleaves preferentially one bond in native
 collagen. Cleavage of the triple helix of collagen at about three-
 quarters of the length of the molecule from the N-terminus, at
 775-Gly-Ile-776 in the alpha-1(I) chain. Cleaves synthetic
 CC substrates and alpha-macroglobulins at bonds where PI' is a
 hydrophobic residue.
 CC -!- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit (By
 similarity).
 CC -!- ENZYME REGULATION: Can be activated without removal of the
 activation peptide.
 CC -!- SIMILARITY: Belongs to peptidase family M10A.
 CC -!- SIMILARITY: Contains 1 hemopexin-like domain.
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 or send an email to license@isb-sib.ch).
 EMBL; M17823; AAB88016.1; -;
 DR EMBL; M17820; AAB88016.1; JOINED.
 DR EMBL; M17821; AAB88016.1; JOINED.
 DR EMBL; M17822; AAB88016.1; JOINED.
 DR EMBL; M19240; AAB88016.1; JOINED.
 DR EMBL; M25653; AAB88016.1; JOINED.
 DR PIR; A27500; KCRBI.
 DR HSSP; P03956; ICGL.
 DR MEROPS; M10.001; -;
 DR InterPro; IPR000585; Hemopexin.
 DR InterPro; IPR006026; Peptidase M.
 DR InterPro; IPR001818; Pept_M10A_M12B.
 DR InterPro; IPR006025; Pept_M_Zn_BS.
 DR InterPro; IPR009070; PGHD_like.
 DR Pfam; PF00045; Hemopexin; 4.
 DR Pfam; PF00413; Peptidase_M10; 1.
 DR Pfam; PF03933; Peptidase_M10_N; 1.
 DR PRINTS; PR00138; MATRXIN.
 DR SMART; SM00120; HX; 4.
 DR SMART; SM00235; ZmC; 1.
 DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
 DR PROSITE; PS00024; HEMOPEXIN; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 KW Calcium-binding; Collagen degradation; Extracellular matrix;
 KW Glycoprotein; Hydrolase; Metal-binding; Metalloprotease; Signal; Zinc;
 KW Zymogen.
 FT SIGNAL 1 18
 FT PROPEP 19 98
 FT CHAIN 99 468
 FT DOMAIN 274 468
 FT SITE 91 91
 FT METAL 123 123
 FT METAL 157 157
 FT METAL 167 167
 FT METAL 169 169
 FT METAL 174 174
 FT METAL 175 175
 FT METAL 177 177
 FT METAL 179 179
 FT METAL 182 182
 FT METAL 189 189
 FT METAL 191 191

Activation peptide.
 Interstitial collagenase.
 Hemopexin-like.
 Cysteine switch (Potential).
 Calcium 1 (By similarity).
 Calcium 2 (By similarity).
 Zinc 1 (By similarity).
 Zinc 1 (By similarity).
 Calcium 3 (By similarity).
 Calcium 3 (via carbonyl oxygen) (By
 similarity).
 Calcium 3 (via carbonyl oxygen) (By
 similarity).
 Calcium 3 (via carbonyl oxygen) (By
 similarity).
 Zinc 1 (By similarity).
 Calcium 2 (via carbonyl oxygen) (By
 similarity).
 Calcium 2 (via carbonyl oxygen) (By
 similarity).
 Calcium 2 (via carbonyl oxygen) (By
 similarity).


```

FT METAL 193 193 similarity).
FT METAL 195 195 Calcium 2 (By similarity).
FT METAL 197 197 Zinc 1 (By similarity).
FT METAL 198 198 Calcium 3 (By similarity).
FT METAL 200 200 Calcium 1 (By similarity).
FT METAL 217 217 Calcium 3 (By similarity).
FT METAL 218 218 Zinc 2 (catalytic) (By similarity).
FT ACT_SITE 219 219 By similarity.
FT METAL 221 221 Zinc 2 (catalytic) (By similarity).
FT METAL 222 222 Zinc 2 (catalytic) (By similarity).
FT METAL 227 227 Calcium 4 (via carbonyl oxygen) (By
FT METAL 284 284 similarity).
FT METAL 328 328 Calcium 4 (via carbonyl oxygen) (By
FT METAL 377 377 similarity).
FT METAL 377 377 Calcium 4 (via carbonyl oxygen) (By
FT METAL 426 426 similarity).
FT METAL 426 426 Calcium 4 (via carbonyl oxygen) (By
FT METAL 119 119 N-linked (GlcNAc...) (Probable).
FT CARBOHYD 119 119 By similarity.
FT DISULFID 277 465
SQ SEQUENCE 468 AA; 53739 MW; DA90538919952B8C CRC64;

Query Match 96.9%; Score 283; DB 1; Length 468;
Best Local Similarity 96.3%; Pred. No. 1.2e-27;
Matches 52; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MQBFFGLKVTGKDPDAETLKVMKQPRCGVPDVAQFVLTGPNRWEQTHLYRIEN 54
Db 66 MQBFFGLKVTGKDPDAETLKVMKQPRCGVPDVAQFVLTGPNRWEQTHLYRIEN 119

RESULT 4
MM01 HORSE STANDARD; PRT; 469 AA.
AC QXK25;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interstitial collagenase precursor (EC 3.4.24.7) (Matrix
DE metalloproteinase-1) (MMP-1).
GN Name=MMP1;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP Richardson D.W.;
RA "Cloning and expression of equine matrix metalloproteinase 1
RT (Interstitial collagenase).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Cleaves collagens of types I, II, and III at one site in
CC the helical domain. Also cleaves collagens of types VII and X.
CC -1- CATALYTIC ACTIVITY: Cleaves preferentially one bond in native
CC collagen. Cleavage of the triple helix of collagen at about three-
CC quarters of the length of the molecule from the N-terminus, at
CC 775-Gly-|-Ile-776 in the alpha-1(I) chain. Cleaves synthetic
CC substrates and alpha-macroglobulins at bonds where P1' is a
CC hydrophobic residue.
CC -1- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit (By
CC similarity).
CC -1- ENZYME REGULATION: Can be activated without removal of the
CC activation peptide.
CC -1- SIMILARITY: Belongs to peptidase family M10A.
CC -1- SIMILARITY: Contains 1 hemopexin-like domain.
CC
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CC EMBL; AF148882; AAD38030.1; -.
DR HSSP; P03956; IAYK.
DR MEROPS; M10.001; -.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR006026; Peptidase_M.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_Bs.
DR InterPro; IPR009070; PGSD-like.
DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF00413; Peptidase_M10; 1.
DR Pfam; PF03933; Peptidase_M10_N; 1.
DR PRINTS; PR00138; MATRIXIN.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZnMc; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Calcium-binding; Collagen degradation; Extracellular matrix;
KW Glycoprotein; Hydrolase; Metal-binding; Metalloprotease; Signal; Zinc;
KW Zymogen.
FT SIGNAL 1 18 By similarity.
FT PROPEP 19 99 Activation peptide.
FT CHAIN 100 469 Interstitial collagenase.
FT DOMAIN 275 469 Hemopexin-like.
FT SITE 92 92 Cysteine switch (Potential).
FT METAL 124 124 Calcium 1 (By similarity).
FT METAL 158 158 Calcium 2 (By similarity).
FT METAL 168 168 Zinc 1 (By similarity).
FT METAL 170 170 Zinc 1 (By similarity).
FT METAL 175 175 Calcium 3 (By similarity).
FT METAL 176 176 Calcium 3 (via carbonyl oxygen) (By
FT METAL 178 178 similarity).
FT METAL 178 178 Calcium 3 (via carbonyl oxygen) (By
FT METAL 180 180 similarity).
FT METAL 180 180 Calcium 3 (via carbonyl oxygen) (By
FT METAL 183 183 Zinc 1 (By similarity).
FT METAL 190 190 Calcium 2 (via carbonyl oxygen) (By
FT METAL 192 192 similarity).
FT METAL 192 192 Calcium 2 (via carbonyl oxygen) (By
FT METAL 194 194 similarity).
FT METAL 196 194 Calcium 2 (By similarity).
FT METAL 198 196 Zinc 1 (By similarity).
FT METAL 199 198 Calcium 3 (By similarity).
FT METAL 201 199 Calcium 1 (By similarity).
FT METAL 218 201 Calcium 3 (By similarity).
FT METAL 219 218 Zinc 2 (catalytic) (By similarity).
FT ACT_SITE 219 219 By similarity.
FT METAL 222 222 Zinc 2 (catalytic) (By similarity).
FT METAL 228 228 Zinc 2 (catalytic) (By similarity).
FT METAL 285 285 Calcium 4 (via carbonyl oxygen) (By
FT METAL 329 329 similarity).
FT METAL 329 329 Calcium 4 (via carbonyl oxygen) (By
FT METAL 378 378 similarity).
FT METAL 378 378 Calcium 4 (via carbonyl oxygen) (By
FT METAL 427 427 similarity).
FT METAL 427 427 Calcium 4 (via carbonyl oxygen) (By
FT DISULFID 278 466 By similarity.
SQ SEQUENCE 469 AA; 54001 MW; ABE6760AB2C529CA CRC64;

Query Match 95.5%; Score 279; DB 1; Length 469;
Best Local Similarity 94.4%; Pred. No. 3.9e-27;
Matches 51; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MQBFFGLKVTGKDPDAETLKVMKQPRCGVPDVAQFVLTGPNRWEQTHLYRIEN 54
Db 67 MQBFFGLKVTGKDPDAETLKVMKQPRCGVPDVAQFVLTGPNRWEQTHLYRIEN 120

RESULT 5
MM01_PIG

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ID MM01_PIG STANDARD; PRT; 469 AA.
AC P21692;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Interstitial collagenase precursor (EC 3.4.24.7) (Matrix
DE metalloproteinase-1) (MMP-1).
GN Name=MMP1;
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RN MEDLINE=91333421; PubMed=1651440;
RX Richards C.B., Rafferty J.A., Reynolds J.J., Saklatvala J.;
RT "Porcine collagenase from synovial fibroblasts: cDNA sequence and
RT modulation of expression of RNA in vitro by various cytokines.";
RL Matrix 11:161-167(1991).
RN [2]
RN SEQUENCE OF '25-469 FROM N.A.
RC TISSUE=Synovial cell;
RX MEDLINE=91067477; PubMed=2174547;
RA Clarke N.J., O'Hare M.C., Cawston T.E., Harper G.P.;
RT "Nucleotide sequence of a cDNA for porcine type I collagenase,
RT obtained by PCR";
RL Nucleic Acids Res. 18:6703-6703(1990).
RN [3]
RN X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 100-469.
RX MEDLINE=96173003; PubMed=8590015;
RA Li J., Brick P., O'Hare M.C., Skarzynski T., Lloyd L.F., Curry V.A.,
RA Clark I.M., Bigg H.F., Hazleman B.L., Cawston T.E., Blow D.M.;
RT "Structure of full-length porcine synovial collagenase reveals a C-
RT terminal domain containing a calcium-linked, four-bladed beta-
RT propeller.";
RL Structure 3:541-549(1995).
RN [4]
RN SEQUENCE OF 100-104 AND 248-282, AND AUTOPROTEOLYTIC CLEAVAGE SITE.
RX MEDLINE=95142615; PubMed=7840605;
RA Clark I.M., Mitchell R.E., Powell L.K., Bigg H.F., Cawston T.E.,
RA O'Hare M.C.;
RT "Recombinant porcine collagenase: purification and autolysis.";
RL Arch. Biochem. Biophys. 316:123-127(1995).
CC -1- FUNCTION: Cleaves collagens of types I, II, and III at one site in
CC the helical domain. Also cleaves collagens of types VII and X.
CC -1- CATALYTIC ACTIVITY: Cleaves preferentially one bond in native
CC collagen. Cleavage of the triple helix of collagen at about three-
CC quarters of the length of the molecule from the N-terminus, at
CC 775-Gly-118-776 in the alpha-1(I) chain. Cleaves synthetic
CC substrates and alpha-macroglobulins at bonds where P1' is a
CC hydrophobic residue.
CC -1- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit.
CC -1- ENZYME REGULATION: Can be activated without removal of the
CC activation peptide.
CC -1- PTM: Undergoes autocatalytic cleavage to produce a N-terminal fragment
CC having reduced collagenolytic activity.
CC -1- SIMILARITY: Belongs to peptidase family M10A.
CC -1- SIMILARITY: Contains 1 hemopexin-like domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X54724; CAA38526.1; -
DR PIR; S15986; KCPGI.
DR PDB; 1FBL; X-ray; @=100-469.
DR MEROPS; M10.001; -
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR006026; Peptidase_M.

DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR009070; PGSD_Like.
DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF00413; Peptidase_M10; 1.
DR Pfam; PF03933; Peptidase_M10_N; 1.
DR PRINTS; PRC0138; MATRININ.
DR SMART; SM00130; HX; 4.
DR SMART; SM00235; ZMNC; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW 3D-structure; Autocatalytic cleavage; Calcium-binding;
KW Collagen degradation; Direct protein sequencing; Extracellular matrix;
KW Glycoprotein; Hydrolase; Metal-binding; Metalloprotease; Signal; Zinc;
KW Zymogen.
FT SIGNAL 1 19 Activation peptide.
FT PROPEP 20 99 Interstitial collagenase.
FT CHAIN 100 469 18 kDa interstitial collagenase.
FT CHAIN 100 258 Hemopexin-like.
FT DOMAIN 275 469 Cysteine switch (Potential).
FT SITE 92 92 Cleavage (autolytic).
FT SITE 258 259 Cleavage (autolytic).
FT METAL 124 124 Calcium 1.
FT METAL 158 158 Calcium 2.
FT METAL 168 168 Zinc 1.
FT METAL 170 170 Zinc 1.
FT METAL 175 175 Calcium 3.
FT METAL 176 176 Calcium 3 (via carbonyl oxygen).
FT METAL 178 178 Calcium 3 (via carbonyl oxygen).
FT METAL 180 180 Calcium 3 (via carbonyl oxygen).
FT METAL 183 183 Zinc 1.
FT METAL 190 190 Calcium 2 (via carbonyl oxygen).
FT METAL 192 192 Calcium 2 (via carbonyl oxygen).
FT METAL 194 194 Calcium 2.
FT METAL 196 196 Zinc 1.
FT METAL 198 198 Calcium 3.
FT METAL 199 199 Calcium 1.
FT METAL 201 201 Calcium 3.
FT METAL 218 218 Zinc 2 (catalytic).
FT ACT_SITE 219 219 Zinc 2 (catalytic).
FT METAL 222 222 Zinc 2 (catalytic).
FT METAL 228 228 Calcium 4 (via carbonyl oxygen).
FT METAL 285 285 Calcium 4 (via carbonyl oxygen).
FT METAL 329 329 Calcium 4 (via carbonyl oxygen).
FT METAL 378 378 Calcium 4 (via carbonyl oxygen).
FT METAL 427 427 Calcium 4 (via carbonyl oxygen).
FT METAL 466 466 N-linked (GlcNAc. .) (Potential).
FT DISULFID 120 120
FT CARBOHYD 101 102
FT STRAND 104 105
FT TURN 104 105
FT STRAND 113 118
FT TURN 123 124
FT TURN 127 142
FT HELIX 143 144
FT TURN 143 144
FT STRAND 148 152
FT STRAND 159 164
FT STRAND 182 184
FT TURN 190 193
FT STRAND 195 198
FT TURN 199 200
FT STRAND 204 204
FT STRAND 211 211
FT STRAND 212 223
FT TURN 224 225
FT STRAND 226 227
FT TURN 232 233
FT TURN 235 236
FT TURN 250 260
FT TURN 277 278
FT TURN 280 281
FT TURN 286 290
FT TURN 291 292

FT STRAND 293 298
 FT TURN 299 300
 FT STRAND 301 305
 FT STRAND 313 316
 FT HELIX 317 320
 FT STRAND 330 334
 FT STRAND 335 338
 FT TURN 339 344
 FT TURN 345 346
 FT STRAND 347 352
 FT TURN 353 354
 FT STRAND 355 356
 FT TURN 358 359
 FT STRAND 362 363
 FT STRAND 364 368
 FT TURN 372 373
 FT STRAND 379 383
 FT TURN 384 387
 FT STRAND 388 393
 FT TURN 394 395
 FT STRAND 396 401
 FT TURN 402 405
 FT STRAND 406 407
 FT STRAND 413 414
 FT HELIX 415 418
 FT TURN 420 421
 FT STRAND 428 432
 FT TURN 433 434
 FT STRAND 435 440
 FT TURN 441 442
 FT STRAND 443 448
 FT TURN 449 452
 FT STRAND 453 459
 FT TURN 460 461
 FT HELIX 462 464
 FT TURN 465 465
 SQ SEQUENCE 469 AA; 53666 MW; 7952D2B2753F682 CRC64;

Query Match 92.5%; Score 270; DB 1; Length 469;
 Best Local Similarity 90.7%; Pred. No. 5.5e-26;
 Matches 49; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MQEFGKVTGKDAETLKVMKQPCGVPDVAQFVLTEGPNRWEQHTLYRIEN 54
 Db 67 MQOFFGLKVTGKDAETLVNWKQPCGVPDVAEFVLTPGNRWENTHLYRIEN 120

RESULT 6

MM01_BOVIN	STANDARD;	PRT;	469 AA.
ID_P28053;			
AC 01-AUG-1992	(Rel. 23, Created)		
DT 01-AUG-1992	(Rel. 23, Last sequence update)		
DT 05-JUL-2004	(Rel. 44, Last annotation update)		
DE	Interstitial collagenase precursor (EC 3.4.24.7) (Matrix		
DE	metalloproteinase-1) (MMP-1) (Fibroblast collagenase).		
GN	Name=MMP1; Synonyms=CLG;		
OS	Bos taurus (Bovine).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Metheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;		
OC	Bovinae; Bos.		
OX	NCBI_TaxID=9913;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Periodontium fibroblast;		
RX	MEDLINE=95201294; PubMed=7894061;		
RA	Tamura M., Shimokawa H., Sasaki S.;		
RT	"Primary structure of bovine interstitial collagenase deduced from		
RT	cDNA sequence."		
RL	DNA Seq. 5:63-66(1994).		
RN	[2]		
RP	SEQUENCE OF 19-39 AND 85-125.		
RX	PubMed=1311165;		

RA Sudbeck B.D., Jeffrey J.J., Welgus H.G., Mecham R.P., McCourt D.,
 RA Parks W.C.;
 RT "Purification and characterization of bovine interstitial collagenase
 and tissue inhibitor of metalloproteinases.";
 RL Arch. Biochem. Biophys. 293:370-376(1992).
 CC -!- FUNCTION: Cleaves collagens of types I, II, and III at one site in
 the helical domain. Also cleaves collagens of types VII and X.
 CC -!- CATALYTIC ACTIVITY: Cleaves preferentially one bond in native
 collagen. Cleavage of the triple helix of collagen at about three-
 quarters of the length of the molecule from the N-terminus, at
 7/5-Gly-Ile-776 in the alpha-1(I) chain. Cleaves synthetic
 substrates and alpha-macroglobulins at bonds where P1' is a
 hydrophobic residue.
 CC -!- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit (By
 similarity).
 CC -!- ENZYME REGULATION: Can be activated without removal of the
 activation peptide.
 CC -!- SIMILARITY: Belongs to peptidase family M10A.
 CC -!- SIMILARITY: Contains 1 hemopexin-like domain.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X58256; CAA41210.1; -;
 DR PIR; S14654; KCBOI.
 DR HSSP; P03956; LHFC.
 DR MEROPS; M10.001; -;
 DR InterPro; IPR000585; Hemopexin.
 DR InterPro; IPR006026; Peptidase M.
 DR InterPro; IPR01818; Pept M10A_M12B.
 DR InterPro; IPR006025; Pept_M_Zn_BS.
 DR InterPro; IPR009070; PGSD_like.
 DR Pfam; PF00045; Hemopexin; 4.
 DR Pfam; PF00413; Peptidase M10; 1.
 DR Pfam; PF03933; Peptidase M10_N; 1.
 DR PRINTS; PR00138; MATRINX.
 DR SMART; SM00120; HX; 4.
 DR SMART; SM00235; ZnMc; 1.
 DR PROSITE; PS00546; CYSTEINE SWITCH; 1.
 DR PROSITE; PS00024; HEMOPEXIN; 1.
 DR PROSITE; PS00142; ZINC PROTEASE; 1.
 DR Calcium-binding; Collagen degradation; Direct protein sequencing;
 KW Extracellular matrix; Glycoprotein; Hydrolase; Metal-binding;
 KW Metalloprotease; Signal; Zinc; zymogen.
 FT SIGNAL 1 18
 FT PROPEP 19 99 Activation peptide.
 FT CHAIN 100 469 Interstitial collagenase.
 FT DOMAIN 275 469 Hemopexin-like.
 FT SITE 92 92 Cysteine switch (potential).
 FT METAL 124 124 Calcium 1 (By similarity).
 FT METAL 158 158 Calcium 2 (By similarity).
 FT METAL 168 168 Zinc 1 (By similarity).
 FT METAL 170 170 Zinc 1 (By similarity).
 FT METAL 175 175 Calcium 3 (By similarity).
 FT METAL 176 176 Calcium 3 (via carbonyl oxygen) (By
 similarity).
 FT METAL 178 178 Calcium 3 (via carbonyl oxygen) (By
 similarity).
 FT METAL 180 180 Calcium 3 (via carbonyl oxygen) (By
 similarity).
 FT METAL 183 183 Zinc 1 (By similarity).
 FT METAL 190 190 Calcium 2 (via carbonyl oxygen) (By
 similarity).
 FT METAL 192 192 Calcium 2 (via carbonyl oxygen) (By
 similarity).
 FT METAL 194 194 Calcium 2 (By similarity).
 FT METAL 196 196 Zinc 1 (By similarity).
 FT METAL 198 198 Calcium 3 (By similarity).

FT METAL 199 199 Calcium 1 (By similarity).
 FT METAL 201 201 Calcium 3 (By similarity).
 FT METAL 218 218 Zinc 2 (catalytic) (By similarity).
 FT ACT SITE 219 219 By similarity.
 FT METAL 222 222 Zinc 2 (catalytic) (By similarity).
 FT METAL 228 228 Zinc 2 (catalytic) (By similarity).
 FT METAL 285 285 Calcium 4 (via carbonyl oxygen) (By similarity).
 FT METAL 329 329 Calcium 4 (via carbonyl oxygen) (By similarity).
 FT METAL 378 378 Calcium 4 (via carbonyl oxygen) (By similarity).
 FT METAL 427 427 Calcium 4 (via carbonyl oxygen) (By similarity).
 FT DISULFID 278 466 By similarity.
 FT CARBOHYD 120 120 N-linked (GlcNAc...) (Potential).
 FT CONFLICT 22 23 AT -> FP (in Ref. 2).
 FT CONFLICT 30 30 D -> L (in Ref. 2).
 FT CONFLICT 35 36 KK -> LL (in Ref. 2).
 FT CONFLICT 85 85 N -> F (in Ref. 2).
 FT CONFLICT 106 108 KSC -> NPR (in Ref. 2).
 FT CONFLICT 113 113 N -> D (in Ref. 2).
 SQ SEQUENCE 469 AA; 53354 MW; 545504CE24BD7B5 CRC64;
 Query Match 80.1%; Score 234; DB 1; Length 469;
 Best Local Similarity 81.5%; Pred. No. 2.4e-21;
 Matches 44; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
 QY 1 MQEFTGLKVTGKPDATLTKVMPKPCGVPDVAQFVLTGPNRWEQTHLYRIEN 54
 DB 67 MQEFTGLKVTGKPDATLTKVMPKPCGVPDVAQFVLTGPNRWEQTHLYRIEN 120
 RESULT 7
 NM01_RANCA STANDARD; PRT; 384 AA.
 ID NM01_RANCA
 AC Q11133;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Interstitial collagenase precursor (EC 3.4.24.7) (Matrix metalloproteinase-1) (MMP-1) (TCL).
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
 OX NCBI_TaxID=8400;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RX MEDLINE=95071832; PubMed=7981043;
 RA Oofusa K., Yomori S., Yoshizato K.;
 RT "Regionally and hormonally regulated expression of genes of collagen and collagenase in the anuran larval skin.";
 RL Int. J. Dev. Biol. 38:345-350(1994).
 CC 1- FUNCTION: Cleaves collagens of types I, II, and III at one site in the helical domain. Also cleaves collagens of types VII and X.
 CC 1- CATALYTIC ACTIVITY: Cleaves preferentially one bond in native collagen. Cleavage of the triple helix of collagen at about three-quarters of the length of the molecule from the N-terminus, at 775-Gly-Ile-776 in the alpha-1(I) chain. Cleaves synthetic substrates and alpha-macroglobulins at bonds where P1' is a hydrophobic residue.
 CC 1- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit (By similarity).
 CC 1- ENZYME REGULATION: Can be activated without removal of the activation peptide (By similarity).
 CC 1- SIMILARITY: Belongs to peptidase family M10A.
 CC 1- SIMILARITY: Contains 1 hemopexin-like domain.
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 CC -----
 CC EMBL; S75623; AAB32661.1; -.
 DR PIR; I51267; I51267.
 DR HSSP; P21692; 1FEL.
 DR MEROPS; M10.001; -.
 DR InterPro; IPR000585; Hemopexin.
 DR InterPro; IPR006026; Peptidase M.
 DR InterPro; IPR001818; Pept M10A_M12B.
 DR InterPro; IPR006025; Pept M_Zn_BS.
 DR InterPro; IPR009070; PGD_like.
 DR Pfam; PF00045; Hemopexin; 2.
 DR Pfam; PF00413; Peptidase_M10; 1.
 DR Pfam; PF03933; Peptidase_M10_N; 1.
 DR PRINTS; PRO0138; MATRILIN.
 DR SMART; SM00120; HX; 2.
 DR SMART; SM00235; ZmG; 1.
 DR PROSITE; PS00546; CYSTEINE_SWITCH; FALSE_NEG.
 DR PROSITE; PS00024; HEMOPEXIN; FALSE_NEG.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 DR Calcium-binding; Collagen degradation; Extracellular matrix;
 KW Hydrolyase; Metal-binding; Metalloprotease; Signal; Zinc; Zymogen.
 FT SIGNAL 1 25 Potential.
 FT PROPEP 26 88 Activation peptide (Potential).
 FT CHAIN 89 384 Interstitial Collagenase.
 FT DOMAIN 239 384 Hemopexin-like.
 FT SITE 81 81 Cysteine switch (Potential).
 FT METAL 113 113 Calcium 1 (By similarity).
 FT METAL 129 129 Calcium 2 (By similarity).
 FT METAL 139 139 Zinc 1 (By similarity).
 FT METAL 141 141 Zinc 1 (By similarity).
 FT METAL 146 146 Calcium 3 (By similarity).
 FT METAL 147 147 Calcium 3 (via carbonyl oxygen) (By similarity).
 FT METAL 149 149 Calcium 3 (via carbonyl oxygen) (By similarity).
 FT METAL 151 151 Calcium 3 (via carbonyl oxygen) (By similarity).
 FT METAL 154 154 Zinc 1 (By similarity).
 FT METAL 161 161 Calcium 2 (via carbonyl oxygen) (By similarity).
 FT METAL 163 163 Calcium 2 (via carbonyl oxygen) (By similarity).
 FT METAL 165 165 Calcium 2 (By similarity).
 FT METAL 167 167 Zinc 1 (By similarity).
 FT METAL 169 169 Calcium 3 (By similarity).
 FT METAL 170 170 Calcium 1 (By similarity).
 FT METAL 172 172 Calcium 3 (By similarity).
 FT METAL 189 189 Zinc 2 (catalytic) (By similarity).
 FT ACT SITE 190 190 By similarity.
 FT METAL 193 193 Zinc 2 (catalytic) (By similarity).
 FT METAL 199 199 Zinc 2 (catalytic) (By similarity).
 FT METAL 249 249 Calcium 4 (via carbonyl oxygen) (By similarity).
 FT METAL 277 277 Calcium 4 (via carbonyl oxygen) (By similarity).
 FT METAL 347 347 Calcium 4 (via carbonyl oxygen) (By similarity).
 FT DISULFID 242 381 By similarity.
 SQ SEQUENCE 384 AA; 43582 MW; A5B5E2FB332239DF CRC64;
 Query Match 79.3%; Score 231.5; DB 1; Length 384;
 Best Local Similarity 79.6%; Pred. No. 4e-21;
 Matches 43; Conservative 5; Mismatches 5; Indels 1; Gaps 1;
 QY 1 MQEFTGLKVTGKPDATLTKVMPKPCGVPDVAQFVLTGPNRWEQTHLYRIEN 54
 DB 57 LKQFFGLKVTGKPDATLTKVMPKPCGVPDVAQFVLTGPNRWEQTHLYRIEN 109
 RESULT 8

MM08 HUMAN
 ID _MM08 HUMAN STANDARD; PRT; 467 AA.
 AC P22854;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Neutrophil collagenase precursor (EC 3.4.24.34) (Matrix
 DE metalloproteinase-8) (MMP-8) (PMNL collagenase) (PMNL-CL).
 GN Name=MMP8; Synonyms=CLG1;
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 314-337; 347-363 AND 424-441.
 RC TISSUE=Neutrophils;
 RX MEDLINE=90307647; PubMed=2164002;
 RA Hasty K.A., Pourmotabbed T.F., Goldberg G.I., Thompson J.P.,
 RA Spinella D.G., Stevens R.M., Mainardi C.L.;
 RT "Human neutrophil collagenase. A distinct gene product with homology
 RT to other matrix metalloproteinases.";
 RL J. Biol. Chem. 265:11421-11424(1990).
 RN [2]
 RP SEQUENCE OF 21-140.
 RC TISSUE=Neutrophils;
 RX MEDLINE=90249372; PubMed=2159879;
 RA Knaeuper V., Kraemer S., Reinke H., Tschesche H.;
 RT "Characterization and activation of procollagenase from human
 RT polymorphonuclear leukocytes. N-terminal sequence determination of the
 RT proenzyme and various proteolytically activated forms.";
 RL Eur. J. Biochem. 189:295-300(1990).
 RN [3]
 RP SEQUENCE OF 21-103.
 RC TISSUE=Neutrophils;
 RX MEDLINE=92111500; PubMed=1662606;
 RA Blaese J., Knaeuper V., Osthus A., Reinke H., Tschesche H.;
 RT "Mercurial activation of human polymorphonuclear leucocyte
 RT procollagenase.";
 RL Eur. J. Biochem. 202:1223-1230(1991).
 RN [4]
 RP SEQUENCE OF 85-120, AND CHARACTERIZATION.
 RC TISSUE=Neutrophils;
 RX MEDLINE=91104978; PubMed=2176876;
 RA Mallva S.K., Mookthiar K.A., Gao Y., Brew K., Dioszegi M.,
 RA Birkedal-Hansen H., van Wart H.B.;
 RT "Characterization of 58-kilodalton human neutrophil collagenase:
 RT comparison with human fibroblast collagenase.";
 RL Biochemistry 29:10628-10634(1990).
 RN [5]
 RP PARTIAL SEQUENCE.
 RC MEDLINE=90380298; PubMed=2169256;
 RA Knaeuper V., Kraemer S., Reinke H., Tschesche H.;
 RT "Partial amino acid sequence of human PMN leukocyte procollagenase.";
 RL Biol. Chem. Hoppe-Seyler 371:295-304(1990).
 RN [6]
 RP ERRATUM.
 RC MEDLINE=91000455; PubMed=2169766;
 RA Knaeuper V., Kraemer S., Reinke H., Tschesche H.;
 RL Biol. Chem. Hoppe-Seyler 371:733-733(1990).
 RN [7]
 RP CYSTEINE-SWITCH MECHANISM.
 RC TISSUE=Neutrophils;
 RX MEDLINE=93050220; PubMed=1330697;
 RA Blaese J., Triebel S., Reinke H., Tschesche H.;
 RT "Formation of a covalent Hg-Cys-bond during mercurial activation of
 RT PMNL procollagenase gives evidence of a cysteine-switch mechanism.";
 RL FEBS Lett. 313:59-61(1992).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 100-262.
 RX MEDLINE=94185631; PubMed=8137810;
 RA Bode W., Reinemer P., Huber R., Klein T., Schnierer S., Tschesche H.;
 RT "The X-ray crystal structure of the catalytic domain of human
 RT neutrophil collagenase inhibited by a substrate analogue reveals the

essentials for catalysis and specificity.";
 RL EMBO J. 13:1263-1269(1994).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 100-262.
 RX MEDLINE=94139930; PubMed=8307185;
 RA Reinemer P., Grams F., Huber R., Kleine T., Schnierer S., Piper M.,
 RA Tschesche H., Bode W.;
 RT "Structural implications for the role of the N terminus in the
 RT 'superactivation' of collagenases. A crystallographic study.";
 RL FEBS Lett. 338:227-233(1994).
 RN [10]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 100-262.
 RX MEDLINE=95384762; PubMed=7656015;
 RA Stams T., Spurlino J.C., Smith D.L., Wahl R.C., Ho T.F.,
 RA Oronfleh M.W., Banks T.M., Rubin B.;
 RT "Structure of human neutrophil collagenase reveals large S1'
 RT specificity pocket.";
 RL Nat. Struct. Biol. 1:119-123(1994).
 RN [11]
 RP X-RAY CRYSTALLOGRAPHY (1.81 ANGSTROMS) OF 100-262.
 RX MEDLINE=97390108; PubMed=9249047;
 RA Betz M., Huxley P., Davies S.J., Mushtaq Y., Pieper M., Tschesche H.,
 RA Bode W., Gomis-Ruth F.-X.;
 RT "1.8-A crystal structure of the catalytic domain of human neutrophil
 RT collagenase (matrix metalloproteinase-8) complexed with a
 RT peptidomimetic hydroxamate primed-side inhibitor with a distinct
 RT selectivity profile.";
 RL Eur. J. Biochem. 247:356-363(1997).
 RN [12]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 105-262.
 RX MEDLINE=98318039; PubMed=9655333;
 RA Brandstetter H., Engh R.A., von Roeder E.G., Moroder L., Huber R.,
 RA Bode W., Grams F.;
 RT "Structure of malonic acid-based inhibitors bound to human neutrophil
 RT collagenase. A new binding mode explains apparently anomalous data.";
 RL Protein Sci. 7:1303-1309(1998).
 CC -!- FUNCTION: Can degrade fibrillar type I, II, and III collagens.
 CC -!- CATALYTIC ACTIVITY: Cleavage of interstitial collagens in the
 CC triple helical domain. Unlike EC 3.4.24.7, this enzyme cleaves
 CC type III collagen more slowly than type I.
 CC -!- COFACTOR: Binds 2 zinc ions and 3 calcium ions per subunit.
 CC -!- ENZYME REGULATION: Cannot be activated without removal of the
 CC activation peptide.
 CC -!- SUBCELLULAR LOCATION: Stored in intracellular granules.
 CC -!- TISSUE SPECIFICITY: Neutrophils.
 CC -!- SIMILARITY: Belongs to peptidase family M10A.
 CC -!- SIMILARITY: Contains 1 hemopexin-like domain.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; J05556; AAA88021.1; -.
 CC PIR; A37073; KCHUN
 CC PDB; 1A85; X-ray; A=105-262.
 CC PDB; 1A86; X-ray; A=105-262.
 CC PDB; 1B2S; X-ray; A=99-263.
 CC PDB; 1I73; X-ray; A=100-262.
 CC PDB; 1I76; X-ray; A=100-262.
 CC PDB; 1JAN; X-ray; A=99-262.
 CC PDB; 1JAO; X-ray; A=100-262.
 CC PDB; 1JAF; X-ray; A=100-262.
 CC PDB; 1JAO; X-ray; A=100-262.
 CC PDB; 1JH1; X-ray; A=105-262.
 CC PDB; 1JU9; X-ray; A=100-262.
 CC PDB; 1KBC; X-ray; A/B=99-262.
 CC PDB; 1MVB; X-ray; A=100-262.
 CC PDB; 1MNC; X-ray; A=101-263.
 CC MEROPS; M10.002; -.

Genew; HGNC:7175; MMP8.
DR MIW; 120355; -
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0008330; F:neutrophil collagenase activity; TAS.
DR GO; GO:0008270; F:zinc ion binding; TAS.
DR GO; GO:0006508; F:proteolysis and peptidolysis; TAS.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR009070; PGBD_like.
DR Pfam; PF00045; Hemopexin_4.
DR Pfam; PF00413; Peptidase_M10_1.
DR PRINTS; PF03933; Peptidase_M10_N; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
DR 3D-structure; Calcium-binding; Collagen degradation;
KW Direct protein sequencing; Extracellular matrix; Glycoprotein;
KW Hydroxylase; Metal-binding; Metalloprotease; Signal; Zinc; Zymogen.
FT SIGNAL 1 20
FT PROPEP 21 100 Activation peptide.
FT CHAIN 101 467 Neutrophil collagenase.
FT DOMAIN 276 467 Hemopexin-like.
FT SITE 91 91 Cysteine switch.
FT METAL 157 157 Calcium 1.
FT METAL 167 167 Zinc 1.
FT METAL 169 169 Zinc 1.
FT METAL 174 174 Calcium 2.
FT METAL 175 175 Calcium 2 (via carbonyl oxygen).
FT METAL 177 177 Calcium 2 (via carbonyl oxygen).
FT METAL 179 179 Calcium 2 (via carbonyl oxygen).
FT METAL 182 182 Zinc 1.
FT METAL 189 189 Calcium 1 (via carbonyl oxygen).
FT METAL 191 191 Calcium 1 (via carbonyl oxygen).
FT METAL 193 193 Calcium 1.
FT METAL 195 195 Zinc 1.
FT METAL 197 197 Calcium 2.
FT METAL 200 200 Calcium 2.
FT METAL 217 217 Zinc 2 (catalytic).
FT ACT_SITE 218 218 Zinc 2 (catalytic).
FT METAL 221 221 Zinc 2 (catalytic).
FT METAL 227 227 Calcium 3 (via carbonyl oxygen) (By
FT METAL 286 286 similarity).
FT METAL 378 378 Calcium 3 (via carbonyl oxygen) (By
FT METAL 425 425 similarity).
FT METAL 425 425 Calcium 3 (via carbonyl oxygen) (By
FT CARBOHYD 54 54 N-linked (GlcNAc...) (Probable).
FT CARBOHYD 73 73 N-linked (GlcNAc...) (Probable).
FT CARBOHYD 112 112 N-linked (GlcNAc...) (Probable).
FT CARBOHYD 204 204 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 246 246 N-linked (GlcNAc...) (Potential).
FT DISULFID 279 464 Probable.
Query Match 73.3%; Score 214; DB 1; Length 467;
Best Local Similarity 70.4%; Pred. No. 8.9e-19;
Matches 38; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
Qy 1 MQEFGKLVTKGPDATLKVMPKRCGVPDVAQFVLTGPNRWEQTHLYRIEN 54
Db 66 MQRFGLNVTKGPDATLKVMPKRCGVPDVAQFVLTGPNRWEQTHLYRIEN 119
RESULT 9
Q81022 PRELIMINARY; PRT; 205 AA.
AC Q81022
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Collagenase-like B (Fragment).

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RA Brathwaite M., Waelitz P., Nagaraja R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY211543; AAC37584.1; -
DR MEROPS; M10.034; -
DR CO; GO:0005578; C:extracellular matrix; IEA.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; F:proteolysis and peptidolysis; IEA.
DR InterPro; IPR006026; Peptidase M.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR009070; PGBD_like.
DR Pfam; PF00413; Peptidase_M10_1.
DR Pfam; PF03933; Peptidase_M10_N; 1.
DR PRINTS; PR00138; MATRININ.
DR SMART; SM00235; ZNMC; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
DR NON_TER 205 205
SQ SEQUENCE 205 AA; 23403 MW; DBD1E974B8769643 CRC64;
Query Match 69.9%; Score 204; DB 2; Length 205;
Best Local Similarity 66.7%; Pred. No. 7.2e-18;
Matches 36; Conservative 6; Mismatches 12; Indels 0; Gaps 0;
Qy 1 MQEFGKLVTKGPDATLKVMPKRCGVPDVAQFVLTGPNRWEQTHLYRIEN 54
Db 64 MQRFGLNVTKGPDATLKVMPKRCGVPDVAQFVLTGPNRWEQTHLYRIEN 117
RESULT 10
Q8EPL6 PRELIMINARY; PRT; 463 AA.
AC Q8EPL6
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative matrix metalloproteinase.
GN Name=Mmp1b; Synonyms=McolB;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=21167837; PubMed=1113146;
RX Balbin M., Fuyo A., Knauper V., Lopez J.M., Alvarez J., Sanchez L.M.,
RA Quesada V., Bordallo J., Murphy, G., Lopez-Otin C.;
RT Identification and enzymatic characterization of two diverging murine
RT counterparts of human interstitial collagenase (MMP-1) expressed at
RT sites of embryo implantation.;
RL J. Biol. Chem. 276:10253-10262 (2001).
DR EMBL; AJ278461; CAC18879.1; -
DR HSSP; P08254; 1HY7.
DR MEROPS; M10.034; -
DR MGD; MGI:1933847; Mmp1b.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR006026; Peptidase M.
DR InterPro; IPR001843; Pept_M10A_M10C.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR009070; PGBD_like.
DR Pfam; PF02051; Fragilysin; 1.
DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF00413; Peptidase_M10_1.
DR Pfam; PF03933; Peptidase_M10_N; 1.
DR PRINTS; PR00138; MATRININ.

DE Neutrophil collagenase precursor (EC 3.4.24.34) (Matrix
DE metalloproteinase-8) (MMP-8).
GN Name=Mmp8;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Lewis;
RC Overall C.M., Lowe D., Wells G., Clements J.M.;
RT "cloning, expression, characterization and activation properties of
rat neutrophil collagenase (MMP-8)";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC -|- FUNCTION: Can degrade fibrillar type I, II, and III collagens.
CC -|- CATALYTIC ACTIVITY: Cleavage of interstitial collagens in the
triple helical domain. Unlike EC 3.4.24.7, this enzyme cleaves
type III collagen more slowly than type I.
CC -|- COFACTOR: Binds 2 zinc ions and 3 calcium ions per subunit (By
similarity).
CC -|- ENZYME REGULATION: Cannot be activated without removal of the
activation peptide (By similarity).
CC -|- SUBCELLULAR LOCATION: Stored in intracellular granules.
CC -|- SIMILARITY: Belongs to peptidase family M10A.
CC -|- SIMILARITY: Contains 1 hemopexin-like domain.
CC -----
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entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AJ007288; CAA07432.1; -;
CC HSP; P22894; 1B2S.
CC MEROPS; M10.002; -;
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_Mzn_BS.
DR InterPro; IPR009070; PGSD-like.
DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF00413; Peptidase_M10; 1.
DR Pfam; PF03933; Peptidase_M10_N; 1.
DR PRINTS; PR00138; MATRXIN.
DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
DR Calcium-binding; Collagen degradation; Extracellular matrix;
KW Glycoprotein; Hydrolase; Metal-binding; Metalloprotease; Signal; Zinc;
KW Zymogen.
FT SIGNAL 1 20 By similarity.
FT PROPEP 21 101 Activation peptide (By similarity).
FT CHAIN 102 466 Neutrophil collagenase.
FT DOMAIN 277 466 Hemopexin-like.
FT SITE 92 92 Cysteine switch (By similarity).
FT METAL 158 158 Calcium 1 (By similarity).
FT METAL 168 168 Zinc 1 (By similarity).
FT METAL 170 170 Zinc 1 (By similarity).
FT METAL 175 175 Calcium 2 (By similarity).
FT METAL 176 176 Calcium 2 (via carbonyl oxygen) (By
similarity).
FT METAL 178 178 Calcium 2 (via carbonyl oxygen) (By
similarity).
FT METAL 180 180 Calcium 2 (via carbonyl oxygen) (By
similarity).
FT METAL 183 183 Zinc 1 (By similarity).
FT METAL 190 190 Calcium 1 (via carbonyl oxygen) (By
similarity).
FT METAL 192 192 Calcium 1 (via carbonyl oxygen) (By
similarity).
FT METAL 194 194 Calcium 1 (By similarity).
FT METAL 196 196 Zinc 1 (By similarity).

FT METAL 198 198 Calcium 2 (By similarity).
FT METAL 201 201 Calcium 2 (By similarity).
FT METAL 218 218 Zinc 2 (catalytic) (By similarity).
FT ACT_SITE 219 219 By similarity.
FT METAL 222 222 Zinc 2 (catalytic) (By similarity).
FT METAL 228 228 Zinc 2 (catalytic) (By similarity).
FT METAL 287 287 Calcium 3 (via carbonyl oxygen) (By
similarity).
FT METAL 379 379 Calcium 3 (via carbonyl oxygen) (By
similarity).
FT METAL 426 426 Calcium 3 (via carbonyl oxygen) (By
similarity).
FT DISULFID 280 465 Probable.
FT CARBOHYD 56 56 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 113 113 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 466 AA; 53277 MW; 8B9DB97576E76C90 CRC64;
Query Match 67.1%; Score 196; DB 1; Length 466;
Best Local Similarity 63.0%; Pred. No. 1.8e-16;
Matches 34; Conservative 9; Mismatches 11; Indels 0; Gaps 0;
QY 1 MQEFGGLKVTGKPDATLKVNMKQPCGVDPVAQFVLTEGPNRWEQTHLYRIEN 54
Db 67 MQRFGLPETGKPDATIEINEKRCGVDPDGDGDFLLTPGSKWHTNLTIRIN 120
RESULT 13
MM10 HUMAN
ID MM10 HUMAN STANDARD; PRT; 476 AA.
AC P09238;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, last sequence update)
DT 05-JUL-2004 (Rel. 44, last annotation update)
DE Stromelysin-2 precursor (EC 3.4.24.22) (Matrix metalloproteinase-10)
DE (MMP-10) (Transin-2) (SL-2).
GN Name=MMP10; Synonyms=STMY2;
GN Homo sapiens (Human)
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=6833985; PubMed=2844164;
RA Muller D., Quantin B., Gesnel M.-C., Millon-Collard R., Abecassis J.,
RA Breathnach R.;
RA "The collagenase gene family in humans consists of at least four
RT members";
RL Biochem. J. 253:187-192(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Wallahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gauratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -|- FUNCTION: Can degrade fibronectin, Gelatins of type I, III, IV,

RA Nickerson D.A.;
RT "SeattleSNPs. NHLBI HL6682 program for genomic applications, UW-
PHRC, Seattle, WA (URL: <http://pga.gs.washington.edu/>).";
RL Submitted (AUG-2001) to the ENBL/GenBank/DBS databases.
[6]
RN ZYMOGEN ACTIVATION.
RP MEDLINE=90344802; PubMed=2383557;
RX Nagase H., Englund J.J., Suzuki K., Salvesen G.;
RT "Stepwise activation mechanisms of the precursor of matrix
RT metalloproteinase 3 (stromelysin) by proteinases and (4-
RT anisophenyl)mercuric acetate";
RL Biochemistry 29:5783-5789(1990).
[7]
RN STRUCTURE BY NMR OF CATALYTIC DOMAIN.
RP MEDLINE=95384761; PubMed=7656014;
RX Gooley P.R., O'Connell J.F., Marcy A.I., Cuca G.C., Salowe S.P.,
RA Bush B.L., Hermes J.D., Esser C.K., Hagmann W.K., Springer J.P.,
RA Johnson B.A.;
RT "The NMR structure of the inhibited catalytic domain of human
RT stromelysin-1";
RL Nat. Struct. Biol. 1:111-118(1994).
[8]
RN STRUCTURE BY NMR OF 100-267.
RP MEDLINE=99043696; PubMed=9827994;
RX Stockman B.J., Waldon D.J., Gates J.A., Scallill T.A.,
RA Kloosterman D.A., Miazak S.A., Jacobsen E.J., Belonga K.L.,
RA Mitchell M.A., Mao B., Petke J.D., Goodman L., Powers E.A.,
RA Ledbetter S.R., Kayes P.S., Vogeli G., Marshall V.P., Petzold G.L.,
RA Poorman R.A.;
RT "Solution structures of stromelysin complexed to thiazolidone
RT inhibitors";
RL Protein Sci. 7:2281-2286(1998).
[9]
RN X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 18-272.
RP MEDLINE=96117647; PubMed=8535233;
RX Becker J.W., Marcy A.I., Rokosz L.L., Axel M.G., Burbaum J.J.,
RA Fitzgerald P.M.D., Cameron P.M., Esser C.K., Hagmann W.K.,
RA Hermes J.D., Springer J.P.;
RT "Stromelysin-1: three-dimensional structure of the inhibited catalytic
RT domain and of the C-truncated proenzyme";
RL Protein Sci. 4:1966-1976(1995).
[10]
RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 100-266.
RP MEDLINE=96311273; PubMed=8740360;
RX Dhanaraj V., Ye Q.-Z., Johnson L.L., Hupe D.J., Ortwein D.F.,
RA Dhanaraj V., Ye Q.-Z., Johnson L.L., Hupe D.J., Ortwein D.F.,
RA Dunbar J.B. Jr., Rubin J.R., Pavlovsky A., Humblet C., Blundell T.L.;
RT "X-ray structure of a hydroxamate inhibitor complex of stromelysin
RT catalytic domain and its comparison with members of the zinc
RT metalloproteinase superfamily";
RL Structure 4:375-386(1996).
[11]
RN X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 105-264.
RP MEDLINE=97236985; PubMed=9083493;
RX Esser C.K., Bugianesi R.L., Caldwell C.G., Chapman K.T., Durette P.L.,
RA Girotra N.N., Kopka I.E., Lanza T.J., LeVorse D.A., Maccoss M.,
RA Owens K.A., Pomplum M.M., Smeone J.P., Harrison R.K.,
RA Nedzwiecki L., Becker J.W., Marcy A.I., Axel M.G., Christen A.J.,
RA McDonnell J., Moore V.L., Olaszewski J.M., Saphos C., Visco D.M.,
RA Shen F., Colletti A., Krieger P.A., Hagmann W.K.;
RT "Inhibition of stromelysin-1 (MMP-3) by P1'-biphenylylethyl
RT carboxyalkyl dipeptides";
RL J. Med. Chem. 40:1026-1040(1997).
[12]
RN X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 100-267 IN COMPLEX WITH
RP TIMP1.
RX MEDLINE=97433330; PubMed=9288970;
RA Gomis-Ruth P.-X., Maskos K., Betz M., Bergner A., Huber R.,
RA Suzuki K., Yoshida N., Nagase H., Brew K., Bourenkov G.P.,
RA Bartunik H., Bode W.;
RT "Mechanism of inhibition of the human matrix metalloproteinase
RT stromelysin-1 by TIMP-1";
RL Nature 389:77-81(1997).
[13]
RN X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 100-264.
RP MEDLINE=9906562; PubMed=9792098;
RX Finzel B.C., Baldwin E.T., Bryant G.L. Jr., Hess G.F., Wilks J.W.,
RA Trepoed C.M., Mott J.E., Marshall V.P., Petzold G.L., Poorman R.A.,
RA O'Sullivan T.J., Schostarez H.J., Mitchell M.A.;
RT "Structural characterizations of nonpeptidic thiazolidone inhibitors of
RT matrix metalloproteinases reveal the basis for stromelysin
RT selectivity";
RL Protein Sci. 7:2118-2126(1998).
[14]
RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 100-272.
RP MEDLINE=20013067; PubMed=10543949;
RX Chen L., Rydel T.J., Gu F., Dunaway C.M., Pikul S., Dunham K.M.,
RA Barnett B.L.;
RT "Crystal structure of the stromelysin catalytic domain at 2.0-A
RT resolution: inhibitor-induced conformational changes";
RL J. Mol. Biol. 293:545-557(1999).
[15]
RN X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 100-267.
RP MEDLINE=99349695; PubMed=10422833;
RX Pavlovsky A.G., Williams M.G., Ye Q.-Z., Ortwein D.F., Johnson L.L.,
RA Purchase C.F. II, White A.D., Dhanaraj V., Roth B.D., Johnson L.L.,
RA Hupe D., Humblet C., Blundell T.L.;
RT "X-ray structure of human stromelysin catalytic domain complexed with
RT nonpeptide inhibitors: implications for inhibitor selectivity";
RL Protein Sci. 8:1455-1462(1999).
[16]
RN STRUCTURE BY NMR OF 100-272.
RP MEDLINE=98434377; PubMed=9760240;
RX Li Y.C., Zhang X., Melton R., Ganu V., Gonnella N.C.;
RA "Solution structure of the catalytic domain of human stromelysin-1
RT complexed to a potent, nonpeptidic inhibitor";
RL Biochemistry 37:14048-14056(1998).
[17]
RN FUNCTION: Can degrade fibronectin, laminin, gelatins of type I,
CC III, IV, and V; collagens III, IV, X, and IX, and cartilage
CC proteoglycans. Activates procollagenase.
CC CATALYTIC ACTIVITY: Preferential cleavage where P1', P2' and P3'
CC are hydrophobic residues.
CC COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit.
CC SIMILARITY: Belongs to peptidase family M10A.
CC SIMILARITY: Contains 1 hemopexin-like domain.

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CC or send an email to license@isb-sib.ch).

CC EMBL: X05232; CAA28859.1; -
CC EMBL: J03209; AAA36321.1; -
CC EMBL: U78045; AAB36942.1; -
CC EMBL: AF405705; AAK95247.1; -
CC FIR: A28156; KCHUS1.
CC PDB: 1B3D; X-ray; A/B=100-272.
CC PDB: 1B8Y; X-ray; A=100-266.
CC PDB: 1B1W; X-ray; A/B=100-272.
CC PDB: 1BM6; NMR; @=100-272.
CC PDB: 1BQO; X-ray; A/B=100-272.
CC PDB: 1C31; X-ray; A/B=100-272.
CC PDB: 1C8T; X-ray; A/B=103-269.
CC PDB: 1CAQ; X-ray; A=100-267.
CC PDB: 1CIZ; X-ray; A=100-267.
CC PDB: 1CQR; X-ray; A/B=100-272.
CC PDB: 1D5J; X-ray; A/B=100-272.
CC PDB: 1D7X; X-ray; A/B=100-272.
CC PDB: 1D8F; X-ray; A/B=100-272.
CC PDB: 1D8M; X-ray; A/B=100-272.
CC PDB: 1G05; X-ray; A/B=100-272.
CC PDB: 1G49; X-ray; A/B=100-272.
CC PDB: 1G4K; X-ray; A/B/C=100-267.
CC PDB: 1HFS; X-ray; @=105-264.

DR PDB; 1HY7; X-ray; A/B=100-272.
 DR PDB; 1M1W; Model; A=100-268.
 DR PDB; 1OO9; NMR; A=100-267.
 DR PDB; 1Q1A; X-ray; A/B/C/D=106-267.
 DR PDB; 1Q1C; X-ray; A/B/C/D=106-266.
 DR PDB; 1SLN; X-ray; @=18-272.
 Query Match 64.7%; Score 189; DB 1; Length 477;
 Best Local Similarity 63.0%; Pred. No. 1.5e-15;
 Matches 34; Conservative 9; Mismatches 11; Indels 0; Gaps 0;
 QY 1 MQEFGKVTGKPDASTLKVMKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 54
 Db 67 MQRFGLGVTKLSDPTLEVNRKPCGVPDVGHFRTFPGIPKWRKTHLYRIYN 120

Search completed: November 15, 2004, 14:06:38
 Job time : 50.8462 secs

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OM protein - protein search, using sw model

Run on: November 15, 2004, 14:01:34 ; Search time 50.4167 Seconds
(without alignments)
391.341 Million cell updates/sec

Title: US-10-032-376a-10

Perfect score: 307

Sequence: 1 MQRFFGLNVTKPNEETLDM.....LTPGNPKWNTLTIRNY 55

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 1022821

Minimum DB seq length: 47

Maximum DB seq length: 660

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_238Sep04.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	307	100.0	55	6	ABP97132 Human mat
2	307	100.0	55	6	ABG76318 Human mat
3	307	100.0	55	8	ADQ17093 Human mat
4	307	100.0	444	4	AAG65357 Human MMP
5	307	100.0	467	4	AAB84610 Amino aci
6	307	100.0	467	4	AAE10416 Human mat
7	307	100.0	467	4	AAG65358 Human neu
8	307	100.0	467	6	ABO32581 Secreted
9	307	100.0	467	8	ADQ10212 Human pol
10	226	73.6	454	8	ADL93947 Human G-c
11	221	72.0	454	7	ADE16002 G-coupled
12	221	72.0	454	7	ADE16004 G-coupled
13	221	72.0	454	7	ADE16008 G-coupled
14	221	72.0	454	7	ADE16006 G-coupled
15	221	72.0	454	8	ADL93945 Human G-c
16	221	72.0	454	8	ADL93943 Human G-c
17	221	72.0	455	8	ADL93941 Human G-c
18	221	72.0	469	4	AAB84606 Amino aci
19	221	72.0	469	4	AAE10415 Human mat
20	221	72.0	469	6	ABU03466 Angiogene
21	221	72.0	469	6	ABR59543 Human can
22	221	72.0	469	6	ABR59542 Human can
23	221	72.0	469	6	ABR48148 Human bla
24	221	72.0	469	6	ABU56596 Lung canc
25	221	72.0	469	6	ABU56597 Lung canc

ALIGNMENTS

RESULT 1

ABP97132

ID ABP97132 standard; peptide; 55 AA.

XX AC ABP97132;

XX DT 24-JUN-2003 (first entry)

XX DE Human matrix metalloproteinase 8 cleavage region peptide SEQ ID NO:10.

XX KW Human; matrix metalloproteinase; MMP; anticancer; wound healing;
matrix metalloproteinase inhibitor; antitumor; antiangiogenic; cardiant;
vascular endothelial growth factor inhibitor; VEGF inhibitor; cytostatic;
vulnary; cerebroprotective; antidiabetic; opthalmological; tumour;
dermatological; metastatic; non-metastatic; vascularised; heart disease;
non-vascularised; surgical incision; chronic wound; stroke; angiogenesis;
macular degeneration; diabetic retinopathy; cleavage region.

XX OS Homo sapiens.

XX FN WO2003018748-A2.

XX PD 06-MAR-2003.

XX PF 15-AUG-2002; 2002WO-US026319.

XX PR 16-AUG-2001; 2001US-0312726P.

XX PR 21-DEC-2001; 2001US-00032376.

XX PR 21-MAY-2002; 2002US-00153185.

XX PA (KIMB) KIMBERLY-CLARK WORLDWIDE INC.

XX PI Quirk S, Weart IF;

XX DR WPI; 2003-381408/36.

XX PT Anti-angiogenic composition comprising peptide inhibitor of matrix metalloproteinase, useful for decreasing the expression of vascular endothelial growth factor and treating cancers and tissue injuries.

XX PS Claim 17; Page 16; 103pp; English.

XX CC The present invention describes an anti-angiogenic composition (I) for inhibiting expression of vascular endothelial growth factor (VEGF). (I) comprises an effective amount of a peptide inhibitor of matrix metalloproteinase (MMP), where the peptide can inhibit the expression of VEGF. (I) has cytostatic, vulnary, cardiant, cerebroprotective, antidiabetic, opthalmological and dermatological activities. (I) can be

Abu07454 Protein d
Abp54454 Matrix me
Adb79176 Matrix me
Ade34550 Human ski
Ade16000 G-coupled
Ade16010 G-coupled
Adn38849 Cancer/an
Adn38694 Cancer/an
Adn38696 Cancer/an
Adn39850 Cancer/an
Adn95538 Human BEC
Adl93949 Human G-c
Adl93939 Human G-c
Adn07695 Human mat
Ade07882 Novel pro
Aag75509 Human col
Aap93628 Sequence
Aap70611 Sequence
Adq18359 Human sof
Abp97131 Human mat

26 221 72.0 469 6 ABU07454
27 221 72.0 469 6 ABE54454
28 221 72.0 469 6 ADB79176
29 221 72.0 469 7 ADE34550
30 221 72.0 469 7 ADE16000
31 221 72.0 469 7 ADE16010
32 221 72.0 469 7 ADN39849
33 221 72.0 469 7 ADN38694
34 221 72.0 469 7 ADN38696
35 221 72.0 469 7 ADN39850
36 221 72.0 469 7 ADN95538
37 221 72.0 469 8 ADL93949
38 221 72.0 469 8 ADL93939
39 221 72.0 470 8 ADN07695
40 221 72.0 490 7 ADN07882
41 221 72.0 496 4 AAG75509
42 215 70.0 457 1 AAP93628
43 215 70.0 469 1 AAP70611
44 215 70.0 469 8 ADQ18359
45 214 69.7 54 6 ABP97131

CC used for inhibiting expression of VEGF, and so can be used for inhibiting
 CC growth of tumours and diminishing tumours size. The tumour can be
 CC metastatic, non-metastatic, vascularised, non-vascularised, hard or soft.
 CC (1) is also useful for treating injuries including wounds, surgical
 CC incisions, chronic wounds, heart diseases and stroke. (1) is also useful
 CC for treating disorders characterised by excessive angiogenesis e.g.
 CC macular degeneration and diabetic retinopathy. The present sequence
 CC represents a human MMP cleavage region peptide, which is used in the
 CC exemplification of the present invention

XX Sequence 55 AA;

Query Match 100.0%; Score 307; DB 6; Length 55;
 Best Local Similarity 100.0%; Pred. No. 3.4e-34;
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORFFGLNVTGKPNBETLDMMKPRCGVPSGGFMLTPGNPKWERTNLTIRNY 55
 DB 1 MORFFGLNVTGKPNBETLDMMKPRCGVPSGGFMLTPGNPKWERTNLTIRNY 55

RESULT 2

ABG76318
 ID ABG76318 standard; protein; 55 AA.

AC ABG76318;

DT 10-MAY-2003 (first entry)

DE Human matrix metalloproteinase (MMP) peptide inhibitor #10.

XX Human; peptide inhibitor; matrix metalloproteinase-8; MMP-8;
 KW cleavage region; proenzyme form; cellular proliferation; fibroblast;
 KW keratinocyte; healthy skin development; wound healing; scarring;
 KW skin tone; wrinkle; anti-aging; vulnerary.

XX Homo sapiens.

XX WO2003016520-A1.

XX 27-FEB-2003.

XX 15-AUG-2002; 2002WO-US026198.

XX 16-AUG-2001; 2001US-0312726P.

XX 21-DEC-2001; 2001US-00032376.

XX 21-MAY-2002; 2002US-00153185.

XX (KIMB) KIMBERLY-CLARK WORLDWIDE INC.

XX Quirk S, Malik S, Villanueva JM;

XX WPI; 2003-289980/28.

XX Novel peptide inhibitor of proteinase activity of matrix

PT metalloproteinases, e.g. matrix metalloproteinase-2, useful for

PT stimulating cellular proliferation of fibroblasts or keratinocytes.

PS Claim 1; Page 16; 120pp; English.

XX The present invention relates to peptide inhibitors of metalloproteinases
 CC (MMPs), particularly metalloproteinase-2 (MMP-2). The inhibitors have
 CC peptide sequences related to the cleavage regions of the proenzyme forms
 CC of the MMPs. The peptide inhibitors are useful for stimulating cellular
 CC proliferation of fibroblasts or keratinocytes, promoting healthy skin
 CC development, treating wounds, preventing scarring, improving skin tone,
 CC reducing wrinkling and for simulating the development of smooth, healthy
 CC skin. The peptide inhibitors are useful as anti-aging and wound healing
 CC compounds. ABG76309-ABG76321 represent peptide inhibitors of MMPs

XX Sequence 55 AA;

Query Match 100.0%; Score 307; DB 6; Length 55;

Best Local Similarity 100.0%; Pred. No. 3.4e-34;
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MORFFGLNVTGKPNBETLDMMKPRCGVPSGGFMLTPGNPKWERTNLTIRNY 55
 DB 1 MORFFGLNVTGKPNBETLDMMKPRCGVPSGGFMLTPGNPKWERTNLTIRNY 55

RESULT 3

ADQ17093
 ID ADQ17093 standard; peptide; 55 AA.

XX ADQ17093;

DT 23-SEP-2004 (first entry)

DE Human matrix metalloproteinase-8 (MMP8) cleavage region peptide.

XX Fibronectin; healthy skin; wrinkle; wound; vulnerary; dermatological;
 KW human; matrix metalloproteinase; MMP.

XX Homo sapiens.

XX US2004127421-A1.

XX 01-JUL-2004.

XX 30-DEC-2002; 2002US-00335207.

XX 30-DEC-2002; 2002US-00335207.

XX (MALI/) MALIK S.

XX (QUIR/) QUIRK S.

XX Malik S, Quirk S;

XX WPI; 2004-506456/48.

XX Composition used for preventing and treating wrinkles and treating wounds
 PT comprises peptide having sequence related to matrix metalloproteinase
 PT proenzyme.

PS Example 1; SEQ ID NO 10; 60pp; English.

XX The present invention provides peptides and compositions containing such
 CC peptides that are useful as agents to maintain healthy skin and to
 CC promote the condition of the skin. The invention is useful for increasing
 CC the amount of fibronectin in tissue. The invention is also useful for
 CC encouraging the maintenance and development of healthy skin, preventing
 CC and treating wrinkles and for treating wounds. The invention acts as
 CC vulnerary and dermatological agents. The present sequence is human matrix
 CC metalloproteinase (MMP) cleavage region peptide. This sequence is used in
 CC the exemplification of the invention.

XX Sequence 55 AA;

Query Match 100.0%; Score 307; DB 8; Length 55;

Best Local Similarity 100.0%; Pred. No. 3.4e-34;
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORFFGLNVTGKPNBETLDMMKPRCGVPSGGFMLTPGNPKWERTNLTIRNY 55

DB 1 MORFFGLNVTGKPNBETLDMMKPRCGVPSGGFMLTPGNPKWERTNLTIRNY 55

RESULT 4

AAG65357

ID AAG65357 standard; protein; 444 AA.

XX AAG65357;

XX 30-NOV-2001 (first entry)

DE Human MMP-8alt polypeptide.
XX
KW MMP-8alt; MMP-8; matrix metalloproteinase; neutrophil collagenase;
KW anti-arthritis; cytostatic; anti-Parkinsonian; neuroprotective;
KW neutrotic; cancer; apoptosis; Parkinson's disease; Alzheimer's disease;
KW Huntington's disease; human; splice variant.
XX
OS Homo sapiens.
XX
PN US1973-H.
XX
PD 03-JUL-2001.
XX
PF 22-OCT-1998; 98US-00178002.
XX
PR 22-OCT-1998; 98US-00178002.
XX
PA (NOVS) NOVARTIS AG.
XX
PI Hu S;
XX
DR WPI; 2001-431511/46.
DR N-PSDB; AAH47515.
XX
XX New MMP-8alt polynucleotides and polypeptides useful as research reagents
PT and materials for discovering treatments and diagnostics to human
PT disease, or as targets for identifying inhibitors of MMP-8alt expression.
XX
PS Claim 11; Col 25-30; 25pp; English.
XX
XX The invention relates to human MMP-8alt polypeptide and polynucleotides.
CC MMP-8alt is a splice variant of the MMP-8 (matrix metalloproteinase)
CC cDNA. The MMP-8alt polypeptide can be expressed by standard recombinant
CC methodology. The polynucleotides and polypeptides may be used as research
CC reagents and materials for the discovery of treatments and diagnostics to
CC human disease, and as targets for identifying modulators. Inhibitors of
CC MMP-8alt polynucleotide or polypeptide expression may be used to treat
CC and/or prevent arthritis, cancer and cancer metastasis, and diseases
CC caused by cellular apoptosis including Parkinson's disease, Alzheimer's
CC disease and Huntington's disease. The present sequence represents the
CC human MMP-8alt polypeptide
XX
SQ Sequence 444 AA;
Query Match 100.0%; Score 307; DB 4; Length 444;
Best Local Similarity 100.0%; Pred. No. 4.4e-33;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MORFFGLNVTGKNEETLDMKKPCGVPDGGFMLTPGNPKWERTNLTIRNY 55
DB 43 MORFFGLNVTGKNEETLDMKKPCGVPDGGFMLTPGNPKWERTNLTIRNY 97
RESULT 5
AAB84610
ID AAB84610 standard; protein; 467 AA.
XX
AC AAB84610;
XX
DT 05-SEP-2001 (first entry)
XX
DE Amino acid sequence of matrix metalloproteinase-8.
XX
KW Growth factor; protein inhibitor; protease; damaged tissue;
KW platelet-derived growth factor; PDGF; fibroblast growth factor; FGF;
KW connective tissue derived growth factor; CTGF; chrysalin; VEGF;
KW keratinocyte-derived growth factor; KGF; epidermal growth factor; EGF;
KW transforming growth factor-beta; TGF-beta; matrix metalloproteinase; MMP;
KW granulocyte macrophage colony stimulating factor; GM-CSF; uPA;
KW vascular endothelial growth factor; urokinase plasminogen activator;
KW dermal ulcer; wound.
XX
OS Homo sapiens.

XX WO200149309-A2.
XX
XX 12-JUL-2001.
XX
XX 21-DEC-2000; 200CWO-IB001935.
XX
XX 29-DEC-1999; 99GB-00030768.
XX
XX (PFIZ) PFIZER LTD.
XX (PFIZ) PFIZER INC.
XX
XX Davies MJ, Huggins JP, McIntosh FS, Occleston NL;
XX
XX WPI; 2001-418351/44.
XX N-PSDB; AAH28225.
XX
XX Composition for the treatment of damaged tissue i.e. chronic wounds and
XX dermal ulcers comprises an inhibitor agent i.e. a protease and a growth
XX factor.
XX
XX Disclosure; Page 555; 572pp; English.
XX
XX The specification describes a pharmaceutical composition, comprising a
XX growth factor, an inhibitor agent, i.e. a protease. The inhibitor agent
XX inhibits the action of at least one specific adverse protein, i.e. a
XX protease, that is upregulated in a damaged tissue such as a wound
XX environment. Growth factors which are included in the composition of the
XX invention are platelet-derived growth factor (PDGF), fibroblast growth
XX factor (FGF), connective tissue derived growth factor (CTGF),
XX keratinocyte-derived growth factor (KGF), transforming growth factor-beta
XX (TGF-beta), granulocyte macrophage colony stimulating factor (GM-CSF),
XX epidermal growth factor (EGF), vascular endothelial growth factor (VEGF),
XX and chrysalin. Inhibitors which are included in the composition of the
XX invention include inhibitors of urokinase-type plasminogen activator
XX (uPA) and matrix metalloproteinase (MMP). The composition is useful for
XX the treatment of chronic damaged tissue, i.e. wounds and dermal ulcers.
XX The present sequence represents a human MMP-8, and is used to produce the
XX composition of the invention
XX
SQ Sequence 467 AA;
Query Match 100.0%; Score 307; DB 4; Length 467;
Best Local Similarity 100.0%; Pred. No. 4.7e-33;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MORFFGLNVTGKNEETLDMKKPCGVPDGGFMLTPGNPKWERTNLTIRNY 55
DB 66 MORFFGLNVTGKNEETLDMKKPCGVPDGGFMLTPGNPKWERTNLTIRNY 120
RESULT 6
AAE10416
ID AAE10416 standard; protein; 467 AA.
XX
AC AAE10416;
XX
DT 10-DEC-2001 (first entry)
XX
DE Human matrix metalloproteinase-8 (MMP-8) protein.
XX
KW Human; matrix metalloproteinase; MMP-8; hair growth; antisense therapy;
KW endopeptidase; skin cell; breast cancer; hair follicle; chromosome 11q22.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..20
XX /label= Signal_peptide
XX Protein 21..467
XX /label= Mature_MMP_8_protein
XX Domain 89..95
XX /label= Cysteine_switch_domain

PA (FRAS/) FRASER C C.
 PA (BARN/) BARNES T M.
 PA (SHAR/) SHARP J D.
 PA (KIRS/) KIRST S J.
 PA (MYER/) MYERS P S.
 PA (LEIB/) LEIBY K R.
 PA (HOLT/) HOLTZMAN D A.
 PA (MCCA/) MCCARTHY S A.
 PA (WRIGHT/) WRIGHTON N.
 PA (MACK/) MACKAY C R.
 PA (GOOD/) GOODEARL A D J.
 XX
 PI Fraser CC, Barnes TM, Sharp JD, Kirst SJ, Myers PS, Leiby KR;
 PI Holtzman DA, McCarthy SA, Wrighton N, Mackay CR, Goodearl ADJ;
 DR WPI; 2003-456230/43.
 DR N-PSDB; ACD66741.
 XX
 XX New nucleic acid molecule encoding a secreted protein (e.g. TANGO 202,
 PT TANGO 210 or INTERCEPT 217), useful for diagnosing, preventing or
 PT treating disorders such as cancer, diabetes or atherosclerosis, and in
 PT forensic biology.
 XX
 XX Disclosure; Fig 15V-15W; 482pp; English.
 PS
 PS The invention relates to secreted polypeptide-related proteins and
 CC nucleic acids (TANGO and INTERCEPT proteins and nucleic acids). The
 CC nucleic acids, proteins and antibodies specific to the proteins are
 CC useful in screening assays, predictive medicine (e.g. diagnostic assays,
 CC prognostic assays, monitoring clinical trials and pharmacogenetics) and
 CC prophylactic and therapeutic methods. The sequences are used in
 CC diagnosing, preventing or treating proliferative disorders (e.g.
 CC cancers), hormonal disorders (e.g. diabetes or thyroid disorders), immune
 CC disorders (e.g. multiple sclerosis or lupus), neurological disorders
 CC (e.g. Alzheimer's disease or Parkinson's disease), cardiovascular
 CC disorders (e.g. myocardial infarction or congestive heart disease), blood
 CC platelet disorders (e.g. thrombocytopenia or anaemia) and disorders
 CC involving blood vessels (e.g. atherosclerosis or vasculitis). The nucleic
 CC acids may also be used in chromosome mapping, tissue typing and forensic
 CC biology, and as surrogate markers. This sequence represents a secreted
 CC polypeptide-related protein of the invention. Note: The sequence data for
 CC this patent was obtained in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html
 XX
 XX Sequence 467 AA;
 SQ
 Query Match 100.0%; Score 307; DB 6; Length 467;
 Best Local Similarity 100.0%; Pred. No. 4.7e-33;
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 MORFFGLNVTGKPNBETLDMKKPCRGVDSGGFMLTPGNPKWERTNLTIRNY 55
 Db 56 MORFFGLNVTGKPNBETLDMKKPCRGVDSGGFMLTPGNPKWERTNLTIRNY 120
 RESULT 9
 ADQ10212
 ID ADQ10212 standard; protein; 467 AA.
 AC ADQ10212;
 XX
 XX 09-SEP-2004 (first entry)
 DT
 DE Human polypeptide #75.
 XX
 XX Human; cancer; obesity; gastritis; diarrhoea; haemorrhoid; asthma;
 KW anaemia; graft-versus-host reaction; allergic reaction; cystic fibrosis;
 KW hypogonadism; cardiovascular disorder; arthritis; osteoarthritis;
 KW arteriosclerosis; hypertension; bacterial infection; psoriasis;
 KW diabetes mellitus; hepatitis; Alzheimer's disease; Huntington's disease;
 KW Parkinson's disease; AIDS; tuberculosis; viral infection; malaria;
 KW goiter; infertility; endometriosis; muscular disorder.

OS Homo sapiens.
 XX
 PN US2004121396-A1.
 XX
 PD 24-JUN-2004.
 XX
 PF 19-DEC-2003; 2003US-00741790.
 XX
 PR 14-JUN-1999; 99US-00333159.
 PR 29-JUN-1999; 99US-00342364.
 PR 10-SEP-1999; 99US-00393996.
 PR 19-OCT-1999; 99US-00420707.
 PR 07-JAN-2000; 2000US-00479249.
 PR 27-APR-2000; 2000US-00559497.
 PR 24-MAY-2000; 2000US-00578063.
 PR 16-JUN-2000; 2000US-00596194.
 PR 23-JUN-2000; 2000US-00602871.
 PR 30-JUN-2000; 2000US-00608452.
 PR 12-JAN-2001; 2001US-00759130.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.

PI Fraser CC, Barnes TM, Sharp JD, Kirst SJ, Myers PS, Leiby KR;
 PI Holtzman DA, McCarthy SA, Wrighton N, Mackay CR, Goodearl ADJ;
 DR WPI; 2004-479675/45.

XX New TANGO, INTERCEPT, and MANGO, useful in diagnosing, preventing, and
 PT treating cancer, constipation, hemorrhoids, cystic fibrosis, and
 PT hypogonadism, psoriasis, hepatitis, Alzheimer's disease, AIDS,
 PT tuberculosis, malaria, goiter, infertility.

XX Disclosure; SEQ ID NO 176; 483pp; English.

XX The invention relates to human polynucleotides and the polypeptides they
 CC encode. The invention also relates to a host cell containing a
 CC polynucleotide of the invention, an antibody which selectively binds with
 CC a polypeptide of the invention, a method of detecting the presence of a
 CC polypeptide in a sample, a method of identifying a compound which binds
 CC with a polypeptide, and a method of modulating the activity of a
 CC polypeptide. The polynucleotides, polypeptides and compositions are
 CC useful for diagnosing, preventing and/or treating cancer, obesity,
 CC gastritis, diarrhoea, haemorrhoids, asthma, anaemia, graft-versus-host
 CC reactions, allergic reactions, cystic fibrosis, hypogonadism,
 CC cardiovascular disorders, arthritis, osteoarthritis, arteriosclerosis,
 CC hypertension, bacterial infections, psoriasis, diabetes mellitus,
 CC hepatitis, Alzheimer's disease, Huntington's disease, Parkinson's
 CC disease, AIDS, tuberculosis, viral infections, malaria, goiter,
 CC infertility, endometriosis, wounds and muscular disorders. This sequence
 CC represents a human polypeptide of the invention. Note: The sequence data
 CC for this patent did not form part of the printed specification but was
 CC obtained in electronic format from USPTO at
 CC seqdata.uspto.gov/sequence.html.

XX Sequence 467 AA;

Query Match 100.0%; Score 307; DB 8; Length 467;
 Best Local Similarity 100.0%; Pred. No. 4.7e-33;
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MORFFGLNVTGKPNBETLDMKKPCRGVDSGGFMLTPGNPKWERTNLTIRNY 55
 Db 66 MORFFGLNVTGKPNBETLDMKKPCRGVDSGGFMLTPGNPKWERTNLTIRNY 120

RESULT 10
 ADL93947
 ID ADL93947 standard; protein; 454 AA.

XX ADL93947;

DT 20-MAY-2004 (first entry)

DE Human G-coupled protein receptor-related protein #19.

XX human; transgenic; Gene Therapy; Protein Therapy; cardiomyopathy;

KW atherosclerosis; hypertension; congenital heart defect; aortic stenosis;

KW atrial septal defect; atrioventricular canal defect; ductus arteriosus;

KW pulmonary stenosis; subaortic stenosis; ventricular septal defect;

KW valve disease; tuberculous sclerosis; scleroderma; obesity; transplantation;

KW adrenoleukodystrophy; congenital adrenal hyperplasia; prostate cancer;

KW neoplasm; adenocarcinoma; lymphoma; uterus cancer; fertility;

KW haemophilia; hypercoagulation; idiopathic thrombocytopenic purpura;

KW immunodeficiency; graft versus host disease; AIDS; bronchial asthma;

KW Crohn's disease; G-coupled protein receptor; metabolic disorder;

XX neurodegenerative disorder; receptor.

OS Homo sapiens.

XX US2004006205-A1.

XX 08-JAN-2004.

XX 02-APR-2002; 2002US-00115479.

XX 03-APR-2001; 2001US-0281136P.

PR 05-APR-2001; 2001US-0281863P.

PR 10-APR-2001; 2001US-0282934P.

PR 13-APR-2001; 2001US-0283657P.

PR 13-APR-2001; 2001US-0283678P.

PR 13-APR-2001; 2001US-0283687P.

PR 13-APR-2001; 2001US-0283710P.

PR 17-APR-2001; 2001US-0284234P.

PR 19-APR-2001; 2001US-0285323P.

PR 20-APR-2001; 2001US-0285609P.

PR 23-APR-2001; 2001US-0285748P.

PR 23-APR-2001; 2001US-0285890P.

PR 24-APR-2001; 2001US-0286068P.

PR 27-APR-2001; 2001US-0287213P.

PR 03-MAY-2001; 2001US-0288509P.

PR 30-NAY-2001; 2001US-0294495P.

PR 31-MAY-2001; 2001US-0294801P.

PR 31-JUL-2001; 2001US-0309216P.

PR 25-SEP-2001; 2001US-0324775P.

PR 28-NOV-2001; 2001US-0333900P.

XX (LIL/)/ LI L.

PA (GERL/)/ GERLACH V.

PA (LIUX/)/ LIU X.

PA (MILL/)/ MILLER C E.

PA (SPYT/)/ SPYTER K A.

PA (ZERR/)/ ZERHUSEN B D.

PA (PENA/)/ PENA C E A.

PA (SHEN/)/ SHENOY S G.

PA (ZHON/)/ ZHONG H.

PA (SMIT/)/ SMITHSON G.

PA (CASK/)/ CASKMAN S J.

PA (BOLD/)/ BOLDOG F L.

PA (VOSS/)/ VOSS E Z.

PA (VERN/)/ VERNET C A.

PA (MACD/)/ MACDOUGALL J R.

PA (RAST/)/ RASTELLI L.

PA (ANDE/)/ ANDERSON D W.

PA (ZHON/)/ ZHONG M.

PA (MEZE/)/ MEZES P S.

PA (FURT/)/ FURTAK K.

PA (PATT/)/ PATTURAJAN M.

PA (BURG/)/ BURGESS C E.

PA (WALY/)/ MALYANKAR U M.

PA (SHIM/)/ SHIMKETS R A.

PA (TAUP/)/ TAUFIER R J.

PA (EDIN/)/ EDINGER S.

PA (MAZU/)/ MAZUR A.

PI Li L, Gerlach V, Liu X, Miller CE, Spytek KA, Zerhusen BD;

PI Pena CEA, Shenoy SG, Zhong H, Smithson G, Casman SJ, Boldog FL;

PI Voss EZ, Vernet CA, Macdougall JR, Rastelli L, Anderson DW, Zhong M;

PI Mezes PS, Furtak K, Patturajan M, Burgess CE, Malyankar UM;

PI Shimkets RA, Taupier RJ, Edinger S, Mazur A;

XX WPI; 2004-224146/21.

DR N-PSDB; ADL93946.

XX New G-coupled protein-receptor related polypeptides, for preventing

PT treating or ameliorating, e.g. acquired immunodeficiency syndrome,

PT bronchial asthma, Crohn's disease, prostate cancer, hemophilia,

PT scleroderma or obesity.

XX Claim 1; Page 69; 220pp; English.

XX The invention relates to isolated human G-coupled protein receptor-

CC related polypeptides and polynucleotides. The proteins are useful for

CC preventing, treating or ameliorating medical disorders by protein or gene

CC therapy. Disorders include cardiomyopathy, atherosclerosis, hypertension,

CC congenital heart defects, aortic stenosis, atrial septal defect,

CC atrioventricular canal defect, ductus arteriosus, pulmonary stenosis,

CC subaortic stenosis, ventricular septal defect, valve diseases, tubercous

CC sclerosis, scleroderma, obesity, transplantation, adrenoleukodystrophy,

CC congenital adrenal hyperplasia, prostate cancer, neoplasm,

CC adenocarcinoma, lymphoma, uterus cancer, fertility, haemophilia,

CC hypercoagulation, idiopathic thrombocytopenic purpura,

CC immunodeficiencies, graft versus host disease, AIDS, bronchial asthma,

CC metabolic disorders, neurodegenerative disorders or Crohn's disease. They

CC are also useful as diagnostic or research tools. The present sequence

CC represents a human G-coupled protein receptor-related protein of the

CC invention.

XX Sequence 454 AA;

SQ Query Match 73.6%; Score 226; DB 8; Length 454;

Best Local Similarity 72.7%; Pred. No. 6e-22;

Matches 40; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 MQRFGLNVTGKPNNEETLDMKKPCGVPDSCGGMVLTGCPKWTNLTIRNY 55

DB 50 MQEFGFLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGPNRWEQNTLTIRNY 104

RESULT 11

ADE16002

ID ADE16002 standard; protein; 454 AA.

XX ADE16002;

XX 29-JAN-2004 (first entry)

XX G-coupled protein receptor related polypeptide, SEQ ID No 32.

XX G-coupled protein receptor; antidiabetic; anorectic; antibacterial;

KW virucide; fungicide; cytostatic; nootropic; neuroprotective;

KW antiparkinsonian; haemostatic; antilipaeamic; neurogenesis;

KW cell differentiation; cell proliferation; hematopoiesis; wound healing;

KW angiogenesis; gene therapy; chromosome mapping; tissue typing;

XX preventive medicine; pharmacogenomics; human.

XX Homo sapiens.

XX WO200283841-A2.

XX 24-OCT-2002.

XX 03-APR-2002; 2002WO-US010713.

XX 03-APR-2001; 2001US-0281136P.

PR 05-APR-2001; 2001US-0281863P.

PR 10-APR-2001; 2001US-0281906P.

PR 13-APR-2001; 2001US-0282934P.

PR 13-APR-2001; 2001US-0283657P.

us-10-032-376a-10._.rag

Mon Nov 15 14:23:29 2004

CC the following activities: antidiabetic, anorectic, antibacterial,
CC virucide, fungicide, cytostatic, nootropic, neuroprotective,
CC antiparkinsonian, haemostatic, and antilipemic. The G-coupled protein
CC receptor related polypeptides are useful in a method of treating or
CC preventing in a human, a pathology associated with the G-coupled protein
CC receptor related polypeptides. The polypeptides are useful in the
CC manufacture of a medicament for treating a syndrome associated with a
CC human disease, preferably a NOX-associated disorder. The novel
CC polypeptides are useful for treating, preventing or diagnosing diseases,
CC such as metabolic disorders, diabetes, obesity, infectious diseases,
CC anorexia, cancer-associated diseases, neurodegenerative disorders,
CC Alzheimer's disease, Parkinson's disease, immune disorders, hematopoietic
CC disorders, and various dyslipidaemias, metabolic disturbances associated
CC with obesity, metabolic X syndrome and wasting disorders associated with
CC chronic diseases and various cancers. The nucleic acids and polypeptides
CC may also be used as targets for the identification of small molecules
CC that modulate or inhibit e.g. neurogenesis, cell differentiation, cell
CC proliferation, hematopoiesis, wound healing and angiogenesis, in gene
CC therapy, in generation of antibodies that bind immunospecifically to NOX
CC substances for use in therapeutic or diagnostic methods. The nucleic
CC acids are further used as hybridization probes, in chromosome mapping,
CC tissue typing, preventive medicine, and pharmacogenomics. This sequence
CC represents one of the novel G-coupled protein receptor related
CC polypeptides of the invention.

XX Sequence 454 AA;

Query Match 72.0%; Score 221; DB 7; Length 454;
Best Local Similarity 70.9%; Pred. No. 2.9e-21;
Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 MQRFFGLNVTGKNEETLDMKKPRCGVPSDGGFMLTPGNKWTNLTIRNY 55
DB 50 MQEFFGLKVTGPDATLTKWKQPRCGVDPVAQFVLTEGNPRWEQTHLYRIENY 104

RESULT 13
ADE16008
ID ADE16008 standard; protein; 454 AA.

XX ADE16008;
DT 29-JAN-2004 (first entry)
XX G-coupled protein receptor related polypeptide, SEQ ID NO 38.
XX G-coupled protein receptor; antidiabetic; anorectic; antibacterial;
KW virucide; fungicide; cytostatic; nootropic; neuroprotective;
KW antiparkinsonian; haemostatic; antilipemic; neurogenesis;
KW cell differentiation; cell proliferation; hematopoiesis; wound healing;
KW angiogenesis; gene therapy; chromosome mapping; tissue typing;
KW preventive medicine; pharmacogenomics; human.

OS Homo sapiens.
XX WO200283841-A2.
PN 24-OCT-2002.

XX 03-APR-2002; 2002WO-US010713.
XX 03-APR-2001; 2001US-0281136P.
XX 05-APR-2001; 2001US-0281863P.
XX 10-APR-2001; 2001US-0281906P.
XX 13-APR-2001; 2001US-0282334P.
XX 13-APR-2001; 2001US-0283657P.
XX 13-APR-2001; 2001US-0283678P.
XX 13-APR-2001; 2001US-0283687P.
XX 13-APR-2001; 2001US-0283710P.
XX 17-APR-2001; 2001US-0284234P.
XX 19-APR-2001; 2001US-0285325P.
XX 20-APR-2001; 2001US-0285609P.
XX 23-APR-2001; 2001US-0285748P.

PR 23-APR-2001; 2001US-0285890P.
PR 24-APR-2001; 2001US-0286068P.
PR 27-APR-2001; 2001US-0287213P.
PR 03-MAY-2001; 2001US-0288503P.
PR 30-MAY-2001; 2001US-0294495P.
PR 31-MAY-2001; 2001US-0294801P.
PR 31-JUL-2001; 2001US-0309216P.
PR 25-SEP-2001; 2001US-0324775P.
PR 28-NOV-2001; 2001US-0333900P.
PR 02-APR-2002; 2002US-00115479.

XX (CURA-) CURAGEN CORP.

XX Li L, Gerlach V, Liu X, Miller CE, Spytek KA, Zerhusen BD;
PI Pena CEA, Shenoy SG, Zhong H, Smithson G, Casman SJ, Boldog FI;
PI Voss EZ, Vernet CAM, Macdougall JR, Rastelli L, Anderson DW;
PI Zhong M, Mezes PD, Furtak K, Patturajan M, Burgess CE, Malyankar UM;
PI Shimkets RA, Taupier RV, Edinger SR, Mazur A;
XX WPI; 2003-067574/06.
DR N-PSDB; ADE16007.

XX New isolated NOX polypeptides and polynucleotides, useful for
PT preventing diagnosing or treating NOX-associated disorders e.g.
PT diabetes, obesity, dyslipidemias, cancer, Parkinson's disease,
PT Alzheimer's disease, infections.

XX Claim 1; SEQ ID NO 38; 320pp; English.

XX The invention relates to a novel isolated G-coupled protein receptor
CC related polypeptides. The novel polypeptide comprise any of the 22 fully
CC defined sequences of 87-1780 amino acids, given in the specification;
CC their mature forms; and possible variants. The novel polypeptides have
CC the following activities: antidiabetic, anorectic, antibacterial,
CC virucide, fungicide, cytostatic, nootropic, neuroprotective,
CC antiparkinsonian, haemostatic, and antilipemic. The G-coupled protein
CC receptor related polypeptides are useful in a method of treating or
CC preventing in a human, a pathology associated with the G-coupled protein
CC receptor related polypeptides. The polypeptides are useful in the
CC manufacture of a medicament for treating a syndrome associated with a
CC human disease, preferably a NOX-associated disorder. The novel
CC polypeptides are useful for treating, preventing or diagnosing diseases,
CC such as metabolic disorders, diabetes, obesity, infectious diseases,
CC anorexia, cancer-associated diseases, neurodegenerative disorders,
CC Alzheimer's disease, Parkinson's disease, immune disorders, hematopoietic
CC disorders, and various dyslipidaemias, metabolic disturbances associated
CC with obesity, metabolic X syndrome and wasting disorders associated with
CC chronic diseases and various cancers. The nucleic acids and polypeptides
CC may also be used as targets for the identification of small molecules
CC that modulate or inhibit e.g. neurogenesis, cell differentiation, cell
CC proliferation, hematopoiesis, wound healing and angiogenesis, in gene
CC therapy, in generation of antibodies that bind immunospecifically to NOX
CC substances for use in therapeutic or diagnostic methods. The nucleic
CC acids are further used as hybridization probes, in chromosome mapping,
CC tissue typing, preventive medicine, and pharmacogenomics. This sequence
CC represents one of the novel G-coupled protein receptor related
CC polypeptides of the invention.

XX Sequence 454 AA;

Query Match 72.0%; Score 221; DB 7; Length 454;
Best Local Similarity 70.9%; Pred. No. 2.9e-21;
Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 MQRFFGLNVTGKNEETLDMKKPRCGVPSDGGFMLTPGNKWTNLTIRNY 55
DB 50 MQEFFGLKVTGPDATLTKWKQPRCGVDPVAQFVLTEGNPRWEQTHLYRIENY 104

RESULT 14
ADE16006
ID ADE16006 standard; protein; 454 AA.
XX

AC ADE16006;
XX
DT 29-JAN-2004 (first entry)
XX
DE G-coupled protein receptor related polypeptide, SEQ ID NO 36.
DE
XX
KW G-coupled protein receptor; antidiabetic; anorectic; antibacterial;
KW virucide; fungicide; cytostatic; nootropic; neuroprotective;
KW antiparkinsonian; haemostatic; antilipemic; neurogenesis;
KW cell differentiation; cell proliferation; hematopoiesis;
KW angiogenesis; gene therapy; chromosome mapping; tissue typing;
KW preventive medicine; pharmacogenomics; human.
XX
XX Homo sapiens.
XX
XX WO200283841-A2.
XX
XX 24-OCT-2002.
XX
XX 03-APR-2002; 2002WO-US010713.
XX
XX 03-APR-2001; 2001US-0281136P.
XX 05-APR-2001; 2001US-0281863P.
XX 05-APR-2001; 2001US-0281906P.
XX 10-APR-2001; 2001US-0282934P.
XX 13-APR-2001; 2001US-0283657P.
XX 13-APR-2001; 2001US-0283678P.
XX 13-APR-2001; 2001US-0283687P.
XX 13-APR-2001; 2001US-0283710P.
XX 17-APR-2001; 2001US-0284234P.
XX 19-APR-2001; 2001US-0285325P.
XX 20-APR-2001; 2001US-0285609P.
XX 23-APR-2001; 2001US-0285748P.
XX 23-APR-2001; 2001US-0285890P.
XX 24-APR-2001; 2001US-0286068P.
XX 27-APR-2001; 2001US-0287213P.
XX 03-MAY-2001; 2001US-0288509P.
XX 30-MAY-2001; 2001US-0294495P.
XX 31-JUL-2001; 2001US-0309218P.
XX 25-SEP-2001; 2001US-0324775P.
XX 28-NOV-2001; 2001US-0333900P.
XX 02-APR-2002; 2002US-00115479.
XX (CURA-) CURAGEN CORP.
XX
XX Li L, Gerlach V, Liu X, Miller CE, Spytek KA, Zerhusen BD;
XX Pena CRA, Shenoy SG, Zhong H, Smithson G, Casman SJ, Boldog FL;
XX Voss EZ, Vernet CAM, Macdougall JR, Rastelli L, Anderson DW;
XX Zhong M, Mezes PD, Furtak K, Patturajan M, Burgess CE, Malyankar UM;
XX Shinkets RA, Taupier RJ, Edinger SR, Mazur A;
XX
XX WPI; 2003-067574/06.
XX N-PSDB; ADE16005.
XX
XX New isolated NOVX polypeptides and polynucleotides, useful for
XX preventing, diagnosing or treating NOVX-associated disorders e.g.
XX diabetes, obesity, dyslipidemias, cancer, Parkinson's disease,
XX Alzheimer's disease, infections.
XX
XX Claim 1; SEQ ID NO 36; 320pp; English.
XX
XX The invention relates to a novel isolated G-coupled protein receptor
XX related polypeptides. The novel polypeptide comprise any of the 22 fully
XX defined sequences of 87-1780 amino acids, given in the specification;
XX their mature forms; and possible variants. The novel polypeptides have
XX the following activities: antidiabetic, anorectic, antibacterial,
XX virucide, fungicide, cytostatic, nootropic, neuroprotective,
XX antiparkinsonian, haemostatic, and antilipemic. The G-coupled protein
XX receptor related polypeptides are useful in a method of treating or
XX preventing in a human, a pathology associated with the G-coupled protein
XX receptor related polypeptides. The polypeptides are useful in the
XX manufacture of a medicament for treating a syndrome associated with a

CC human disease, preferably a NOVX-associated disorder. The novel
CC polypeptides are useful for treating, preventing or diagnosing diseases,
CC such as metabolic disorders, diabetes, obesity, infectious diseases,
CC anorexia, cancer-associated diseases, neurodegenerative disorders,
CC Alzheimer's disease, Parkinson's disease, immune disorders, hematopoietic
CC disorders, and various dyslipidemias, metabolic disturbances associated
CC with obesity, metabolic X syndrome and wasting disorders associated with
CC chronic diseases and various cancers. The nucleic acids and polypeptides
CC may also be used as targets for the identification of small molecules
CC that modulate or inhibit e.g. neurogenesis, cell differentiation, cell
CC proliferation, hematopoiesis, wound healing and angiogenesis, in gene
CC therapy, in generation of antibodies that bind immunospecifically to NOVX
CC acids are further used as hybridization or diagnostic methods. The nucleic
CC tissue typing, preventive medicine, and pharmacogenomics. This sequence
CC represents one of the novel G-coupled protein receptor related
CC polypeptides of the invention.
XX
XX Sequence 454 AA;
SQ

Query Match 72.0%; Score 221; DB 7; Length 454;
Best Local Similarity 70.9%; Pred. No. 2.9e-21;
Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
Qy 1 MQRFFGLNVTGKNEETLDMKKXPRCGVDSGGFMLTPGNKWERNTLTYRIYNY 55
Db 50 MQEFFGLKVTGKPDATLTKVMKQRCGVPDVAQFVLTEGNPRWEOTHLTYRIENY 104

RESULT 15
ADL93945
ID ADL93945 standard; protein; 454 AA.
XX
XX AC ADL93945;
XX
XX 20-MAY-2004 (first entry)
XX
XX Human G-coupled protein receptor-related protein #18.
XX
XX human; transgenic; Gene Therapy; Protein Therapy; cardiomyopathy;
KW atherosclerosis; hypertension; congenital heart defect; aortic stenosis;
KW atrial septal defect; atrioventricular canal defect; ductus arteriosus;
KW pulmonary stenosis; subaortic stenosis; ventricular septal defect;
KW valve disease; tuberculous sclerosis; scleroderma; obesity; transplantation;
KW adrenoleukodystrophy; congenital adrenal hyperplasia; prostate cancer;
KW neoplasm; adenocarcinoma; lymphoma; uterus cancer; fertility;
KW hemophilia; hypercoagulation; idiopathic thrombocytopenic purpura;
KW immunodeficiency; graft versus host disease; AIDS; bronchial asthma;
KW Crohn's disease; G-coupled protein receptor; metabolic disorder;
KW neurodegenerative disorder; receptor.
XX
XX Homo sapiens.
XX
XX US2004006205-A1.
XX
XX 08-JAN-2004.
XX
XX 02-APR-2002; 2002US-00115479.
XX
XX 03-APR-2001; 2001US-0281136P.
XX 05-APR-2001; 2001US-0281863P.
XX 05-APR-2001; 2001US-0281906P.
XX 10-APR-2001; 2001US-0282934P.
XX 13-APR-2001; 2001US-0283657P.
XX 13-APR-2001; 2001US-0283678P.
XX 13-APR-2001; 2001US-0283687P.
XX 13-APR-2001; 2001US-0283710P.
XX 17-APR-2001; 2001US-0284234P.
XX 19-APR-2001; 2001US-0285325P.
XX 20-APR-2001; 2001US-0285609P.
XX 23-APR-2001; 2001US-0285748P.
XX 23-APR-2001; 2001US-0285890P.
XX 24-APR-2001; 2001US-0286068P.

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OM protein - protein search, using sw model

Run on: November 15, 2004, 14:01:35 ; Search time 14.8077 Seconds
(without alignments)
246.324 Million cell updates/sec

Title: US-10-032-376A-10

Perfect score: 307

Sequence: 1 MQRFFGLNVTGKPNETLDM.....LTPGNPKWERNLTIRINY 55

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 205538

Minimum DB seq length: 47

Maximum DB seq length: 660

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	307	100.0	444	1	US-09-178-002-2
2	307	100.0	466	3	US-08-704-711A-17
3	307	100.0	466	3	US-09-521-220-17
4	307	100.0	467	1	US-09-178-002-4
5	307	100.0	467	3	US-09-391-104-24
6	307	100.0	468	3	US-08-448-489-13
7	221	72.0	469	3	US-08-704-711A-16
8	221	72.0	469	3	US-08-448-489-12
9	221	72.0	469	3	US-09-521-220-16
10	221	72.0	469	3	US-09-391-104-23
11	196	63.8	477	3	US-08-704-711A-20
12	196	63.8	477	3	US-08-448-489-15
13	196	63.8	477	3	US-08-281-313-1
14	196	63.8	477	3	US-09-521-220-20
15	196	63.8	477	3	US-09-391-104-21
16	195	63.5	476	3	US-08-704-711A-21
17	195	63.5	476	3	US-08-448-489-14
18	195	63.5	476	3	US-09-521-220-21
19	195	63.5	476	3	US-09-391-104-22
20	188	61.2	471	3	US-09-391-104-25
21	179	58.3	471	4	US-08-994-689C-1
22	172	56.0	471	4	US-08-994-689C-21
23	164	53.4	513	4	US-10-140-002-192
24	164	53.4	513	4	US-09-862-631-4
25	160	52.1	264	3	US-09-009-156-6
26	160	52.1	264	3	US-09-372-154-6
27	160	52.1	267	3	US-08-448-489-18

28 160 52.1 267 3 US-09-391-104-27
29 160 52.1 271 3 US-08-896-062-2
30 160 52.1 470 3 US-08-088-392-2
31 160 52.1 470 3 US-08-396-988-2
32 160 52.1 470 3 US-09-391-104-26
33 159 51.8 135 4 US-09-513-999C-4163
34 153 49.8 631 3 US-08-448-489-17
35 153 49.8 660 3 US-08-704-711A-18
36 153 49.8 660 3 US-09-521-220-18
37 153 49.8 660 3 US-09-391-104-19
38 153 49.8 660 4 US-09-917-254-89
39 143.5 46.7 604 3 US-09-391-104-30
40 143.5 46.7 607 3 US-09-000-041A-2
41 143.5 46.7 607 3 US-09-211-704A-10
42 143.5 46.7 607 4 US-09-734-002-2
43 142 46.3 136 4 US-09-513-999C-4639
44 138 45.0 462 3 US-08-068-392-3
45 138 45.0 462 3 US-08-396-988-3

ALIGNMENTS

RESULT 1
US-09-178-002-2
; Sequence 2, Application US/09178002
; Patent No. H001973
; GENERAL INFORMATION:
; APPLICANT: Hu, Shou-Ih
; TITLE OF INVENTION: Human Neutrophil Collagenase Splice Variant
; FILE REFERENCE: CGC 2048
; CURRENT APPLICATION NUMBER: US/09/178,002
; CURRENT FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-178-002-2

Query Match 100.0%; Score 307; DB 1; Length 444;
Best Local Similarity 100.0%; Pred. No. 5, 2e-32;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQRFFGLNVTGKPNETLDMKKKPCGVPDGGFMLTPGNPKWERNLTIRINY 55
DB 43 MQRFFGLNVTGKPNETLDMKKKPCGVPDGGFMLTPGNPKWERNLTIRINY 97

RESULT 2
US-08-704-711A-17
; Sequence 17, Application US/08704711A
; Patent No. 6114159
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; APPLICANT: HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/704,711A
; FILING DATE: 20-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/DE95/00357
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 466 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-08-704-711A-17
Query Match 100.0%; Score 307; DB 3; Length 466;
Best Local Similarity 100.0%; Pred. No. 5.5e-32;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQRFFGLNVTGKNEETLDMKKPRCGVDSGGFMLTPGNPKWERTNLTIRNY 55
Db 66 MQRFFGLNVTGKNEETLDMKKPRCGVDSGGFMLTPGNPKWERTNLTIRNY 120

RESULT 3
US-09-521-220-17
; Sequence 17, Application US/09521220
; Patent No. 639348
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/521,220
; FILING DATE: 08-Mar-2000
; CLASSIFICATION: <Unknown>
; 21-OCT-1994
; 17-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/704,711
; FILING DATE: <Unknown>
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 466 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-521-220-17
Query Match 100.0%; Score 307; DB 3; Length 466;
Best Local Similarity 100.0%; Pred. No. 5.5e-32;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQRFFGLNVTGKNEETLDMKKPRCGVDSGGFMLTPGNPKWERTNLTIRNY 55
Db 66 MQRFFGLNVTGKNEETLDMKKPRCGVDSGGFMLTPGNPKWERTNLTIRNY 120

RESULT 4
US-09-178-002-4
; Sequence 4, Application US/09178002
; Patent No. H001973
; GENERAL INFORMATION:
; APPLICANT: Hu, Shou-Ih
; TITLE OF INVENTION: Human Neutrophil Collagenase Splice Variant
; FILE REFERENCE: CGC 2048
; CURRENT APPLICATION NUMBER: US/09/178,002
; CURRENT FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-178-002-4
Query Match 100.0%; Score 307; DB 1; Length 467;
Best Local Similarity 100.0%; Pred. No. 5.6e-32;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQRFFGLNVTGKNEETLDMKKPRCGVDSGGFMLTPGNPKWERTNLTIRNY 55
Db 66 MQRFFGLNVTGKNEETLDMKKPRCGVDSGGFMLTPGNPKWERTNLTIRNY 120

RESULT 5
US-09-391-104-24
; Sequence 24, Application US/09391104
; Patent No. 639371
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Falduto, Michael T.
; APPLICANT: Magnuson, Scott R.
; APPLICANT: Morgan, Douglas W.
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE.
; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
; TITLE OF INVENTION: OF USING SAME
; FILE REFERENCE: 6073.US.P1
; CURRENT APPLICATION NUMBER: US/09/391,104
; CURRENT FILING DATE: 1999-09-07
; PRIOR APPLICATION NUMBER: US 08/814,394
; PRIOR FILING DATE: 1997-03-11
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 467
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-391-104-24

Query Match      100.0%; Score 307; DB 3; Length 467;
Best Local Similarity 100.0%; Pred. No. 5.6e-32;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MORFFGLNVTGKPNETLDMKKPRCGVDSGGFMLTGNPKWERTNLTIRNY 55
Db      66 MORFFGLNVTGKPNETLDMKKPRCGVDSGGFMLTGNPKWERTNLTIRNY 120

RESULT 6
US-08-448-489-13
; Sequence 13, Application US/08448489
; Patent No. 6184022
; GENERAL INFORMATION:
; APPLICANT: SEIKI, Motoharu
; APPLICANT: SATO, Hiroshi
; APPLICANT: SHINAGAWA, Akira
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
; FILE REFERENCE: 55-290P
; CURRENT APPLICATION NUMBER: US/08/448,489
; CURRENT FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 13
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; FEATURE:
; OTHER INFORMATION: X = UNKNOWN
; OTHER INFORMATION: Description of Unknown Organism: Known Member of
; OTHER INFORMATION: Matrix Metalloproteinase Family
US-08-448-489-13

Query Match      100.0%; Score 307; DB 3; Length 468;
Best Local Similarity 100.0%; Pred. No. 5.6e-32;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MORFFGLNVTGKPNETLDMKKPRCGVDSGGFMLTGNPKWERTNLTIRNY 55
Db      66 MORFFGLNVTGKPNETLDMKKPRCGVDSGGFMLTGNPKWERTNLTIRNY 120

RESULT 7
US-08-704-711A-16
; Sequence 16, Application US/08704711A
; Patent No. 614159
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; APPLICANT: HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,711A
; FILING DATE: 20-NOV-1996
; CLASSIFICATION: 435

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-391-104-24

PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/DE95/00357
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 438838.1
; FILING DATE: 21-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 469 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-704-711A-16

Query Match      72.0%; Score 221; DB 3; Length 469;
Best Local Similarity 70.9%; Pred. No. 1.1e-20;
Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Qy      1 MORFFGLNVTGKPNETLDMKKPRCGVDSGGFMLTGNPKWERTNLTIRNY 55
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RESULT 8
US-08-448-489-12
; Sequence 12, Application US/08448489
; Patent No. 6184022
; GENERAL INFORMATION:
; APPLICANT: SEIKI, Motoharu
; APPLICANT: SATO, Hiroshi
; APPLICANT: SHINAGAWA, Akira
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
; FILE REFERENCE: 55-290P
; CURRENT APPLICATION NUMBER: US/08/448,489
; CURRENT FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 12
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Known Member of
; OTHER INFORMATION: Matrix Metalloproteinase Family
US-08-448-489-12

Query Match      72.0%; Score 221; DB 3; Length 469;
Best Local Similarity 70.9%; Pred. No. 1.1e-20;
Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Qy      1 MQEFGKLVTKGKPNETLDMKKPRCGVDSGGFMLTGNPKWERTNLTIRNY 55
Db      67 MQEFGKLVTKGKPDATLKVMPKQRCGVDPVQAQFVLTEGNPRWEQTHLTIRNY 121

RESULT 9
US-09-521-220-16
; Sequence 16, Application US/09521220
; Patent No. 6399348
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; APPLICANT: HINZMANN, Bernd
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/ TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
/ METALLOPROTEASES, THEIR PRODUCTION AND USE
/ NUMBER OF SEQUENCES: 22
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Foley & Lardner
/ STREET: 3000 K Street, N.W., Suite 500
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20007-5109
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/521,220
/ FILING DATE: 08-Mar-2000
/ CLASSIFICATION: <Unknown>
/ 21-OCT-1994
/ 17-MAR-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/704,711
/ FILING DATE: <Unknown>
/ APPLICATION NUMBER: DE 4438838.1
/ FILING DATE: 21-OCT-1994
/ APPLICATION NUMBER: DE 4409663.1
/ FILING DATE: 17-MAR-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: GRANADOS, Patricia D.
/ REGISTRATION NUMBER: 33,683
/ REFERENCE/DOCKET NUMBER: 26083/124
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202)672-5300
/ TELEFAX: (202)672-5399
/ TELEX: 904136
/ INFORMATION FOR SEQ ID NO: 16:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 469 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ SEQUENCE DESCRIPTION: SEQ ID NO: 16:
/ US-09-521-220-16
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/ Best Local Similarity 70.9%; Pred. No. 1.1e-20;
/ Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
/ QY 1 MQRFFGLNVTGKNEETLDMKKPRCGVDPDSGGFVLTGPNPKWERTNLTIRNY 55
/ Db 67 MQEFGKLVTKGKPDATLKVWKQPRCGVDPVAQFVLTGPNRWEQTHLTIRYNI 121
/ RESULT 10
/ US-09-391-104-23
/ Sequence 23, Application US/09391104
/ Patent No. 6399371
/ GENERAL INFORMATION:
/ APPLICANT: Abbott Laboratories
/ APPLICANT: Falduto, Michael T.
/ APPLICANT: Magnuson, Scott R.
/ APPLICANT: Morgan, Douglas W.
/ TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,
/ TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
/ FILE REFERENCE: 6073.US.P1
/ CURRENT APPLICATION NUMBER: US/09/391,104
/ CURRENT FILING DATE: 1999-09-07
/ PRIOR APPLICATION NUMBER: US 08/814,394
/ PRIOR FILING DATE: 1997-03-11
/ NUMBER OF SEQ ID NOS: 35
/ SOFTWARE: FastSeq for Windows Version 3.0

/ SEQ ID NO 23
/ LENGTH: 469
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-09-391-104-23
/ Query Match 72.0%; Score 221; DB 3; Length 469;
/ Best Local Similarity 70.9%; Pred. No. 1.1e-20;
/ Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
/ QY 1 MQRFFGLNVTGKNEETLDMKKPRCGVDPDSGGFVLTGPNPKWERTNLTIRNY 55
/ Db 67 MQEFGKLVTKGKPDATLKVWKQPRCGVDPVAQFVLTGPNRWEQTHLTIRYNI 121
/ RESULT 11
/ US-08-704-711A-20
/ Sequence 20, Application US/08704711A
/ Patent No. 6114159
/ GENERAL INFORMATION:
/ APPLICANT: WILL, Horst
/ APPLICANT: HINZMANN, Bernd
/ TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
/ TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
/ NUMBER OF SEQUENCES: 22
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Foley & Lardner
/ STREET: 3000 K Street, N.W., Suite 500
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20007-5109
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/704,711A
/ FILING DATE: 20-NOV-1996
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: WO PCT/DE95/00357
/ FILING DATE: 17-MAR-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: DE 4438838.1
/ FILING DATE: 21-OCT-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: DE 4409663.1
/ FILING DATE: 17-MAR-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: GRANADOS, Patricia D.
/ REGISTRATION NUMBER: 33,683
/ REFERENCE/DOCKET NUMBER: 26083/124
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202)672-5300
/ TELEFAX: (202)672-5399
/ TELEX: 904136
/ INFORMATION FOR SEQ ID NO: 20:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 477 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-704-711A-20
/ Query Match 63.8%; Score 196; DB 3; Length 477;
/ Best Local Similarity 63.6%; Pred. No. 2.1e-17;
/ Matches 35; Conservative 8; Mismatches 12; Indels 0; Gaps 0;
/ QY 1 MQRFFGLNVTGKNEETLDMKKPRCGVDPDSGGFVLTGPNPKWERTNLTIRNY 55
/ Db 67 MQEFGKLVTKGKPDATLKVWKQPRCGVDPVAQFVLTGPNRWEQTHLTIRYNI 121


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RESULT 12
US-08-448-489-15
; Sequence 15, Application US/08448489
; Patent No. 6184022
; GENERAL INFORMATION:
; APPLICANT: SEIKI, Motoharu
; APPLICANT: SATO, Hiroshi
; APPLICANT: SHINAGAWA, Akira
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
; FILE REFERENCE: 55-290P
; CURRENT APPLICATION NUMBER: US/08/448,489
; CURRENT FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 15
; LENGTH: 477
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Known Member of
; OTHER INFORMATION: Matrix Metalloproteinase family
US-08-448-489-15
Query Match 63.8%; Score 196; DB 3; Length 477;
Best Local Similarity 63.6%; Pred. No. 2.1e-17;
Matches 35; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 MQRFFGLNVTGKNEETLDMKKPCGVPDSCGFMLTGPNPKWERTNLTIRINY 55
Db 67 MQKFLGLEVTGKLDSDTLEVMKPCGVPDVGHFRTFGIPKWKTHLTIRINY 121

RESULT 13
US-08-281-313-1
; Sequence 9, Application US/09368169
; Patent No. 6284511
; GENERAL INFORMATION:
; APPLICANT: Tetsuya INAKA et al.
; TITLE OF INVENTION: HEAT-STABLE PROLYNDOPEPTIDASE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Wenderoth, Lind & Ponack, L.L.P.
; STREET: 2033 K Street, N.W., Suite 800
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/368,169
; FILING DATE: August 5, 1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/750,816
; FILING DATE: January 8, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee Cheng
; REGISTRATION NUMBER: 40,949
; REFERENCE/DOCKET NUMBER: 99-0868/LC(WMC)49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-721-8200
; TELEFAX: 202-721-8250
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acid residues
; TYPE: amino acid
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; ORIGINAL SOURCE:
; ORGANISM: Flavobacterium meningosepticum
; ORGANISM: Met Lys Tyr Asn Lys Leu Ser Val Ala Val Ala Phe Ala Phe Ala Ala V
; ORGANISM: 1
; Sequence 1, Application US/08281313
; Patent No. 6284513
; GENERAL INFORMATION:
; APPLICANT: Ye, Qi-Zhuang
; APPLICANT: Johnson, Linda L.
; APPLICANT: Hupe, Donald J.
; APPLICANT: Baragi, Vijaykumar
; TITLE OF INVENTION: Process for the Production of
; TITLE OF INVENTION: Stromelysin Catalytic Domain Protein
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Warner-Lambert Company
; STREET: 2800 Plymouth Rd.
; CITY: Ann Arbor
; STATE: MI
; COUNTRY: US
; ZIP: 48105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/281,313
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/012,705
; FILING DATE: 03-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Tinney, Francis J.
; REGISTRATION NUMBER: 33,069
; REFERENCE/DOCKET NUMBER: 4415-01-FUT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 313 996-7295
; TELEFAX: 313 996-1553
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 477 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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; LOCATION: 1..17
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; US-08-281-313-1
Query Match 63.8%; Score 196; DB 3; Length 477;
Best Local Similarity 63.6%; Pred. No. 2.1e-17;
Matches 35; Conservative 8; Mismatches 12; Indels 0; Gaps 0;
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QY 1 MQRFFGLNVTGKNEETLDMKKPCGVPDSCGFMLTGPNPKWERTNLTIRINY 55
Db 67 MQKFLGLEVTGKLDSDTLEVMKPCGVPDVGHFRTFGIPKWKTHLTIRINY 121
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US-09-521-220-20
; Sequence 20, Application US/09521220
; Patent No. 6399348
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/521,220
; FILING DATE: 08-Mar-2000
; CLASSIFICATION: <Unknown>
; 21-OCT-1994
; 17-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/704,711
; FILING DATE: <Unknown>
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 477 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-521-220-20
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Query Match 63.8%; Score 196; DB 3; Length 477;
Best Local Similarity 63.6%; Pred. No. 2.1e-17;
Matches 35; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 MQEFFGLNVTGKPNETLDMKKPCGVPDSCGFMLTGPNPKWERTNLTIRNY 55
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Db 67 MQKFLGLEVTGKLDSDTLEVMRPRCGVPDVGHFRTFGIPKWKTHLTIRVNY 121
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Search completed: November 15, 2004, 14:08:08
Job time : 15.8077 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 15, 2004, 14:06:45 ; Search time 142.436 Seconds
(without alignments)
136.623 Million cell updates/sec

Title: US-10-032-376A-10

Perfect score: 307
Sequence: 1 MORFFGLNVTGKPNBEETLDM.....LTPGNPKWERTNLTIRNY 55

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1568699 seqs, 353819137 residues

Total number of hits satisfying chosen parameters: 1077212

Minimum DB seq length: 47

Maximum DB seq length: 660

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*
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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	307	100.0	55	14	US-10-219-329-10
2	307	100.0	55	14	US-10-153-185-10
3	307	100.0	55	14	US-10-219-561-10
4	307	100.0	55	16	US-10-032-376A-10
5	307	100.0	55	16	US-10-335-207-10
6	307	100.0	467	9	US-08-331-104-24
7	307	100.0	467	9	US-08-801-196-20
8	307	100.0	467	10	US-09-759-130B-176
9	307	100.0	467	14	US-10-131-985-31
10	307	100.0	467	16	US-10-741-790-176
11	221	72.0	454	15	US-10-115-479-32
12	221	72.0	454	15	US-10-115-479-34
13	221	72.0	454	15	US-10-115-479-36

14	221	72.0	454	15	US-10-115-479-38	Sequence 38, Appl
15	221	72.0	469	9	US-09-391-104-23	Sequence 23, Appl
16	221	72.0	469	9	US-09-801-196-19	Sequence 19, Appl
17	221	72.0	469	9	US-09-853-386-100	Sequence 100, Appl
18	221	72.0	469	14	US-10-301-822-119	Sequence 119, Appl
19	221	72.0	469	14	US-10-021-660-76	Sequence 76, Appl
20	221	72.0	469	14	US-10-308-279-34	Sequence 34, Appl
21	221	72.0	469	14	US-10-131-985-23	Sequence 23, Appl
22	221	72.0	469	14	US-10-295-027-12	Sequence 12, Appl
23	221	72.0	469	14	US-10-295-027-14	Sequence 14, Appl
24	221	72.0	469	14	US-10-295-027-1167	Sequence 1167, Appl
25	221	72.0	469	14	US-10-295-027-1168	Sequence 1168, Appl
26	221	72.0	469	15	US-10-115-479-30	Sequence 30, Appl
27	221	72.0	469	15	US-10-115-479-40	Sequence 40, Appl
28	221	72.0	469	15	US-10-211-462-22	Sequence 22, Appl
29	221	72.0	469	15	US-10-188-832-6	Sequence 6, Appl
30	221	72.0	469	16	US-10-734-564-109	Sequence 109, Appl
31	221	72.0	470	15	US-10-447-315-1	Sequence 1, Appl
32	221	72.0	496	14	US-10-106-698-6283	Sequence 6283, Appl
33	214	69.7	54	14	US-10-219-329-9	Sequence 9, Appl
34	214	69.7	54	14	US-10-153-185-9	Sequence 9, Appl
35	214	69.7	54	14	US-10-219-561-9	Sequence 9, Appl
36	214	69.7	54	16	US-10-032-376A-9	Sequence 9, Appl
37	214	69.7	54	16	US-10-335-207-9	Sequence 9, Appl
38	198	64.5	173	15	US-10-115-479-48	Sequence 48, Appl
39	196	63.8	267	14	US-10-133-797-73	Sequence 73, Appl
40	196	63.8	477	9	US-09-391-104-21	Sequence 21, Appl
41	196	63.8	477	9	US-09-801-196-24	Sequence 24, Appl
42	196	63.8	477	14	US-10-171-311-137	Sequence 137, Appl
43	196	63.8	477	14	US-10-301-822-127	Sequence 127, Appl
44	196	63.8	477	14	US-10-131-985-27	Sequence 27, Appl
45	196	63.8	477	14	US-10-295-027-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1
US-10-219-329-10
; Sequence 10, Application US/10219329
; Publication No. US20030096757A1
; GENERAL INFORMATION:
; APPLICANT: Quirk, Stephen
; APPLICANT: Weart, Ilona f.
; TITLE OF INVENTION: Anti-Cancer and Wound Healing Compounds
; FILE REFERENCE: 1443.035WO1
; CURRENT APPLICATION NUMBER: US/10/219,329
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-219-329-10

Query Match 100.0%; Score 307; DB 14; Length 55;
Best Local Similarity 100.0%; Pred. No. 1e-32; Indels 0; Gaps 0;
Matches 55; Conservative 0; Mismatches 0;
Qy 1 MORFFGLNVTGKPNBEETLDMKKPCRGVDPDSGGFMLTFCGNPKWERTNLTIRNY 55
Db 1 MORFFGLNVTGKPNBEETLDMKKPCRGVDPDSGGFMLTFCGNPKWERTNLTIRNY 55

RESULT 2
US-10-153-185-10
; Sequence 10, Application US/10153185
; Publication No. US2003014895A1

Mon Nov 15 14:23:29 2004

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; GENERAL INFORMATION:
; APPLICANT: Quirk, Stephen
; APPLICANT: Malik, Sohail
; TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds
; FILE REFERENCE: 1443.034US1
; CURRENT APPLICATION NUMBER: US/10/153,185
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-153-185-10

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Query Match 100.0%; Score 307; DB 14; Length 55;
Best Local Similarity 100.0%; Pred. No. 1e-32;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
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; Sequence 10, Application US/10219561
; Publication No. US20030166567A1
; GENERAL INFORMATION:
; APPLICANT: Quirk, Stephen
; APPLICANT: Malik, Sohail
; APPLICANT: Villanueva, Julie M.
; TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds
; FILE REFERENCE: 1443.008US2
; CURRENT APPLICATION NUMBER: US/10/219,561
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 10/153,185
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-219-561-10

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Query Match 100.0%; Score 307; DB 14; Length 55;
Best Local Similarity 100.0%; Pred. No. 1e-32;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
US-10-032-376A-10
; Sequence 10, Application US/10032376A
; Publication No. US20040127420A1
; GENERAL INFORMATION:
; APPLICANT: Quirk, Steven
; TITLE OF INVENTION: Metalloproteinase Inhibitors for Wound Healing
; FILE REFERENCE: 1443.008US1
; CURRENT APPLICATION NUMBER: US/10/032,376A
; CURRENT FILING DATE: 2001-12-21

```

```

; PRIOR APPLICATION NUMBER: 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-032-376A-10

```

```

Query Match 100.0%; Score 307; DB 16; Length 55;
Best Local Similarity 100.0%; Pred. No. 1e-32;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MORFFGLNVTGKPNNEETLDMKKPRCGVDSGGFMLTPGNPKWERTNLTIRNY 55
DB 1 MORFFGLNVTGKPNNEETLDMKKPRCGVDSGGFMLTPGNPKWERTNLTIRNY 55

```

```

RESULT 5
US-10-335-207-10
; Sequence 10, Application US/10335207
; Publication No. US20040127421A1
; GENERAL INFORMATION:
; APPLICANT: Malik, Sohail
; APPLICANT: Quirk, Stephen
; TITLE OF INVENTION: Method to Increase Fibronectin
; FILE REFERENCE: 1443.047US1
; CURRENT APPLICATION NUMBER: US/10/335,207
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-335-207-10

```

```

Query Match 100.0%; Score 307; DB 16; Length 55;
Best Local Similarity 100.0%; Pred. No. 1e-32;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MORFFGLNVTGKPNNEETLDMKKPRCGVDSGGFMLTPGNPKWERTNLTIRNY 55
DB 1 MORFFGLNVTGKPNNEETLDMKKPRCGVDSGGFMLTPGNPKWERTNLTIRNY 55

```

```

RESULT 6
US-09-391-104-24
; Sequence 24, Application US/09391104
; Publication No. US20020031817A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Falduto, Michael T.
; APPLICANT: Magnuson, Scott R.
; APPLICANT: Morgan, Douglas W.
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEINASE GENE,
; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
; TITLE OF INVENTION: OF USING SAME
; FILE REFERENCE: 6073.US.P1
; CURRENT APPLICATION NUMBER: US/09/391,104
; CURRENT FILING DATE: 1999-09-07
; PRIOR APPLICATION NUMBER: US 08/814,394
; PRIOR FILING DATE: 1997-03-11
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-391-104-24

```

```

Query Match 100.0%; Score 307; DB 9; Length 467;

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Best Local Similarity 100.0%; Pred. No. 1.3e-31; Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQRFFGLNVTGKNEETLDMKKPRCGVDSGGFMLTPGNPKWERTNLTIRNY 55
Db 66 MQRFFGLNVTGKNEETLDMKKPRCGVDSGGFMLTPGNPKWERTNLTIRNY 120

RESULT 7
US-09-801-196-20
; Sequence 20, Application US/09801196
; Patent No. US20020037827A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Kai
; APPLICANT: Smith, Ryan
; APPLICANT: Fajardo, Mark
; APPLICANT: Moss, Patrick
; TITLE OF INVENTION: A NOVEL MATRIX METALLOPROTEINASE (MMP-25)
; FILE REFERENCE: 240083.509
; CURRENT APPLICATION NUMBER: US/09/801,196
; CURRENT FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-801-196-20

Query Match 100.0%; Score 307; DB 9; Length 467;
Best Local Similarity 100.0%; Pred. No. 1.3e-31; Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQRFFGLNVTGKNEETLDMKKPRCGVDSGGFMLTPGNPKWERTNLTIRNY 55
Db 66 MQRFFGLNVTGKNEETLDMKKPRCGVDSGGFMLTPGNPKWERTNLTIRNY 120

RESULT 8
US-09-759-130B-176
; Sequence 176, Application US/09759130B
; Publication No. US2003002279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirt, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; FILE REFERENCE: MP100-5350VIM
; CURRENT APPLICATION NUMBER: US/09/759,130B
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364

; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 176
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-130B-176

Query Match 100.0%; Score 307; DB 10; Length 467;
Best Local Similarity 100.0%; Pred. No. 1.3e-31; Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQRFFGLNVTGKNEETLDMKKPRCGVDSGGFMLTPGNPKWERTNLTIRNY 55
Db 66 MQRFFGLNVTGKNEETLDMKKPRCGVDSGGFMLTPGNPKWERTNLTIRNY 120

RESULT 9
US-10-131-985-31
; Sequence 31, Application US/10131985
; Publication No. US2003019940A1
; GENERAL INFORMATION:
; APPLICANT: Dack, Kevin N
; APPLICANT: Davies, Michael J
; APPLICANT: Fish, Paul V
; APPLICANT: Huggins, Jonathan P
; APPLICANT: McIntosh, Fraser S
; APPLICANT: Occleston, Nicholas L
; TITLE OF INVENTION: Composition
; FILE REFERENCE: PCS 10391A
; CURRENT APPLICATION NUMBER: US/10/131,985
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US/09/726,295
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: GB 9930768.8
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-131-985-31

Query Match 100.0%; Score 307; DB 14; Length 467;
Best Local Similarity 100.0%; Pred. No. 1.3e-31; Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQRFFGLNVTGKNEETLDMKKPRCGVDSGGFMLTPGNPKWERTNLTIRNY 55
Db 66 MQRFFGLNVTGKNEETLDMKKPRCGVDSGGFMLTPGNPKWERTNLTIRNY 120

RESULT 10
US-10-741-790-176
; Sequence 176, Application US/10741790
; Publication No. US20040121396A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirt, Susan J

us-10-032-376a-10..rapb

Mon Nov 15 14:23:29 2004

APPLICANT: Mackay, Charles R
 APPLICANT: Myers, Paul S
 APPLICANT: Leiby, Kevin R
 APPLICANT: Wrighton, Nicolas
 APPLICANT: Goodearl, Andrew
 APPLICANT: Holtzman, Douglas A
 TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
 TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
 TITLE OF INVENTION: USES
 FILE REFERENCE: MP100-5350NMIM
 CURRENT APPLICATION NUMBER: US/10/741,790
 CURRENT FILING DATE: 2003-12-19
 PRIOR APPLICATION NUMBER: US 09/479,249
 PRIOR FILING DATE: 2000-01-07
 PRIOR APPLICATION NUMBER: US 09/559,497
 PRIOR FILING DATE: 2000-04-27
 PRIOR APPLICATION NUMBER: US 09/578,063
 PRIOR FILING DATE: 2000-05-24
 PRIOR APPLICATION NUMBER: US 09/333,159
 PRIOR FILING DATE: 1999-06-14
 PRIOR APPLICATION NUMBER: US 09/596,194
 PRIOR FILING DATE: 2000-07-14
 PRIOR APPLICATION NUMBER: US 09/342,364
 PRIOR FILING DATE: 1998-06-29
 PRIOR APPLICATION NUMBER: US 09/608,452
 PRIOR FILING DATE: 2000-06-30
 PRIOR APPLICATION NUMBER: US 09/393,996
 PRIOR FILING DATE: 1998-09-10
 PRIOR APPLICATION NUMBER: US 09/502,871
 PRIOR FILING DATE: 2000-06-23
 PRIOR APPLICATION NUMBER: US 09/420,707
 PRIOR FILING DATE: 1999-10-19
 NUMBER OF SEQ ID NOS: 460
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 176
 LENGTH: 467
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-741-790-176

Query Match 100.0%; Score 307; DB 16; Length 467;
 Best Local Similarity 100.0%; Pred. No. 1.3e-31;
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQRFFGLNVTGKNEETLDMKKPRCGVDSGGFMLTPGNPKWERTNLTIRNY 55
 Db 66 MQRFFGLNVTGKNEETLDMKKPRCGVDSGGFMLTPGNPKWERTNLTIRNY 120

RESULT 11

US-10-115-479-32
 Sequence 32, Application US/10115479
 Publication No. US20040006205A1
 GENERAL INFORMATION:

APPLICANT: Li, Li
 APPLICANT: Gerlach, Valerie L.
 APPLICANT: Liu, Xiaohong
 APPLICANT: Miller, Charles E.
 APPLICANT: Spytek, Kimberly A.
 APPLICANT: Zerhusen, Bryan D.
 APPLICANT: Pena, Carol E.A.
 APPLICANT: Shenoy, Suresh G.
 APPLICANT: Zhong, Haihong
 APPLICANT: Smithson, Glendda
 APPLICANT: Casman, Stacie J.
 APPLICANT: Boldog, Ferenc L.;
 APPLICANT: Voss, Edward
 APPLICANT: Vernet, Corine
 APPLICANT: MacDougall, John A.
 APPLICANT: Rastelli, Luca
 APPLICANT: Anderson, David W.
 APPLICANT: Zhong, Mei
 APPLICANT: Mezes, Peter S.

APPLICANT: Purtak, Katarzyna
 APPLICANT: Patturajan, Meera
 APPLICANT: Burgess, Catherine E.
 APPLICANT: Malyanker, Uriel M.
 APPLICANT: Shinkets, Richard A.
 APPLICANT: Taupier, Raymond J.
 APPLICANT: Edinger, Shlomit R.
 APPLICANT: Mazur, Ann
 TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
 FILE REFERENCE: 21402-322 B (Cura 622 PT)
 CURRENT APPLICATION NUMBER: US/10/115,479
 CURRENT FILING DATE: 2002-11-18
 PRIOR APPLICATION NUMBER: 60/281,136
 PRIOR FILING DATE: 2001-04-03
 PRIOR APPLICATION NUMBER: 60/281,863
 PRIOR FILING DATE: 2001-04-05
 PRIOR APPLICATION NUMBER: 60/281,906
 PRIOR FILING DATE: 2001-04-05
 PRIOR APPLICATION NUMBER: 60/282,934
 PRIOR FILING DATE: 2001-04-10
 PRIOR APPLICATION NUMBER: 60/283,657
 PRIOR FILING DATE: 2001-04-13
 PRIOR APPLICATION NUMBER: 60/283,678
 PRIOR FILING DATE: 2001-04-13
 PRIOR APPLICATION NUMBER: 60/283,687
 PRIOR FILING DATE: 2001-04-13
 PRIOR APPLICATION NUMBER: 60/283,710
 PRIOR FILING DATE: 2001-04-13
 PRIOR APPLICATION NUMBER: 60/284,234
 PRIOR FILING DATE: 2001-04-17
 PRIOR APPLICATION NUMBER: 60/285,325
 PRIOR FILING DATE: 2001-04-19
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 198
 SEQ ID NO 32
 LENGTH: 454
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-115-479-32

Query Match 72.0%; Score 221; DB 15; Length 454;
 Best Local Similarity 70.9%; Pred. No. 2.7e-20;
 Matches 33; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MQRFFGLNVTGKNEETLDMKKPRCGVDSGGFMLTPGNPKWERTNLTIRNY 55
 Db 50 MQRFFGLNVTGKNEETLDMKKPRCGVDSGGFMLTPGNPKWERTNLTIRNY 104

RESULT 12

US-10-115-479-34
 Sequence 34, Application US/10115479
 Publication No. US20040006205A1
 GENERAL INFORMATION:

APPLICANT: Li, Li
 APPLICANT: Gerlach, Valerie L.
 APPLICANT: Liu, Xiaohong
 APPLICANT: Miller, Charles E.
 APPLICANT: Spytek, Kimberly A.
 APPLICANT: Zerhusen, Bryan D.
 APPLICANT: Pena, Carol E.A.
 APPLICANT: Shenoy, Suresh G.
 APPLICANT: Zhong, Haihong
 APPLICANT: Smithson, Glendda
 APPLICANT: Casman, Stacie J.
 APPLICANT: Boldog, Ferenc L.;
 APPLICANT: Voss, Edward
 APPLICANT: Vernet, Corine
 APPLICANT: MacDougall, John A.
 APPLICANT: Rastelli, Luca
 APPLICANT: Anderson, David W.
 APPLICANT: Zhong, Mei
 APPLICANT: Mezes, Peter S.

APPLICANT: Furtak, Katarzyna
APPLICANT: Patturajan, Meera
APPLICANT: Burgess, Catherine E.
APPLICANT: Malvanker, Uriel M.
APPLICANT: Shimkets, Richard A.
APPLICANT: Taupier, Raymond J.
APPLICANT: Edinger, Shlomit R.
APPLICANT: Mazur, Ann
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REFERENCE: 21402-322 B (Cura 622 PT)
CURRENT APPLICATION NUMBER: US/10/115,479
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: 60/281,136
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/281,863
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/281,906
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/282,934
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: 60/283,657
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/283,678
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/283,687
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/283,710
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/284,234
PRIOR FILING DATE: 2001-04-17
PRIOR APPLICATION NUMBER: 60/285,325
PRIOR FILING DATE: 2001-04-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 198
SEQ ID NO 34
LENGTH: 454
TYPE: PRT
ORGANISM: Homo sapiens
US-10-115-479-34

Query Match 72.0%; Score 221; DB 15; Length 454;
Best Local Similarity 70.9%; Pred. No. 2.7e-20;
Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
Oy 1 MQRFFGLNVTGKNEETLDMKKPRCGVDPDSGGFMLTPGNPKWERTNLTIRNY 55
Db 50 MQEFGKLVGTGPDATLTKYMKQRCGVDPDVAQFVLTEGNPRWEQTHLTIRIENY 104

RESULT 13
US-10-115-479-36
Sequence 36, Application US/10115479
Publication No. US2004006205A1
GENERAL INFORMATION:
APPLICANT: Li, Li
APPLICANT: Gerlach, Valerie L.
APPLICANT: Liu, Xiaohong
APPLICANT: Miller, Charles E.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Zerhusen, Bryan D.
APPLICANT: Pena, Carol E.A.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Zhong, Haihong
APPLICANT: Smithson, Glendda
APPLICANT: Casman, Stacie J.
APPLICANT: Boldog, Ferenc L.;
APPLICANT: Voss, Edward
APPLICANT: Vernet, Corine
APPLICANT: MacDougall, John A.
APPLICANT: Rastelli, Luca
APPLICANT: Anderson, David W.
APPLICANT: Zhong, Mei
APPLICANT: Mezes, Peter S.

APPLICANT: Furtak, Katarzyna
APPLICANT: Patturajan, Meera
APPLICANT: Burgess, Catherine E.
APPLICANT: Malvanker, Uriel M.
APPLICANT: Shimkets, Richard A.
APPLICANT: Taupier, Raymond J.
APPLICANT: Edinger, Shlomit R.
APPLICANT: Mazur, Ann
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHO
FILE REFERENCE: 21402-322 B (Cura 622 PT)
CURRENT APPLICATION NUMBER: US/10/115,479
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: 60/281,136
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/281,863
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/281,906
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/282,934
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: 60/283,657
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/283,678
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/283,687
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/283,710
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/284,234
PRIOR FILING DATE: 2001-04-17
PRIOR APPLICATION NUMBER: 60/285,325
PRIOR FILING DATE: 2001-04-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 198
SEQ ID NO 36
LENGTH: 454
TYPE: PRT
ORGANISM: Homo sapiens
US-10-115-479-36

Query Match 72.0%; Score 221; DB 15; Length 454;
Best Local Similarity 70.9%; Pred. No. 2.7e-20;
Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
Oy 1 MQRFFGLNVTGKNEETLDMKKPRCGVDPDSGGFMLTPGNPKWERTNLTIRNY 55
Db 50 MQEFGKLVGTGPDATLTKYMKQRCGVDPDVAQFVLTEGNPRWEQTHLTIRIENY 104

RESULT 14
US-10-115-479-38
Sequence 38, Application US/10115479
Publication No. US2004006205A1
GENERAL INFORMATION:
APPLICANT: Li, Li
APPLICANT: Gerlach, Valerie L.
APPLICANT: Liu, Xiaohong
APPLICANT: Miller, Charles E.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Zerhusen, Bryan D.
APPLICANT: Pena, Carol E.A.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Zhong, Haihong
APPLICANT: Smithson, Glendda
APPLICANT: Casman, Stacie J.
APPLICANT: Boldog, Ferenc L.;
APPLICANT: Voss, Edward
APPLICANT: Vernet, Corine
APPLICANT: MacDougall, John A.
APPLICANT: Rastelli, Luca
APPLICANT: Anderson, David W.
APPLICANT: Zhong, Mei
APPLICANT: Mezes, Peter S.

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OM protein - protein search, using sw model

Run on: November 15, 2004, 14:01:35 ; Search time 12.3397 Seconds
(without alignments)
428.852 Million cell updates/sec

Title: US-10-032-376A-10

Perfect score: 307

Sequence: 1 MQRFFGLNVTKPNEETLDM.....LTPGNPKWERNLTLYRINY 55

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 246014

Minimum DB seq length: 47

Maximum DB seq length: 660

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_79:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	307	100.0	467	1 KCHUN	neutrophil collage
2	233	75.9	468	1 KCPBI	interstitial colla
3	231	75.2	469	1 KCPGI	interstitial colla
4	221	72.0	469	1 KCHUI	interstitial colla
5	218	71.0	469	1 KCB01	interstitial colla
6	201.5	65.6	384	2 I51267	collagenase (EC 3.
7	196	63.8	477	1 KCHUS1	stromelysin 1 (EC
8	195	63.5	476	1 KCHUS2	stromelysin 2 (EC
9	193	62.9	476	1 KC6505	stromelysin 1 (EC
10	193	62.9	477	1 KMS51	stromelysin 1 (EC
11	192	62.5	478	1 KCRBS1	stromelysin 1 (EC
12	190	61.9	476	1 KCRTS2	stromelysin 2 (EC
13	189	61.6	466	2 A23685	interstitial colla
14	189	61.6	472	2 S29243	interstitial colla
15	188	61.2	471	2 A53711	collagenase 3 (EC
16	188	61.2	475	1 KERTIH	stromelysin 1 (EC
17	183	59.6	483	2 JC5743	matrix metalloprot
18	163	53.1	267	2 A57490	matrilysin (EC 3.4
19	160	52.1	267	1 KCHUM	matrilysin (EC 3.4
20	160	52.1	470	2 A49499	metalloelastase HM
21	153	49.8	660	1 A28153	Gelatinase A (EC 3
22	138	45.0	462	2 A24201	macrophage elastas
23	134.5	43.8	582	2 I38028	matrix metalloprot
24	134.5	43.8	582	2 I34471	matrix metalloprot
25	129.5	42.2	582	2 I48673	matrix metalloprot
26	120	39.1	82	2 PM0052	pro-matrix metallo
27	111	36.2	521	2 T37252	probable matrix me
28	108	35.2	341	2 T51957	metalloproteinase
29	108	35.2	342	2 G84885	probable metallopr

RESULT 1
KCHUN
neutrophil collagenase (EC 3.4.24.34) precursor [validated] - human
N:Alternate names: matrix metalloproteinase 8
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1992 #sequence, revision 30-Sep-1992 #text change 09-Jul-2004
C:Accession: A37073; A61175; A36230; S09680; S11026; S19576; S27225; S32527; S6
R:Hasty, K.A.; Pourmotabbed, T.F.; Goldberg, G.I.; Thompson, J.P.; Spinella, D.G.; Stev
J. Biol. Chem. 265, 11421-11424, 1990
A:Title: Human neutrophil collagenase. A distinct gene product with homology to other m
A:Reference number: A37073; MUID:90307647; PMID:2164002
A:Accession: A37073
A:Molecule type: mRNA
A:Residues: 1-467 <HAS>
A:Cross-references: UNIPROT:P22894; GB:J05556; NID:G180617; PIDN:AAA88021.1; PID:G18061
R:Davaraian, P.; Mookhtiar, K.; Van Wart, H.; Berliner, N.
Blood 77, 2731-2738, 1991
A:Title: Structure and expression of the cDNA encoding human neutrophil collagenase.
A:Reference number: A61175; MUID:91255696; PMID:1646048
A:Accession: A61175
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-31, 'I', '33-86, 'E', 88-467 <DEV>
A:Accession: B61175
A:Molecule type: protein
A:Residues: 283-264, 'X', 266-270, 'X', 272-273, 'X', 275, 'X', 277 <DE2>
R:Mallya, S.K.; Mookhtiar, K.A.; Gao, Y.; Brew, K.; Dioszegi, M.; Birkedal-Hansen, H.;
Biochemistry 29, 10628-10634, 1990
A:Title: Characterization of 58-kilodalton human neutrophil collagenase: comparison wit
A:Reference number: A36230; MUID:91104978; PMID:2176876
A:Accession: A36230
A:Molecule type: protein
A:Residues: 'X', 86-87, 'X', 89-90, 'X', 92-97, 'X', 99-111, 'X', 113-120 <MAL>
R:Knaeuper, V.; Kraemer, S.; Reinke, H.; Tschesche, H.
Eur. J. Biochem. 189, 295-300, 1990
A:Title: Characterization and activation of procollagenase from human polymorphonuclear
A:Reference number: S09680; MUID:90249372; PMID:2159879
A:Accession: S09680
A:Molecule type: protein
A:Residues: 21-31, 'I', '33-39, 'I', 41-47, 'V', 49-53, 'I', 55-72, 'G', 74-86, 'E', 88-111, 'X', 113-
A>Note: 67-Lys was also found
R:Knaeuper, V.; Kraemer, S.; Reinke, H.; Tschesche, H.
Biol. Chem. Hoppe-Seyler 371, 733, 1990
A:Title: Corrigendum. Partial amino-acid sequence of human PMN leukocyte procollagenase
A:Reference number: S11026; MUID:91000455; PMID:2169766
A>Note: Original publication was Biol. Chem. Hoppe-Seyler 371 (Suppl.), 295-304, 1990
A:Accession: S11026
A:Molecule type: protein
A:Residues: 21-31, 'I', '33-53, 'I', 55-72, 'G', 74-111, 'X', 113-140; 183-203, 'X', 205-209; 248-26
A>Note: 87-Glu was also found
R:Blaeser, J.; Knaeuper, V.; Osthues, A.; Reinke, H.; Tschesche, H.
Eur. J. Biochem. 202, 1223-1230, 1991

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probable dihydroxy
hypothetical prote

RESULT 2
KCRBI
A:Title: Mercurial activation of human polymorphonuclear leucocyte procollagenase.
A:Reference number: S19576; MUID:92111500; PMID:1662606
A:Accession: S19576
A:Molecule type: Protein
A:Residues: 69-103 <Bu2>
R:Blaser, J.; Triebel, S.; Reinke, H.; Tschesche, H.
FEBS Lett. 313, 59-61, 1992
A:Title: Formation of a covalent Hg-Cys-bond during mercurial activation of PMNL procollagenase.
A:Reference number: S27225; MUID:9305020; PMID:1330697
A:Accession: S27225
A:Molecule type: Protein
A:Residues: 68-103 <BuA>
R:Knaeuper, V.; Osthus, A.; Declerck, Y.A.; Langley, K.E.; Blaaser, J.; Tschesche, H.
Biochem. J. 291, 847-854, 1993
A:Title: Fragmentation of human polymorphonuclear-leucocyte collagenase.
A:Reference number: S32527; MUID:93256897; PMID:8489511
A:Accession: S32527
A:Molecule type: Protein
A:Residues: 100-112;263-276 <KN3>
R:Knaeuper, V.; Murphy, G.; Tschesche, H.
Eur. J. Biochem. 235, 187-191, 1996
A:Title: Activation of human neutrophil procollagenase by stromelysin 2.
A:Reference number: S62608; MUID:96202934; PMID:8631328
A:Accession: S62608
A:Molecule type: Protein
A:Residues: 21-39, 'I', '41-47, 'V', '49-122 <KN4>
R:Stams, T.; Spurlino, J.C.; Smith, D.L.; Rubin, B.
Submitted to the Brookhaven Protein Data Bank, January 1994
A:Reference number: A67078; PDB:1MNC
A:Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 'G', '106-149', 'G', '1
R:Stams, T.; Spurlino, J.C.; Smith, D.L.; Wahi, R.C.; Ho, T.F.; Qoronfleh, M.W.; Banks, N.A.
Struct. Biol. 1, 119-123, 1994
A:Title: Structure of human neutrophil collagenase reveals large S1' specificity pocket.
A:Reference number: A58274; MUID:95384762; PMID:7656015
A:Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 'G', '106-149', 'G', '1
C:Comment: This protein is more highly glycosylated than interstitial collagenase and is
C:Genetics:
A:Gene: GDB:MWP8; CLG1
A:Cross-references: GDB:128173; OMIM:120355
A:Map position: 11q22.2-11q22.3
C:Function:
A:Description: hydrolyzes collagen types I, II, and III at Gly-Ile sites in collagenous
A:Note: cleaves type I collagen most rapidly
C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloproteinase
C:Keywords: calcium; extracellular matrix; glycoprotein; hydrolase; metalloproteinase; n
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-467/Product: procollagenase #status predicted <PRO>
F:21-100/Domain: activation peptide #status experimental <ACT>
F:59-262/Domain: matrix metalloproteinase homology <MMP>
F:89-96/Region: autoinhibitory
F:101-467/Product: neutrophil collagenase #status predicted <MAT>
F:273-464/Domain: hemopexin repeat homology <PXN>
F:54,73,112,119,204,246/Binding site: carboxylate (Asn) (covalent) #status predicted
F:73-74/Cleavage site: Asp-Val (autolytic) #status experimental
F:84-85/Cleavage site: Asp-Met (autolytic) #status experimental
F:91-91,217,221,227/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status
F:99-100/Cleavage site: Phe-Met (autolytic) #status experimental
F:167,169,182,195/Binding site: zinc, noncatalytic (His, Asp, His, His) #status experime
F:174,175,177,179,197,200/Binding site: calcium (Asp, Gly, Asn, Ile, Asp, Glu) #status e
F:217,221,227/Binding site: zinc, catalytic (His) (active) #status experimental
F:218/Active site: Glu #status predicted
F:262-263/Cleavage site: Gly-Leu (autolytic) #status experimental
F:279-464/Disulfide bonds: #status predicted

Query Match 100.0%; Score 307; DB 1; Length 467;
Best Local Similarity 100.0%; Pred. No. 6,7e-31;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MORFFGLNVTGKNEETLDMKKPCGVDPDGGFMTLPGNPKWERTNLTIRNY 55
Db 66 MORFFGLNVTGKNEETLDMKKPCGVDPDGGFMTLPGNPKWERTNLTIRNY 120

RESULT 2
KCRBI
A:Title: Interstitial collagenase (EC 3.4.24.7) precursor - rabbit
N:Alternate names: fibroblast collagenase; matrix metalloproteinase 1 (MMP1); tissue col
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text_change 09-Jul-2004
C:Accession: A27500; B27500; I46694
R:Finzi, M.E.; Plucinska, I.M.; Mayer, A.S.; Gross, R.H.; Brinckerhoff, C.E.
Biochemistry 26, 6156-6165, 1987
A:Title: A gene for rabbit synovial cell collagenase: member of a family of metalloprote
A:Reference number: A27500; MUID:88077876; PMID:2825772
A:Accession: A27500
A:Molecule type: mRNA
A:Residues: 1-468 <FIN>
A:Cross-references: UNIPROT:P13943; GB:M19240
A:Accession: B27500
A:Molecule type: DNA
A:Residues: 1-391;399-468 <FIT>
A:Cross-references: GB:M17820
A:Note: the location of the intron between exons 7 and 8 is approximate
R:Finzi, M.E.; Austin, S.D.; Holt, P.T.; Ruby, P.L.; Gross, R.H.; White, H.D.; Brinckerho
Coll. Relat. Res. 6, 239-248, 1986
A:Title: Homology between exon-containing portions of rabbit genomic clones for synovial
A:Reference number: I46694; MUID:87029174; PMID:3021384
A:Accession: I46694
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 449-468 <FIT>
A:Cross-references: GB:M25663; NID:9531211; PIDN:AAA31203.1; PID:9531212
C:Comment: This enzyme cleaves collagens of types I, II, and III at a Gly-Ile site in th
C:Comment: Procollagenase can be activated without removal of the activation peptide. St
tion peptide by other proteinases.
C:Comment: Procollagenase is found in glycosylated and unglycosylated forms, both of whi
C:Genetics:
A:Introns: 34/3; 116/2; 166/1; 208/1; 260/1; 299/2; 344/1; 398/1; 433/1
A:Description: hydrolyzes collagens, in particular types I, II, III, and X, serpins, and
C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotei
C:Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo
F:1-18/Domain: signal sequence #status predicted <SIG>
F:18-468/Product: procollagenase #status predicted <PRO>
F:19-98/Domain: activation peptide #status predicted <ACT>
F:59-260/Domain: matrix metalloproteinase homology <MMP>
F:89-96/Region: autoinhibitory
F:99-468/Product: interstitial collagenase #status predicted <MAT>
F:271-465/Domain: hemopexin repeat homology <PXN>
F:91,217,221,227/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
F:119,142/Binding site: carboxylate (Asn) (covalent) #status predicted
F:217,221,227/Binding site: zinc, catalytic (His) (active) #status predicted
F:218/Active site: Glu #status predicted
F:278-465/Disulfide bonds: #status predicted
Query Match 75.9%; Score 233; DB 1; Length 468;
Best Local Similarity 74.5%; Pred. No. 1.6e-21;
Matches 41; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
Qy 1 MORFFGLNVTGKNEETLDMKKPCGVDPDGGFMTLPGNPKWERTNLTIRNY 55
Db 66 MORFFGLNVTGKNEETLDMKKPCGVDPDGGFMTLPGNPKWERTNLTIRNY 120

RESULT 3
KCPGI

Interstitial collagenase (EC 3.4.24.7) precursor [validated] - pig
N:Alternate names: fibroblast collagenase; matrix metalloproteinase 1 (MMP1); tissue col
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text_change 09-Jul-2004
C:Accession: S15986; S1597
R:Richards, C.D.; Rafferty, J.A.; Reynolds, J.J.; Saklatvala, J.
Matrix 11, 161-167, 1991
A:Title: Porcine collagenase from synovial fibroblasts: cDNA sequence and modulation of
A:Reference number: S15986; MUID:91333421; PMID:1651440
A:Accession: S15986

A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-469 <R1C>
A/Cross-references: UNIPROT:P21692
A/Note: part of the sequence, including the amino end of the proenzyme, was confirmed by R/Clarke, N.J.; O'Hare, M.C.; Cawston, T.E.; Harper, G.P.
Nucleic Acids Res. 18, 6703, 1990
A/Title: Nucleotide sequence of a cDNA for porcine type I collagenase, obtained by PCR.
A/Reference number: S13597; MUID:91067477; PMID:2174547
A/Accession: S13597
A/Molecule type: mRNA
A/Residues: 25-469 <CLA>
A/Cross-references: EMBL:X54724; NID:G2016; PIDN:CAA38526.1; PID:G930269
R/Li, J.; Brick, P.; Blow, D.M.
Submitted to the Brookhaven Protein Data Bank, April 1995
A/Reference number: A65568; PDB:1PBL
A/Contents: annotation; X-ray crystallography, 2.5 angstroms, residues 100-466
C/Comment: Procollagenase can be activated without removal of the activation peptide. St
tion peptide by other proteinases.
C/Comment: Procollagenase is found in glycosylated and unglycosylated forms, both of whi
A/Function:
A/Description: hydrolyzes collagens, in particular types I, II, III, and X, serpins, and
A/Note: also hydrolyzes type X collagen, serpins, and alpha-macroglobulins
C/Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotei
C/Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo
F1-19/Domain: signal sequence #status predicted <SIG>
F1-19/Domain: signal sequence #status predicted <SIG>
F20-59/Product: procollagenase #status predicted <PRO>
F20-59/Domain: activation peptide #status experimental <ACT>
F60-261/Domain: matrix metalloproteinase homology <MMP>
F100-469/Product: interstitial collagenase #status predicted <MAT>
F172-466/Domain: hemopexin repeat homology <PXN>
F192,218,222,228/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status
F120,143/Binding site: carboxylate (Asn) (covalent) #status predicted
F218,222,228/Binding site: zinc, catalytic (His) (active) #status experimental
F219/Active site: Glu #status predicted
F278-466/Disulfide bonds: #status experimental

Query Match 75.2%; Score 231; DB 1; Length 469;
Best Local Similarity 72.7%; Pred. No. 2.8e-21;
Matches 40; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 1 MORFFGLNVTGKPNBTLDMKKPCGVPDSCGFMLTQGNPKWERTNLTIRNY 55
Db 67 MQQFFGLKVTGKPDATLNMVQKPCGVPDVAEFLVTPGNPWNTHLTIRNY 121

RESULT 4
KCHUI
Interstitial collagenase (EC 3.4.24.7) precursor [validated] - human
N/Alternate names: fibroblast collagenase; matrix metalloproteinase 1 (MMP1); tissue col
C/Species: Homo sapiens (man)
C/Date: 13-Aug-1986 #sequence revision 30-Sep-1992 #text change 09-Jul-2004
C/Accession: A3708; S22766; I57620; A00996; D29157; A44516; S06132; B60964; S10595; S53
R/Templeton, N.S.; Brown, P.D.; Levy, A.T.; Margulies, I.M.K.; Liotta, L.A.; Stetler-St
Cancer Res. 50, 5431-5437, 1990
A/Title: Cloning and characterization of human tumor cell interstitial collagenase.
A/Reference number: A37308; MUID:90352887; PMID:2167156
A/Accession: A37308
A/Molecule type: mRNA
A/Residues: 1-469 <TEM>
A/Cross-references: UNIPROT:P03956; GB:X54925; NID:G30125; PIDN:CAA38691.1; PID:G30126
R/Brinckerhoff, C.E.; Ruby, P.L.; Austin, S.D.; Fini, M.E.; White, H.D.
J. Clin. Invest. 79, 542-546, 1987
A/Title: Molecular cloning of human synovial cell collagenase and selection of a single
A/Reference number: S22766; MUID:87109799; PMID:3027129
A/Accession: S22766
A/Molecule type: DNA
A/Residues: 1-63,65-70 <BRI>
A/Cross-references: EMBL:M15996; NID:G180666; PIDN:AAA35700.1; PID:G180667
R/Engel, P.; Baumann, I.; Stein, B.; Delius, H.; Rahmsdorf, H.J.; Herrlich, P.
Mol. Cell. Biol. 7, 2256-2266, 1987
A/Title: 12-O-tetradecanoyl-phorbol-13-acetate induction of the human collagenase gene i
A/Reference number: I57620; MUID:87257941; PMID:3037355

A/Accession: I57620
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-35 <RES>
A/Cross-references: GB:M16567; NID:G180668; PIDN:AAA52033.1; PID:G180669
R/Goldberger, G.I.; Wilhelm, S.M.; Kronberger, A.; Bauer, E.A.; Grant, G.A.; Eisen, A.Z.
J. Biol. Chem. 261, 6600-6605, 1986
A/Title: Human fibroblast collagenase. Complete primary structure and homology to an on
A/Reference number: A00996; MUID:86196089; PMID:3009463
A/Accession: A00996
A/Molecule type: mRNA
A/Residues: 1-114, 'R', '116-409', 'S', '411-469' <GOL>
A/Cross-references: GB:M13509; NID:G180664; PIDN:AAA35699.1; PID:G180665
A/Note: part of this sequence was confirmed by protein sequencing of the proenzyme
R/Witham, S.E.; Murphy, G.; Angel, P.; Rahmsdorf, H.J.; Smith, B.J.; Lyons, A.; Harris
Biochem. J. 240, 913-916, 1986
A/Title: Comparison of human stromelysin and collagenase by cloning and sequence analysis
A/Reference number: A90336; MUID:87156645; PMID:3030290
A/Accession: D29157
A/Molecule type: mRNA
A/Residues: 1-199, 'H', '201-207', 'T', '209-469' <WHI>
A/Cross-references: EMBL:X55231; NID:G38266; PIDN:CAA28858.1; PID:G38267
A/Note: parts of this sequence, including the amino end of the proenzyme and of the mat
R/Birkedal-Hansen, B.; Moore, W.G.I.; Taylor, R.E.; Shown, A.S.; Birkedal-Hansen, H.
Biochemistry 27, 6751-6758, 1988
A/Title: Monoclonal antibodies to human fibroblast procollagenase. Inhibition of enzym
end of the activated enzyme.
A/Reference number: A44518; MUID:89062403; PMID:2461732
A/Accession: A44518
A/Molecule type: protein
A/Residues: 270-305 <BIR>
R/Clark, I.M.; Cawston, T.E.
Biochem. J. 263, 201-206, 1989
A/Title: Fragments of human fibroblast collagenase. Purification and characterization.
A/Reference number: S06132; MUID:90104231; PMID:2557822
A/Accession: S06132
A/Status: preliminary
A/Molecule type: protein
A/Residues: 100-102, 'P', '104-107', 'XX', '110-112', '270-277', 'X', '279-280', 'X', '282-287' <CLA>
R/Rak, M.W.; Walakavits, L.A.; Shah, T.K.; Vanmiddlesworth, J.; Cameton, P.M.; Lin, T.
Connect. Tissue Res. 25, 49-65, 1990
A/Title: Production and purification of prostromelysin and procollagenase from IL-1 bet
A/Reference number: A60964; MUID:91059606; PMID:2173990
A/Accession: B60964
A/Molecule type: protein
A/Residues: 24-35;100-108;270-272, 'X', '274', 'X', '276' <LAR>
R/Suzuki, K.; Nagase, H.; Ito, A.; Englund, J.J.; Salvesen, G.
Biol. Chem. Hoppe-Seyler 371(Suppl.), 305-310, 1990
A/Title: The role of matrix metalloproteinase 3 in the stepwise activation of human rhe
A/Reference number: S10595; MUID:90380300; PMID:2169257
A/Accession: S10595
A/Molecule type: protein
A/Residues: 20-102 <SUZ>
R/Suzuki, K.; Lees, M.; Newlands, G.F.J.; Nagase, H.; Woolley, D.E.
Biochem. J. 305, 301-306, 1995
A/Title: Activation of precursors for matrix metalloproteinases 1 (interstitial collage
A/Reference number: S53438; MUID:95126921; PMID:7826345
A/Accession: S53438
A/Status: preliminary
A/Molecule type: protein
A/Residues: 20-108 <SU2>
R/Springman, E.B.; Angleton, E.L.; Birkedal-Hansen, H.; Van Wart, H.E.
Proc. Natl. Acad. Sci. U.S.A. 87, 364-368, 1990
A/Title: Multiple modes of activation of latent human fibroblast collagenase: evidence
A/Reference number: A44517; MUID:90115877; PMID:2153297
R/Contents: annotation; disulfide bond; activation mechanism
R/Salowe, S.P.; Marcy, A.I.; Guca, G.C.; Smith, C.K.; Kopka, I.E.; Hagmann, W.K.; Herme
Biochemistry 31, 4535-4540, 1992
A/Title: Characterization of zinc-binding sites in human stromelysin-1: stoichiometry o
A/Reference number: A43031; MUID:92256384; PMID:1581308
A/Contents: annotation; zinc ligand in proenzyme
A/Note: Cys-92 binds zinc in the proenzyme. Both active and proenzyme forms of the cata
C/Comment: Procollagenase can be activated without removal of the activation peptide. S

F;218,222,228/Binding site: zinc, catalytic (His) (active) #status predicted

A;Accession: A28399
A;Status: nucleic acid sequence not shown: not compared with conceptual translation

F;219/Active site: Glu #status predicted
F;290-477/Disulfide bonds: #status predicted

Query Match 63.8%; Score 196; DB 1; Length 477;
Best Local Similarity 63.6%; Pred. No. 7.8e-17;
Matches 35; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 MQRFGLVNTGKNEETLDMMKPRCGVPDSGGFMLTGPNPKWERTNLTYYRINY 55
|||:|||:::|||||:::|||||:::|||||
Db 67 MQRFGLGVTKLSDTLEWVRKPRCGVPDVGHFRTFGPIPKWRKTLTYRVIN 121
|||:|||:::|||||:::|||||:::|||||

RESULT 8
KCHUS2

stromelysin 2 (EC 3.4.24.22) precursor [validated] - human
N;Alternate names: matrix metalloproteinase 10 (MMP10); transin-2
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
C;Accession: A28916; A47496
R;Muller, D.; Quantin, B.; Gesnel, M.C.; Millon-Collard, R.; Abecassis, J.; Breathnach,
Biochem. J. 253, 187-192, 1988
A;Title: The collagenase gene family in humans consists of at least four members.
A;Reference number: A90339; PMID:88339885; PMID:2844164
A;Accession: A28916
A;Molecule type: mRNA
A;Residues: 1-476 <ML>
A;Cross-references: UNIPROT:P09238; EMBL:X07820; NID:G36628; PIDN:CAA30679.1; PID:G3662
A;Note: mRNA for this protein was detected in several human tumors
R;Winslow, L.O.; Grenet, H.; Birkedal-Hansen, B.; Boden, M.K.; Engler, J.A.; Birke
J. Biol. Chem. 268, 17341-17347, 1993
A;Title: Cell type-specific regulation of SL-1 and SL-2 genes. Induction of the SL-2 ge
A;Reference number: A47496; PMID:9332520; PMID:8349617
A;Accession: A47496
A;Molecule type: protein
A;Residues: 17-33 <WIN>
C;Comment: This enzyme degrades various extracellular matrix proteins, including fibron
C;Genetics:
A;Gene: GDB:MMP10; STMY2
A;Cross-references: GDB:120392; OMIM:185260
A;Map position: 11q22.3-11q23
A;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprote
C;Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo
F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-476/Product: prostromelysin 2 #status experimental <PRO>
F;17-98/Domain: activation peptide #status predicted <ACT>
F;59-263/Domain: matrix metalloproteinase homology <MMP>
F;89-96/Region: autoinhibitory
F;95-476/Product: stromelysin 2 #status predicted <MAT>
F;203-476/Domain: hemopexin repeat homology <PXN>
F;91,217,221,227/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
F;119/Binding site: carbohydurate (Asn) (covalent) #status predicted
F;217,221,227/Binding site: zinc, catalytic (His) (active) #status predicted
F;218/Active site: Glu #status predicted
F;289-476/Disulfide bonds: #status predicted

Query Match 63.5%; Score 195; DB 1; Length 476;
Best Local Similarity 63.6%; Pred. No. 1e-16;
Matches 35; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 MQRFGLVNTGKNEETLDMMKPRCGVPDSGGFMLTGPNPKWERTNLTYYRINY 55
|||:|||:::|||||:::|||||:::|||||
Db 66 MQRFGLGVTKLSDTLEWVRKPRCGVPDVGHFRTFGPIPKWRKTLTYRVIN 120
|||:|||:::|||||:::|||||:::|||||

RESULT 9
JC6505

stromelysin 2 (EC 3.4.24.22) precursor - mouse
N;Alternate names: matrix metalloproteinase 10
C;Species: Mus musculus (house mouse)
C;Date: 16-Oct-1998 #sequence_revision 16-Oct-1998 #text_change 09-Jul-2004
C;Accession: JC6505
R;Madlener, M.; Werner, S.
Gene 202, 75-81, 1997

A:Gene: GDB:MMPL3; CLG3
A:Cross-references: GDB:373966; OMIM:600108
A:Map position: 11q22.2-11q22.3
C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotease
C:Keywords: hydrolase; metalloproteinase; zinc; zymogen
F:64-267/Domain: matrix metalloproteinase homology <MMP>
F:278-471/Domain: hemopexin repeat homology <PXN>
F:96,222,226,232/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
F:222,226,232/Binding site: zinc, catalytic (His) (active) #status predicted
F:223/Active site: Glu #status predicted

Query Match 61.2%; Score 188; DB 2; Length 471;
Best Local Similarity 63.6%; Pred. No. 7.9e-16;
Matches 35; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

QY 1 MQRFFGLNVTGKPNETLDMKKPCGVPDGGFMLTPGNPKWERTNLTIRNY 55
Db 71 MOSFFLEVTGKLDNTLDMKKPCGVPDGGFMLTPGNPKWERTNLTIRNY 125

Search completed: November 15, 2004, 14:07:19
Job time : 12.3397 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 15, 2004, 14:01:34 ; Search time 50.7692 Seconds
(without alignments)
623.323 Million cell updates/sec

Title: US-10-032-376a-10

Perfect score: 307

Sequence: 1 MQRFFGLVTKPNEETLDM.....LTPGNPKWERTNLTVIRNY 55

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1605865

Minimum DB seq length: 47

Maximum DB seq length: 660

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	307	100.0	467	1 MM08 HUMAN	P22894 homo sapien
2	233	75.9	468	1 MM01 RABIT	P13943 coryctolagus
3	231	75.2	469	1 MM01 PIG	P21692 sus scrofa
4	223	72.6	466	1 MM08 RAT	O88766 rattus norv
5	222	72.3	469	1 MM01 HORSE	Q9X525 equus cabal
6	221	72.0	469	1 MM01 HUMAN	P03956 equus cabal
7	221	72.0	469	2 AAP35520	AAP35520 homo sapi
8	218	71.0	469	1 MM01 BOVIN	P28053 bos taurus
9	201.5	65.6	384	1 MM01 RANCA	Q11133 rana catesb
10	198	64.5	465	2 Q8C209	Q8C209 mus muscu
11	198	64.5	465	2 Q8C230	Q8C230 mus muscu
12	198	64.5	465	2 AAH42742	AAH42742 mus muscu
13	198	64.5	465	2 BAC40805	BAC40805 mus muscu
14	198	64.5	478	2 Q6Y405	Q6Y405 canis fami
15	198	64.5	478	2 QAO63580	QAO63580 canis fam
16	196	63.8	469	1 MM13 XENLA	Q10835 xenopus lae
17	196	63.8	472	2 Q92342	Q92342 gallus gall
18	196	63.8	472	2 Q10833	Q10833 xenopus lae
19	196	63.8	477	1 MM03 HUMAN	P08254 homo sapien
20	196	63.8	477	2 AAH69676	AAH69676 homo sapi
21	196	63.8	477	2 AAH69716	AAH69716 homo sapi
22	195	63.5	476	1 MM10 HUMAN	P09238 homo sapien
23	195	63.5	476	2 AAP36110	AAP36110 homo sapi
24	194	63.2	145	2 Q9N283	Q9N283 bos taurus
25	194	63.2	452	2 Q9T182	Q9T182 canis fami
26	193	62.9	476	1 MM10 MOUSE	O5123 mus muscu
27	193	62.9	477	1 MM03 MOUSE	P28863 mus muscu
28	193	62.9	479	2 Q922W6	Q922W6 mus muscu
29	192	62.5	478	1 MM03 RABIT	P28863 coryctolagus
30	190	61.9	465	1 MM08 MOUSE	O70138 mus muscu
31	190	61.9	476	1 MM10 RAT	P07152 rattus norv

32 189 61.6 466 1 MM13 RAT
33 189 61.6 472 1 MM13 MOUSE
34 188 61.2 383 2 Q7Z5M0
35 188 61.2 393 2 O8M118
36 188 61.2 471 1 MM13 HUMAN
37 188 61.2 471 2 Q6NM66
38 188 61.2 471 2 AAH67522
39 188 61.2 471 2 AAH67523
40 188 61.2 475 1 MM03 RAT
41 188 61.2 489 2 Q7Z5M1
42 187 60.9 472 1 MM13 HORSE
43 185 60.3 139 2 O9QM68
44 185 60.3 471 1 MM13 BOVIN
45 184 59.9 259 2 Q6DF35

ALIGNMENTS

RESULT 1:

MM08_HUMAN
ID MM08_HUMAN STANDARD; PRT; 467 AA.
AC P22894;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Neutrophil collagenase precursor (EC 3.4.24.34) (Matrix metalloproteinase-8) (MMP-8) (PMNL collagenase) (PMNL-CL).
GN Name=MMP8; Synonyms=CLG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 314-337; 347-363 AND 424-441.
RC TISSUE=Neutrophils;
RX MEDLINE=90307647; PubMed=2164002;
RA Hasty K.A., Pourmotabbed T.F., Goldberg G.I., Thompson J.P., Spinella D.G., Stevens R.M., Mainardi C.L.;
RT "Human neutrophil collagenase. A distinct gene product with homology to other matrix metalloproteinases.";
RL J. Biol. Chem. 265:11421-11424(1990).
RN [2]
RP SEQUENCE OF 21-140.
RC TISSUE=Neutrophils;
RX MEDLINE=90249372; PubMed=2159879;
RA Knaeuper V., Kraemer S., Reinke H., Tschesche H.;
RT "Characterization and activation of procollagenase from human polymorphonuclear leucocytes. N-terminal sequence determination of the proenzyme and various proteolytically activated forms.";
RL Eur. J. Biochem. 189:295-300(1990).
RN [3]
RP SEQUENCE OF 21-103.
RC TISSUE=Neutrophils;
RX MEDLINE=92111500; PubMed=1662606;
RA Blaesser J., Knaeuper V., Osthus A., Reinke H., Tschesche H.;
RT "Mercurial activation of human polymorphonuclear leucocyte procollagenase.";
RL Eur. J. Biochem. 202:1223-1230(1991).
RN [4]
RP SEQUENCE OF 85-120, AND CHARACTERIZATION.
RC TISSUE=Neutrophils;
RX MEDLINE=91104978; PubMed=2176876;
RA Malliya S.K., Mookthiar K.A., Gao Y., Brew K., Dioszegi M., Birkedal-Hansen H., van Wart H.E.;
RT "Characterization of 58-kilodalton human neutrophil collagenase: comparison with human fibroblast collagenase.";
RL Biochemistry 29:10628-10634(1990).
RN [5]
RP PARTIAL SEQUENCE.
RX MEDLINE=90380298; PubMed=2169256;
RA Knaeuper V., Kraemer S., Reinke H., Tschesche H.;
RT "Partial amino acid sequence of human PMN leukocyte procollagenase.";

P23097 rattus norv
P33435 mus musculu
Q725M0 homo sapien
O8M118 felis silve
P45452 homo sapien
Q6NM66 homo sapien
AAH67522 homo sapi
AAH67523 homo sapi
P03957 rattus norv
O18927 equus cabal
Q7Z5M1 homo sapien
O9QM68 sus scrofa
O7656 bos taurus
Q6DF35 xenopus tro


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FT CARBOHYD 246 246 N-linked (GlcNAc...) (Potential).
FT DISULFID 279 464 Probable.

Query Match
Best Local Similarity 100.0%; Score 307; DB 1; Length 467;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORFFGLNVTGKPNBETLDMKKPCRGVDPDSGGFMLTPGNPKWERTNLTIRNY 55
DB 66 MORFFGLNVTGKPNBETLDMKKPCRGVDPDSGGFMLTPGNPKWERTNLTIRNY 120

RESULT 2
MM01_RABIT
ID MM01_RABIT STANDARD; PRT; 468 AA.
AC PI3943;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interstitial collagenase precursor (EC 3.4.24.7) (Matrix
DE metalloproteinase-1) (MMP-1).
GN Name=MMP1;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]_SEQUENCE FROM N.A.
RC TISSUE=Synovial cell;
RX MEDLINE=88077876; PubMed=2825772;
RA Fini M.E., Plucinska I.M., Mayer A.S., Gross R.H., Brinckerhoff C.E.;
RT "A gene for rabbit synovial cell collagenase: member of a family of
RT metalloproteinases that degrade the connective tissue matrix.";
RL Biochemistry 26:6156-6165(1987).
RN [2]_
RP SEQUENCE OF 449-468 FROM N.A.
RC STRAIN=New Zealand white;
RX MEDLINE=87029174; PubMed=3021384;
RA Fini M.E., Austin S.D., Holt P.T., Ruby P.L., Gross R.H., White H.D.,
RA Brinckerhoff C.E.;
RT "Homology between exon-containing portions of rabbit genomic clones
RT for synovial cell collagenase and human foreskin and synovial cell
RT mRNAs.";
RL Coll. Relat. Res. 6:239-248(1986).
CC -!- FUNCTION: Cleaves collagens of types I, II, and III at one site in
CC the helical domain. Also cleaves collagens of types VII and X.
CC -!- CATALYTIC ACTIVITY: Cleaves preferentially one bond in native
CC collagen. Cleavage of the triple helix of collagen at about three-
CC quarters of the length of the molecule from the N-terminus, at
CC 775-Gly-Ile-776 in the alpha-1(I) chain. Cleaves synthetic
CC substrates and alpha-macroglobulins at bonds where Pi' is a
CC hydrophobic residue.
CC -!- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit (By
CC similarity).
CC -!- ENZYME REGULATION: Can be activated without removal of the
CC activation peptide.
CC -!- SIMILARITY: Belongs to peptidase family M10A.
CC -!- SIMILARITY: Contains 1 hemopexin-like domain.
CC
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CC
CC EMBL; M17823; AAB88016.1; -
CC EMBL; M17820; AAB88016.1; JOINED.
CC EMBL; M17821; AAB88016.1; JOINED.
CC EMBL; M17822; AAB88016.1; JOINED.
CC EMBL; M19240; AAB88016.1; JOINED.
CC EMBL; M25663; AAA31203.1; -

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DR PIR; A27500; KCRB1.
DR HSSP; P03956; 1CGL.
DR MEROPS; M10.001; -.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR006026; Peptidase_M.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR009070; PGSD-like.
DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF00413; Peptidase_M10; 1.
DR Pfam; PF03933; Peptidase_M10_N; 1.
DR PRINTS; PR00138; MATRXIN.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZnMc; 1.
DR PROSITE; PS00546; CYSTEINE SWITCH; 1.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC PROTEASE; 1.
KW Calcium-binding; Collagen degradation; Extracellular matrix;
KW Glycoprotein; Hydrolase; Metal-binding; Metalloprotease; Signal; Zinc;
KW Zymogen.
FT SIGNAL 1 18 Activation peptide.
FT PROPEP 19 98 Interstitial Collagenase.
FT CHAIN 99 468 Hemopexin-like.
FT DOMAIN 274 468 Cysteine switch (Potential).
FT SITE 91 91 Calcium 1 (By similarity).
FT METAL 123 123 Calcium 2 (By similarity).
FT METAL 157 157 Zinc 1 (By similarity).
FT METAL 167 167 Zinc 1 (By similarity).
FT METAL 169 169 Calcium 3 (By similarity).
FT METAL 174 174 Calcium 3 (via carbonyl oxygen) (By
FT METAL 175 175 similarity).
FT METAL 177 177 Calcium 3 (via carbonyl oxygen) (By
FT METAL 179 179 similarity).
FT METAL 182 182 Calcium 3 (via carbonyl oxygen) (By
FT METAL 189 189 similarity).
FT METAL 191 191 Zinc 1 (By similarity).
FT METAL 193 193 Calcium 2 (via carbonyl oxygen) (By
FT METAL 195 195 similarity).
FT METAL 197 197 Calcium 2 (By similarity).
FT METAL 198 198 Zinc 1 (By similarity).
FT METAL 200 200 Calcium 3 (By similarity).
FT METAL 217 217 Zinc 2 (catalytic) (By similarity).
FT ACT_SITE 218 218 By similarity.
FT METAL 221 221 Zinc 2 (catalytic) (By similarity).
FT METAL 227 227 Zinc 2 (catalytic) (By similarity).
FT METAL 284 284 Calcium 4 (via carbonyl oxygen) (By
FT METAL 328 328 similarity).
FT METAL 377 377 Calcium 4 (via carbonyl oxygen) (By
FT METAL 426 426 similarity).
FT CARBOHYD 119 119 Calcium 4 (via carbonyl oxygen) (By
FT DISULFID 277 465 similarity).
FT SEQUENCE 468 AA; 53739 MW; DA905389195258C CRC64;

Query Match 75.9%; Score 233; DB 1; Length 468;
Best Local Similarity 74.5%; Pred. No. 4.3e-20;
Matches 41; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 MORFFGLNVTGKPNBETLDMKKPCRGVDPDSGGFMLTPGNPKWERTNLTIRNY 55
DB 66 MORFFGLNVTGKPNBETLDMKKPCRGVDPDSGGFMLTPGNPKWERTNLTIRNY 120

RESULT 3
MM01_PIG

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ID AC MM01_PIG STANDARD; PRT; 469 AA.
DI P21692;
DT 01-MAY-1991 (Rel. 18, Created)
DI 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Interstitial collagenase precursor (NC 3.4.24.7) (Matrix
DE metalloproteinase-1) (MMP-1).
GN Name=MMP1;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=91333421; PubMed=1651440;
RA Richards C.D., Rafferty J.A., Reynolds J.J., Saklatvala J.,
RT "Porcine collagenase from synovial fibroblasts: cDNA sequence and
RT modulation of expression of RNA in vitro by various cytokines.";
RL Matrix 11:161-167(1991).
RN [2]
RP SEQUENCE OF 25-469 FROM N.A.
RC TISSUE-Synovial cell.
RX MEDLINE=91067477; PubMed=2174547;
RA Clarke N.J., O'Hare M.C., Cawston T.E., Harper G.P.,
RT "Nucleotide sequence of a cDNA for porcine type I collagenase,
RT obtained by PCR.";
RL Nucleic Acids Res. 18:6703-6703(1990).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 100-469.
RX MEDLINE=96173003; PubMed=8590015;
RA Li J., Brick P., O'Hare M.C., Skarzynski T., Lloyd L.F., Curry V.A.,
RX Clark I.M., Bigg H.F., Hazleman B.L., Cawston T.E., Blow D.M.,
RT "Structure of full-length porcine synovial collagenase reveals a C-
RT terminal domain containing a calcium-linked, four-bladed beta-
RT propeller.";
RL Structure 3:541-549(1995).
RN [4]
RP SEQUENCE OF 100-104 AND 248-282, AND AUTOPROTEOLYTIC CLEAVAGE SITE.
RX MEDLINE=95142615; PubMed=7840605;
RA Clark I.M., Mitchell R.E., Powell L.K., Bigg H.F., Cawston T.E.,
RA O'Hare M.C.,
RT "Recombinant porcine collagenase: purification and autolysis.";
RL Arch. Biochem. Biophys. 316:123-127(1995).
CC -!- FUNCTION: Cleaves collagens of types I, II, and III at one site in
CC the helical domain. Also cleaves collagens of types VII and X.
CC -!- CATALYTIC ACTIVITY: Cleaves preferentially one bond in native
CC collagen. Cleavage of the triple helix of collagen at about three-
CC quarters of the length of the molecule from the N-terminus, at
CC 775-Gly-Ile-776 in the alpha-1(I) chain. Cleaves synthetic
CC substrates and alpha-macroglobulins at bonds where Pi' is a
CC hydrophobic residue.
CC -!- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit.
CC -!- ENZYME REGULATION: Can be activated without removal of the
CC activation peptide.
CC -!- PTM: Undergoes autolytic cleavage to produce a N-terminal fragment
CC having reduced collagenolytic activity.
CC -!- SIMILARITY: Belongs to peptidase family M10A.
CC -!- SIMILARITY: Contains 1 hemopexin-like domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X54724; CAA38526.1; -.
DR PIR; S15986; KCFGI.
DR PDB; 1FBL; X-ray; @=100-469.
DR MEROPS; M10.001; -.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR006026; Peptidase_M.

DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR009070; PGBD_like.
DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF00413; Peptidase_M10; 1.
DR Pfam; PF03933; Peptidase_M10_N; 1.
DR PRINTS; PR00138; MATRXIN.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZmC; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW 3D-structure; Autocatalytic cleavage; Calcium-binding;
KW Collagen degradation; Direct protein sequencing; Extracellular matrix;
KW Glycoprotein; Hydrolase; Metal-binding; Metalloprotease; Signal; Zinc;
KW Zymogen.
FT SIGNAL 1 19
FT PROPEP 20 99 Activation peptide.
FT CHAIN 100 469 Interstitial collagenase.
FT CHAIN 100 258 18 kDa interstitial collagenase.
FT DOMAIN 275 489 Hemopexin-like.
FT SITE 92 92 Cysteine switch (Potential).
FT SITE 258 259 Cleavage (autolytic).
FT METAL 124 124 Calcium 1.
FT METAL 158 158 Calcium 2.
FT METAL 168 168 Zinc 1.
FT METAL 170 170 Zinc 1.
FT METAL 175 175 Calcium 3.
FT METAL 176 176 Calcium 3 (via carbonyl oxygen).
FT METAL 178 178 Calcium 3 (via carbonyl oxygen).
FT METAL 180 180 Calcium 3 (via carbonyl oxygen).
FT METAL 183 183 Zinc 1.
FT METAL 190 190 Calcium 2 (via carbonyl oxygen).
FT METAL 192 192 Calcium 2 (via carbonyl oxygen).
FT METAL 194 194 Calcium 2.
FT METAL 196 196 Zinc 1.
FT METAL 198 198 Calcium 3.
FT METAL 199 199 Calcium 1.
FT METAL 201 201 Calcium 3.
FT METAL 218 218 Zinc 2 (catalytic).
FT ACT_SITE 219 219 Zinc 2 (catalytic).
FT METAL 222 222 Zinc 2 (catalytic).
FT METAL 228 228 Calcium 4 (via carbonyl oxygen).
FT METAL 285 285 Calcium 4 (via carbonyl oxygen).
FT METAL 329 329 Calcium 4 (via carbonyl oxygen).
FT METAL 378 378 Calcium 4 (via carbonyl oxygen).
FT METAL 427 427 Calcium 4 (via carbonyl oxygen).
FT DISULFID 278 466 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 120 120
FT STRAND 101 102
FT TURN 104 105
FT STRAND 113 118
FT TURN 123 124
FT TURN 127 142
FT HELIX 127 142
FT TURN 143 144
FT STRAND 148 152
FT STRAND 159 164
FT STRAND 182 184
FT TURN 190 193
FT STRAND 195 198
FT TURN 199 200
FT STRAND 204 204
FT STRAND 211 211
FT HELIX 212 223
FT TURN 224 225
FT STRAND 226 227
FT TURN 232 233
FT TURN 235 236
FT HELIX 250 260
FT TURN 277 278
FT TURN 280 281
FT STRAND 286 290
FT TURN 291 292

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FT STRAND 293 298
FT TURN 299 300
FT STRAND 301 305
FT STRAND 313 316
FT HELIX 317 320
FT STRAND 330 334
FT TURN 335 338
FT STRAND 339 344
FT TURN 345 346
FT STRAND 347 352
FT TURN 353 354
FT STRAND 355 356
FT TURN 358 359
FT STRAND 362 363
FT STRAND 364 368
FT HELIX 372 373
FT TURN 379 383
FT STRAND 384 387
FT TURN 388 393
FT TURN 394 395
FT STRAND 396 401
FT TURN 402 405
FT STRAND 406 407
FT STRAND 413 414
FT HELIX 415 418
FT TURN 420 421
FT STRAND 428 432
FT TURN 433 434
FT STRAND 435 440
FT TURN 441 442
FT STRAND 443 448
FT TURN 449 452
FT STRAND 453 459
FT TURN 460 461
FT HELIX 462 464
FT TURN 465 465
SQ SEQUENCE 469 AA; 53666 MW; 7952D72B2753F682 CRC64;

Query Match 75.2%; Score 231; DB 1; Length 469;
Best Local Similarity 72.7%; Pred. No. 7.6e-20;
Matches 40; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 1 MORFFGLNVTGKPNBETLDMKKPCGVPDGGFMLTPGNPKWSTNLTYYIRNY 55
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
67 MQQFFGLKVTGTPDAETLNVMKQPCGVPDVAEFLVTFGNPFWNTHLYTYIENY 121

Db

RESULT 4
MM08 RAT
ID MM08 RAT STANDARD; PRT; 466 AA.
AC O88766;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Neutrophil collagenase precursor (EC 3.4.24.34) (Matrix metalloproteinase-8) (MMP-8).
GN Name=Mmp8;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Lewis;
RA Overall C.M., Lowe D., Wells G., Burel S., Clements J.M.;
RT "Cloning, expression, characterization and activation properties of rat neutrophil collagenase (MMP-8).";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Can degrade fibrillar type I, II, and III collagens.
CC -!- CATALYTIC ACTIVITY: Cleavage of interstitial collagens in the triple helical domain. Unlike EC 3.4.24.7, this enzyme cleaves type III collagen more slowly than type I.
CC -!- COFACTOR: Binds 2 zinc ions and 3 calcium ions per subunit (By

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similarity).
-!- ENZYME REGULATION: Cannot be activated without removal of the activation peptide (By similarity).
-!- SUBCELLULAR LOCATION: Stored in intracellular granules.
-!- SIMILARITY: Belongs to peptidase family M10A.
-!- SIMILARITY: Contains 1 hemopexin-like domain.
-----
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EMBL; AJ007288; CAA07432.1; -.
HSP; P22894; IZS.
MEROPS; M10.002; -.
InterPro; IPR000585; Hemopexin.
InterPro; IPR001818; Pept_M10A_M12B.
InterPro; IPR006025; Pept_M_Zn_BS.
InterPro; IPR009070; PGBD-like.
Pfam; PF00045; Hemopexin_4.
Pfam; PF00413; Peptidase_M10; 1.
Pfam; PF03933; Peptidase_M10_N; 1.
PRINTS; PR00138; MATRIXIN.
PROSITE; PS00546; CYSTEINE_SWITCH; 1.
PROSITE; PS00024; HEMOPEXIN; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
Calcium-binding; Collagen degradation; Extracellular matrix; Glycoprotein; Hydrolase; Metal-binding; Metalloprotease; Signal; Zinc; Zymogen.
FT SIGNAL 1 20 By similarity.
FT PROPEP 21 101 Activation peptide (By similarity).
FT CHAIN 102 466 Neutrophil collagenase.
FT DOMAIN 277 466 Hemopexin-like.
FT SITE 92 Cysteine switch (By similarity).
FT METAL 158 158 Calcium 1 (By similarity).
FT METAL 168 168 Zinc 1 (By similarity).
FT METAL 170 170 Zinc 1 (By similarity).
FT METAL 175 175 Calcium 2 (By similarity).
FT METAL 176 176 Calcium 2 (via carbonyl oxygen) (By similarity).
FT METAL 178 178 Calcium 2 (via carbonyl oxygen) (By similarity).
FT METAL 180 180 Calcium 2 (via carbonyl oxygen) (By similarity).
FT METAL 183 183 Zinc 1 (By similarity).
FT METAL 190 190 Calcium 1 (via carbonyl oxygen) (By similarity).
FT METAL 192 192 Calcium 1 (via carbonyl oxygen) (By similarity).
FT METAL 194 194 Calcium 1 (By similarity).
FT METAL 196 196 Zinc 1 (By similarity).
FT METAL 198 198 Calcium 2 (By similarity).
FT METAL 201 201 Calcium 2 (By similarity).
FT METAL 218 218 Zinc 2 (catalytic) (By similarity).
FT ACT_SITE 219 By similarity.
FT METAL 222 Zinc 2 (catalytic) (By similarity).
FT METAL 228 Zinc 2 (catalytic) (By similarity).
FT METAL 287 Calcium 3 (via carbonyl oxygen) (By similarity).
FT METAL 379 Calcium 3 (via carbonyl oxygen) (By similarity).
FT METAL 426 Calcium 3 (via carbonyl oxygen) (By similarity).
FT DISULFID 280 Probable.
FT CARBOHYD 56 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 113 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 466 AA; 53277 MW; 8B9DE97576E76C90 CRC64;

Query Match 72.8%; Score 223; DB 1; Length 466;
Best Local Similarity 70.9%; Pred. No. 7.3e-19;

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RA Harris T.J.R., Reynolds J.J., Herrlich P., Docherty A.J.P.;
RT "Comparison of human stromelysin and collagenase by cloning and
RL sequence analysis.",
RL Biochem. J. 240:913-916(1986).
[3]
RP SEQUENCE FROM N.A.
RX MEDLINE=86196089; PubMed=3009463;
RA Goldberg G.I., Wilhelm S.M., Kronberger A., Bauer E.A., Grant G.A.,
RT Eisen A.Z.;
RA "Human fibroblast collagenase. Complete primary structure and homology
RT to an oncogene transformation-induced rat protein.",
RL J. Biol. Chem. 261:6600-6605(1986).
[4]
RP SEQUENCE FROM N.A.
RA Lin D., Duncan M., Allen E., Araujo R., Aparicio A., Chai A.,
RA Chung E., Davis K., Federspiel N., Hyman R., Kalman S., Komp C.,
RA Kurdi O., Lashkari D., Lew H., Namath A., Oefner P., Roberts D.,
RA Heller R., Davis R.W.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
[5]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Sapetenko M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting J., Helton E., Kretzmar M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Gichman J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.",
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[6]
RP SEQUENCE OF 1-35 FROM N.A.
RX MEDLINE=87257941; PubMed=3037355;
RA Angel P., Baumann I., Stein B., Delius H., Rahmsdorf H.J.,
RA Herrlich P.;
RT "12-O-tetradecanoyl-phorbol-13-acetate induction of the human
RL collagenase gene is mediated by an inducible enhancer element located
RL in the 5'-flanking region.",
RL Mol. Cell. Biol. 7:2256-2266(1987).
[7]
RP SEQUENCE OF 1-70 FROM N.A.
RC TISSUE=Synovial cell;
RX MEDLINE=87109799; PubMed=3027129;
RA Brinckerhoff C.E., Ruby P.L., Austin S.D., Fini M.E., White H.D.;
RT "Molecular cloning of human synovial cell collagenase and selection of
RL a single gene from genomic DNA.",
RL J. Clin. Invest. 79:542-546(1987).
[8]
RP SEQUENCE OF 100-112 AND 270-287.
RC TISSUE=Fibroblast;
RX MEDLINE=90104231; PubMed=2557822;
RA Clark I.M., Cawston T.E.;
RT "Fragments of human fibroblast collagenase. Purification and
RL characterization.",
RL Biochem. J. 263:201-206(1989).
[9]
RP SIMILARITY TO THERMOLYSIN TYPE PROTEASES.
RX MEDLINE=87194799; PubMed=3032950;
RA McKerrow J.H.;
RT "human fibroblast collagenase contains an amino acid sequence

RT homologous to the zinc-binding site of Serratia protease.",
RL J. Biol. Chem. 262:5943-5943(1987).
[10]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 100-269.
RX MEDLINE=95384760; PubMed=7656013;
RA Borkakoti N., Winkler F.K., Williams D.H., D'Arcy A., Broadhurst M.J.,
RA Brown P.A., Johnson W.H., Murray E.J.,
RT "Structure of the catalytic domain of human fibroblast collagenase
RL complexed with an inhibitor.",
RL Nat. Struct. Biol. 1:106-110(1994).
[11]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 102-269.
RX MEDLINE=94304829; PubMed=8031754;
RA Lovejoy B., Hassell A.M., Luther M.A., Weigl D., Jordan S.R.;
RT "Crystal structures of recombinant 19-kDa human fibroblast collagenase
RL complexed to itself.",
RL Biochemistry 33:8207-8217(1994).
[12]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 102-269.
RX MEDLINE=94105765; PubMed=8278810;
RA Lovejoy B., Cleasby A., Hassell A.M., Longley K., Luther M.A.,
RA Weigl D., McEneaney G., McElroy A.B., Drewry D., Lambert M.H.,
RT "Structure of the catalytic domain of fibroblast collagenase complexed
RL with an inhibitor.",
RL Science 263:375-377(1994).
[13]
RP X-RAY CRYSTALLOGRAPHY (1.56 ANGSTROMS) OF 101-269.
RX MEDLINE=94377426; PubMed=8090713;
RA Spurlino J.C., Smallwood A.M., Carlton D.D., Banks K.J.,
RA Johnson J.S., Cook B.R., Falvo J., Wahl R.C., Pulvino T.A., Et A.L.;
RT "1.56-A structure of mature truncated human fibroblast collagenase.",
RL Proteins 19:98-109(1994).
[14]
RP STRUCTURE BY NMR OF 101-269.
RX MEDLINE=98145213; PubMed=9484219;
RA Moy F.J., Chanda P.K., Cosmi S., Pisano M.R., Urbano C., Wilhelm J.,
RA Powers R.;
RT "High-resolution solution structure of the inhibitor-free catalytic
RL fragment of human fibroblast collagenase determined by
RL multidimensional NMR.",
RL Biochemistry 37:1495-1504(1998).
CC -!- FUNCTION: Cleaves collagens of types I, II, and III at one site in
CC the helical domain. Also cleaves collagens of types VII and X.
CC -!- CATALYTIC ACTIVITY: Cleaves preferentially one bond in native
CC collagen. Cleavage of the triple helix of collagen at about three-
CC quarters of the length of the molecule from the N-terminus at
CC 775-Gly-1-Ile-776 in the alpha-1(I) chain. Cleaves synthetic
CC substrates and alpha-macroglobulins at bonds where P1' is a
CC hydrophobic residue.
CC -!- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit.
CC -!- ENZYME REGULATION: Can be activated without removal of the
CC activation peptide.
CC -!- DOMAIN: There are two distinct domains in this protein; the
CC catalytic N-terminal, and the C-terminal which is involved in
CC substrate specificity and in binding TIMP (tissue inhibitor of
CC metalloproteinases).
CC -!- PTM: Undergoes autolytic cleavage to two major forms (22 kDa and
CC 27 kDa). A minor form (25 kDa) is the glycosylated form of the 22
CC kDa form. The 27 kDa form has no activity while the 22/25 kDa form
CC can act as activator for collagenase.
CC -!- SIMILARITY: Belongs to peptidase family M10A.
CC -!- SIMILARITY: Contains 1 hemopexin-like domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (see [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/)
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X05231; CAA28858.1; -

KW Extracellular matrix: Glycoprotein; Hydrolase; Metal-binding;
 KW Metalloprotease; Signal; Zinc; Zymogen.
 FT SIGNAL 1 18
 FT PROPEP 19 99 Activation peptide.
 FT CHAIN 100 469 Interstitial collagenase.
 FT DOMAIN 275 469 Hemopexin-like.
 FT SITE 92 92 Cysteine switch (Potential).
 FT METAL 124 124 Calcium 1 (By similarity).
 FT METAL 158 158 Calcium 2 (By similarity).
 FT METAL 168 168 Zinc 1 (By similarity).
 FT METAL 170 170 Zinc 1 (By similarity).
 FT METAL 175 175 Calcium 3 (By similarity).
 FT METAL 176 176 Calcium 3 (via carbonyl oxygen) (By similarity).
 FT METAL 178 178 Calcium 3 (via carbonyl oxygen) (By similarity).
 FT METAL 180 180 Calcium 3 (via carbonyl oxygen) (By similarity).
 FT METAL 183 183 Zinc 1 (By similarity).
 FT METAL 190 190 Calcium 2 (via carbonyl oxygen) (By similarity).
 FT METAL 192 192 Calcium 2 (via carbonyl oxygen) (By similarity).
 FT METAL 194 194 Calcium 2 (By similarity).
 FT METAL 196 196 Zinc 1 (By similarity).
 FT METAL 198 198 Calcium 3 (By similarity).
 FT METAL 199 199 Calcium 1 (By similarity).
 FT METAL 201 201 Calcium 3 (By similarity).
 FT METAL 218 218 Zinc 2 (catalytic) (By similarity).
 FT ACT SITE 219 219 By similarity.
 FT METAL 222 222 Zinc 2 (catalytic) (By similarity).
 FT METAL 228 228 Zinc 2 (catalytic) (By similarity).
 FT METAL 285 285 Calcium 4 (via carbonyl oxygen) (By similarity).
 FT METAL 329 329 Calcium 4 (via carbonyl oxygen) (By similarity).
 FT METAL 378 378 Calcium 4 (via carbonyl oxygen) (By similarity).
 FT METAL 427 427 Calcium 4 (via carbonyl oxygen) (By similarity).
 FT DISULFID 278 466 By similarity.
 FT CARBOHYD 120 120 N-linked (GlcNAc...) (Potential).
 FT CONFLICT 22 23 AT -> FP (in Ref. 2).
 FT CONFLICT 30 30 D -> L (in Ref. 2).
 FT CONFLICT 35 36 KK -> LL (in Ref. 2).
 FT CONFLICT 85 85 N -> F (in Ref. 2).
 FT CONFLICT 106 108 KSC -> NPR (in Ref. 2).
 FT CONFLICT 113 113 N -> D (in Ref. 2).
 FT SEQUENCE 469 AA; 53354 MW; B4A5504CE24BD7B5 CRC64;
 Query Match 71.0%; Score 218; DB 1; Length 469;
 Best Local Similarity 70.9%; Pred. No. 3.1e-18;
 Matches 39; Conservative 6; Mismatches 10; Indels 0; Gaps 0;
 QY 1 MQRFGLVGTGKNEETLDMKPRGCPVDSGGFMLTPGNPKWERTNLTYYRNY 55
 DB 67 MQRFGLVGTGKDAETLNWKPGRGVPDPAFVLTGKSCWENTNLTYYRNY 121
 RESULT 9
 MM01 RANCA STANDARD; PRT; 384 AA.
 ID MM01 RANCA
 AC Q1113;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Interstitial collagenase precursor (EC 3.4.24.7) (Matrix metalloproteinase-1) (MMP-1) (TC1).
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.
 OX NCBI_TaxID=9400;
 RN [1]

RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RX MEDLINE=95071832; PubMed=7981043;
 RA Oofusa K., Yomori S., Yoshizato K.;
 RT "Regionally and hormonally regulated expression of genes of collagen
 and collagenase in the anuran larval skin.";
 RL Int. J. Dev. Biol. 38:345-350(1994).
 CC -!- FUNCTION: Cleaves collagens of types I, II, and III at one site in
 the helical domain. Also cleaves preferentially one bond in about three-
 quarters of the length of the triple helix of collagen at about three-
 quarters of the length of the molecule from the N-terminus at
 775-Gly-Ile-776 in the alpha-1(I) chain. Cleaves synthetic
 substrates and alpha-macroglobulins at bonds where PI* is a
 hydrophobic residue.
 CC -!- Cofactor: Binds 2 zinc ions and 4 calcium ions per subunit (By
 similarity).
 CC -!- ENZYME REGULATION: Can be activated without removal of the
 activation peptide (By similarity).
 CC -!- SIMILARITY: Belongs to peptidase family M10A.
 CC -!- SIMILARITY: Contains 1 hemopexin-like domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL; S75623; AAB32661.1; -;
 DR PIR; I51267; I51267.
 DR HSPF; P21692; IFLB.
 DR MEROPS; M10.001; -;
 DR InterPro; IPR000585; Hemopexin.
 DR InterPro; IPR006026; Peptidase M.
 DR InterPro; IPR001818; Pept_M10A_M12B.
 DR InterPro; IPR006025; Pept_M_Zn_BS.
 DR InterPro; IPR009070; POED-like.
 DR Pfam; PF00045; Hemopexin; 2.
 DR Pfam; PF00413; Peptidase M10; 1.
 DR Pfam; PF03933; Peptidase M10_N; 1.
 DR PRINTS; PR00138; MATRIXIN.
 DR SMART; SM00120; HX; 2.
 DR SMART; SM00235; ZmC; 1.
 DR PROSITE; PS00546; CYSTEINE SWITCH; FALSE_NEG.
 DR PROSITE; PS00024; HEMOPEXIN; FALSE_NEG.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 DR Calcium-binding; Collagen degradation; Extracellular matrix;
 KW Hydrolase; Metal-binding; Metalloprotease; Signal; Zinc; Zymogen.
 FT SIGNAL 1 25 Potential.
 FT PROPEP 26 88 Activation peptide (Potential).
 FT CHAIN 89 384 Interstitial collagenase.
 FT DOMAIN 239 384 Hemopexin-like.
 FT SITE 81 81 Cysteine switch (Potential).
 FT METAL 113 113 Calcium 1 (By similarity).
 FT METAL 129 129 Calcium 2 (By similarity).
 FT METAL 139 139 Zinc 1 (By similarity).
 FT METAL 141 141 Zinc 1 (By similarity).
 FT METAL 146 146 Calcium 3 (By similarity).
 FT METAL 147 147 Calcium 3 (via carbonyl oxygen) (By similarity).
 FT METAL 149 149 Calcium 3 (via carbonyl oxygen) (By similarity).
 FT METAL 151 151 Calcium 3 (via carbonyl oxygen) (By similarity).
 FT METAL 154 154 Zinc 1 (By similarity).
 FT METAL 161 161 Calcium 2 (via carbonyl oxygen) (By similarity).
 FT METAL 163 163 Calcium 2 (via carbonyl oxygen) (By similarity).
 FT METAL 165 165 Calcium 2 (By similarity).
 FT METAL 167 167 Zinc 1 (By similarity).

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FT METAL 169          Calcium 3 (By similarity).
FT METAL 170          Calcium 1 (By similarity).
FT METAL 172          Calcium 3 (By similarity).
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FT METAL 193          Zinc 2 (catalytic) (By similarity).
FT METAL 199          Zinc 2 (catalytic) (By similarity).
FT METAL 249          Calcium 4 (via carbonyl oxygen) (By
FT METAL 277          similarity).
FT METAL 347          Calcium 4 (via carbonyl oxygen) (By
FT METAL 347          similarity).
FT DISULFID 242 381    Calcium 4 (via carbonyl oxygen) (By
FT SEQUENCE 384 AA; 43582 MW; A5B5E2FB32239DF CRC64;
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Best Local Similarity 65.5%; Pred. No. 2.7e-16;
Matches 36; Conservative 10; Mismatches 8; Indels 1; Gaps 1;
QY 1 MQRFFGLNVTGKPNBETLDMKKPCGVPDSCGFMTPGNPKWERTNLTIRNY 55
Db 57 LKQFFGLKVTGKDAETL-VMKQSTCGVPDVGVEVLTGPNRWENTHLYRIENY 110

RESULT 10
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ID Q8C209
AC Q8C209;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus B6-derived CD11+ve dendritic cells cDNA, RIKEN full-
DE length enriched library, clone: F730044H20 product: matrix
DE metalloprotease 8, full insert sequence.
GN Names=Mmp8;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=9279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RA "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630 (2000).
RN [5]
RP SEQUENCE FROM N.A.

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RC STRAIN=C57BL/6J;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Nakamura S., Hiramoto K., Hiraoka T., Kasukawa T.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Iizawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771 (2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume N.,
RA Hayashida K., Hayatsu N., Hiramoto K., Kagawa I., Kasukawa T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akanita S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
ID Q8C209 PRELIMINARY; PRT; 465 AA.
AC Q8C209;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus B6-derived CD11+ve dendritic cells cDNA, RIKEN full-
DE length enriched library, clone: F730018B13 product: matrix
DE metalloprotease 8, full insert sequence.
GN Names=Mmp8;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=9279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RA "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630 (2000).
RN [5]
RP SEQUENCE FROM N.A.

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Query Match 64.5%; Score 198; DB 2; Length 465;
Best Local Similarity 65.5%; Pred. No. 9e-16;
Matches 36; Conservative 7; Mismatches 12; Indels 0; Gaps 0;
QY 1 MQRFFGLNVTGKPNBETLDMKKPCGVPDSCGFMTPGNPKWERTNLTIRNY 55
Db 66 MQRFFSLAETGKDAATMGIMEMPCGVPDSCGFMTPGNPKWERTNLTIRNY 120

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ID Q8C230
AC Q8C230;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus B6-derived CD11+ve dendritic cells cDNA, RIKEN full-
DE length enriched library, clone: F730018B13 product: matrix
DE metalloprotease 8, full insert sequence.
GN Names=Mmp8;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

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ID BAC40805 PRELIMINARY; PRT; 465 AA.
AC BAC40805;
DT 14-APR-2004 (TEMBLrel. 27, Created)
DT 14-APR-2004 (TEMBLrel. 27, Last sequence update)
DE NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full-length enriched
DE library, clone: F630050H05 product: matrix metalloproteinase 8, full
DE insert sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_SEQUENCE FROM N.A.
RP STRAIN=NOD;
RC MEDLINE=22354683; PubMed=12466851;
RX The FANTOM Consortium,
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630 (2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771 (2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanaoka T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RT Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AK089234; BAC40805.1; -; 448AEC59639E9237 CRC64;
SQ SEQUENCE 465 AA; 53125 MW; 448AEC59639E9237 CRC64;
Query Match 64.5%; Score 198; DB 2; Length 465;
Best Local Similarity 65.5%; Pred. No. 9e-16;
Matches 36; Conservative 7; Mismatches 12; Indels 0; Gaps 0;
Qy 1 MQRFGLNVTGKNEETLDMKKPRGCVDPDSGFMLTGPNPKWERNLTYRINY 55
Db 66 MQRFPSLAETGKLDAAATGMINEMPRCGVDPDSGDFLLTGPSPKWTHTLTYRINH 120
RESULT 14
Q6Y4Q5 PRELIMINARY; PRT; 478 AA.
ID Q6Y4Q5
AC Q6Y4Q5; 27, Created
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DE Stromelysin 1.
DE Stromelysin 1.
GN Name=MMP3;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Sarcoma;
RA Sorensen K.C., Balkin R.G., Kitchell B.E., Siegel A.M., Schaeffer D.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY183143; AAO63580.1; -;
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR006026; Peptidase M.
DR InterPro; IPR001818; Pept M10A_M12B.
DR InterPro; IPR006025; Pept_M_zn_BS.
DR Pfam; PF00045; Hemopexin_4.
DR Pfam; PF00413; Peptidase_M10; 1.
DR Pfam; PF03933; Peptidase_M10_N; 1.
DR PRINTS; PR00138; MATRILIN.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZnMc; 1.
DR PROSITE; PS00546; CYSTEINE SWITCH; 1.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN 1.
SQ SEQUENCE 478 AA; 53633 MW; 5D1B9DA9D57BC041 CRC64;
Query Match 64.5%; Score 198; DB 2; Length 478;
Best Local Similarity 63.6%; Pred. No. 9.3e-16;
Matches 35; Conservative 7; Mismatches 13; Indels 0; Gaps 0;
Qy 1 MQRFGLNVTGKNEETLDMKKPRGCVDPDSGFMLTGPNPKWERNLTYRINY 55
Db 67 MQRFGLGTVTKVSDTLAMRRPRCGVDPVGDFTTFFGMPKWRKTHLTYRIMNY 121
RESULT 15
AAO63580 PRELIMINARY; PRT; 478 AA.
ID AAO63580
AC AAO63580;
DT 02-MAR-2004 (TEMBLrel. 27, Created)
DT 02-MAR-2004 (TEMBLrel. 27, Last sequence update)
DE Stromelysin 1.
DE Stromelysin 1.
GN MMP3;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Sarcoma;
RA Sorensen K.C., Balkin R.G., Kitchell B.E., Siegel A.M., Schaeffer D.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

Search completed: November 15, 2004, 14:06:39
Job time : 51.7692 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 13, 2004, 14:57:16 ; Search time 89.1795 Seconds
(without alignments)
189.060 Million cell updates/sec

Title: US-10-032-376A-8
Perfect score: 258
Sequence: 1 LQKLSLPETGELDSATLKA.....VPDLGRFOTFGDLKWHHN 47

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04: *
1: Geneseqp1980s: *
2: Geneseqp1990s: *
3: Geneseqp2000s: *
4: Geneseqp2001s: *
5: Geneseqp2002s: *
6: Geneseqp2003as: *
7: Geneseqp2003bs: *
8: Geneseqp2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	258	100.0	47	6	ABP97130 Human mat
2	258	100.0	47	6	ABG76316 Human mat
3	258	100.0	47	8	ADQ17091 Human mat
4	258	100.0	432	5	ABP69247 Human pol
5	258	100.0	702	5	ABP69246 Human pol
6	258	100.0	707	2	AAK07077 92-KDa hu
7	258	100.0	707	3	AAY58015 Matrix me
8	258	100.0	707	4	AAE10432 Human mat
9	258	100.0	707	4	AAE10432 Human mat
10	258	100.0	707	4	AAE10432 Human mat
11	258	100.0	707	6	ABU56680 Lung canc
12	258	100.0	707	6	ABU56680 Lung canc
13	258	100.0	707	6	AAO16609 Human mat
14	258	100.0	707	6	ABP92116 Human cer
15	258	100.0	707	7	ADL14993 Human typ
16	258	100.0	707	7	ADN39040 Cancer/an
17	258	100.0	707	7	ADN39335 Cancer/an
18	258	100.0	707	8	ADH17067 Human mat
19	258	100.0	707	8	ADJ75581 Marker ge
20	258	100.0	707	8	ADM67186 Human adi
21	258	100.0	707	8	ADM07701 Human mat
22	258	100.0	707	8	ADQ19168 Human sof
23	228	88.4	43	6	ABP97138 Human mat
24	228	88.4	43	6	ABG76324 Partial s
25	228	88.4	43	8	ADQ17099 Human mat

ALIGNMENTS

RESULT 1

ABP97130
ID ABP97130 standard; peptide; 47 AA.
XX AC ABP97130;
XX AC
XX DT 24-JUN-2003 (first entry)
XX DE Human matrix metalloproteinase 9 cleavage region peptide SEQ ID NO:8.
XX KW Human; matrix metalloproteinase; MMP; anticancer; wound healing;
XX KW matrix metalloproteinase inhibitor; antitumor; antiangiogenic; cardiant;
XX KW vascular endothelial growth factor inhibitor; VEGF inhibitor; cytosolic;
XX KW vulnarary; cerebroprotective; antidiabetic; ophthalmological; tumour;
XX KW dermatological; metastatic; non-metastatic; vascularised; heart disease;
XX KW non-vascularised; surgical incision; chronic wound; stroke; angiogenesis;
XX KW macular degeneration; diabetic retinopathy; cleavage region.
XX OS Homo sapiens.
XX PN W02003018748-A2.
XX PD 06-MAR-2003.
XX PF 15-AUG-2002; 2002WO-US026319.
XX PR 16-AUG-2001; 2001US-0312726P.
XX PR 21-DEC-2001; 2001US-00032376.
XX PR 21-MAY-2002; 2002US-00153185.
XX (KIMS) KIMBERLY-CLARK WORLDWIDE INC.
XX Quirk S, Weart IF;
XX WPI; 2003-381408/36.
XX Anti-angiogenic composition comprising peptide inhibitor of matrix metalloproteinase, useful for decreasing the expression of vascular endothelial growth factor and treating cancers and tissue injuries.
XX Claim 17; Page 16; 103pp; English.

The present invention describes an anti-angiogenic composition (I) for inhibiting expression of vascular endothelial growth factor (VEGF). (I) comprises an effective amount of a peptide inhibitor of matrix metalloproteinase (MMP), where the peptide can inhibit the expression of VEGF. (I) has cytostatic, vulnarary, cardiant, cerebroprotective, antidiabetic, ophthalmological and dermatological activities. (I) can be

used for inhibiting expression of VEGF, and so can be used for inhibiting growth of tumours and diminishing tumours size. The tumour can be metastatic, non-metastatic, vascularised, non-vascularised, hard or soft. (I) is also useful for treating injuries, including wounds, surgical incisions, chronic wounds, heart diseases and stroke. (I) is also useful for treating disorders characterised by excessive angiogenesis e.g. macular degeneration and diabetic retinopathy. The present sequence represents a human MMP cleavage region peptide, which is used in the exemplification of the present invention

XX Sequence 47 AA;

Query Match 100.0%; Score 258; DB 6; Length 47;
Best Local Similarity 100.0%; Pred. No. 3.2e-29;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKQSLPETGELDSATLKAMETPRCGVDPDLGRFOTFEGDLKWHHN 47
DB 1 LKQSLPETGELDSATLKAMETPRCGVDPDLGRFOTFEGDLKWHHN 47

RESULT 2

ABG76316
ID ABG76316 standard; protein; 47 AA.

XX AC ABG76316;

XX DT 10-MAY-2003 (first entry)

XX DE Human matrix metalloproteinase (MMP) peptide inhibitor #8.

XX KW Human; peptide inhibitor; matrix metalloproteinase-9; MMP-9;
XX KW cleavage region; proenzyme form; cellular proliferation; fibroblast;
XX KW keratinocyte; healthy skin development; wound healing; scarring;
XX KW skin tone; wrinkle; anti-aging; vulnerary.

XX OS Homo sapiens.

XX PN WO2003016520-A1.

XX PD 27-FEB-2003.

XX PF 15-AUG-2002; 2002WO-US026138.

XX PR 16-AUG-2001; 2001US-0312726P.

XX PR 21-DEC-2001; 2001US-00023236.

XX PR 21-MAY-2002; 2002US-00153185.

XX PA (KIMB) KIMBERLY-CLARK WORLDWIDE INC.

XX PI Quirk S, Malik S, Villanueva JM;

XX PS WPI; 2003-289980/28.

XX PT Novel peptide inhibitor of proteinase activity of matrix

XX PT metalloproteinases, e.g. matrix metalloproteinase-2, useful for

XX PT stimulating cellular proliferation of fibroblasts or keratinocytes.

XX PS Claim 1; Page 16; 120pp; English.

XX CC The present invention relates to peptide inhibitors of metalloproteinases (MMPs), particularly metalloproteinase-2 (MMP-2). The inhibitors have peptide sequences related to the cleavage regions of the proenzyme forms of the MMPs. The peptide inhibitors are useful for stimulating cellular proliferation of fibroblasts or keratinocytes, promoting healthy skin development, treating wounds, preventing scarring, improving skin tone, reducing wrinkling and for simulating the development of smooth, healthy skin. The peptide inhibitors are useful as anti-aging and wound healing compounds. ABG76309-ABG76321 represent peptide inhibitors of MMPs

XX Sequence 47 AA;

Query Match 100.0%; Score 258; DB 6; Length 47;

Best Local Similarity 100.0%; Pred. No. 3.2e-29;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKQSLPETGELDSATLKAMETPRCGVDPDLGRFOTFEGDLKWHHN 47
DB 1 LKQSLPETGELDSATLKAMETPRCGVDPDLGRFOTFEGDLKWHHN 47

RESULT 3

ADQ17091
ID ADQ17091 standard; peptide; 47 AA.

XX AC ADQ17091;

XX DT 23-SEP-2004 (first entry)

XX DE Human matrix metalloproteinase-9 (MMP9) cleavage region peptide.

XX KW Fibronectin; healthy skin; wrinkle; wound; vulnerary; dermatological;
XX KW human; matrix metalloproteinase; MMP.

XX OS Homo sapiens.

XX PN US2004127421-A1.

XX PD 01-JUL-2004.

XX PF 30-DEC-2002; 2002US-00335207.

XX PR 30-DEC-2002; 2002US-00335207.

XX PA (MALI/) MALIK S.

XX PA (QUIR/) QUIRK S.

XX PI Malik S, Quirk S;

XX PS WPI; 2004-506456/48.

XX PT Composition used for preventing and treating wrinkles and treating wounds
XX PT comprises peptide having sequence related to matrix metalloproteinase
XX PT proenzyme.

XX PS Example 1; SEQ ID NO 8; 60pp; English.

XX CC The present invention provides peptides and compositions containing such
XX CC peptides that are useful as agents to maintain healthy skin and to
XX CC promote the condition of the skin. The invention is useful for increasing
XX CC the amount of fibronectin in tissue. The invention is also useful for
XX CC encouraging the maintenance and development of healthy skin, preventing
XX CC and treating wrinkles and for treating wounds. The invention acts as
XX CC vulnerary and dermatological agents. The present sequence is human matrix
XX CC metalloproteinase (MMP) cleavage region peptide. This sequence is used in
XX CC the exemplification of the invention.

XX SQ Sequence 47 AA;

Query Match 100.0%; Score 258; DB 8; Length 47;
Best Local Similarity 100.0%; Pred. No. 3.2e-29;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKQSLPETGELDSATLKAMETPRCGVDPDLGRFOTFEGDLKWHHN 47
DB 1 LKQSLPETGELDSATLKAMETPRCGVDPDLGRFOTFEGDLKWHHN 47

RESULT 4

ABP69247
ID ABP69247 standard; protein; 432 AA.

XX AC ABP69247;

XX DT 20-JAN-2003 (first entry)


```

DE Human polypeptide SEQ ID NO 1294.
XX
XX Human; genome mapping; gene therapy; food supplement; virus; fungus;
KW cell-proliferative disorder; neurodegenerative disease; bacterial;
KW Parkinson's disease; Alzheimer's disease; autoimmune disease;
KW multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
KW arthritis; cytostatic; immunomodulator; nootropic; neuroprotective;
KW antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
KW haemostatic; vulnery; fungicide; antibacterial; virucide; protozoacide;
KW antiarthritic.
XX
OS Homo sapiens.
XX
PN WO200270539-A2.
XX
PD 12-SEP-2002.
XX
PF 05-MAR-2002; 2002WO-US005095.
XX
PR 05-MAR-2001; 2001US-00799451.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;
PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;
PI Wehrman T, Wang J, Wang D, Drmanac RT;
XX
DR WPI; 2002-759812/82.
DR N-PSDB; AB211464.
XX
XX New polynucleotides comprising sequences assembled from expressed
PT sequence tags (ESTs), useful for treating cell-proliferative,
PT neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
PT or coagulation disorders.
XX
XX Claim 9; SEQ ID NO 1294; 1012bp + Sequence Listing; English.
PS
XX
XX The invention relates to an isolated polynucleotide (I) comprising a
CC nucleotide sequence selected from any of 948 sequences (AB211119-
CC AB212066) or their mature protein coding portion, active domain coding
CC protein or complementary sequences. The polynucleotides are useful for
CC identifying expressed genes or for physical mapping of human genome. The
CC encoded polypeptides (ABP6902-ABP6949) are useful as molecular weight
CC markers, as a food supplement, for generating antibodies, in medical
CC imaging, screening and diagnostic assays and for treating cell-
CC proliferative disorders (cancer), neurodegenerative diseases (Parkinson's
CC or Alzheimer's disease), autoimmune diseases (multiple sclerosis,
CC diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,
CC platelet or coagulation disorders, wound, burns, incision, ulcers, liver
CC or lung fibrosis, infections (bacterial, viral, fungal, parasitic),
CC arthritis, etc. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 432 AA;
Query Match 100.0%; Score 258; DB 5; Length 432;
Best Local Similarity 100.0%; Pred. No. 4.8e-28;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LQKQLSLPETGELDSATLKAMRTPCGVDPDLGRFOTFEGDLKWHHN 47
DB 74 LQKQLSLPETGELDSATLKAMRTPCGVDPDLGRFOTFEGDLKWHHN 120
RESULT 5
ABP69246
ID ABP69246 standard; protein; 702 AA.
XX
AC ABP69246;
XX
DT 20-JAN-2003 (first entry)
XX
DE Human polypeptide SEQ ID NO 1293.
XX
XX Human; genome mapping; gene therapy; food supplement; virus; fungus;
KW cell-proliferative disorder; neurodegenerative disease; bacterial;
KW Parkinson's disease; Alzheimer's disease; autoimmune disease;
KW multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
KW arthritis; cytostatic; immunomodulator; nootropic; neuroprotective;
KW antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
KW haemostatic; vulnery; fungicide; antibacterial; virucide; protozoacide;
KW antiarthritic.
XX
OS Homo sapiens.
XX
PN WO200270539-A2.
XX
PD 12-SEP-2002.
XX
PF 05-MAR-2002; 2002WO-US005095.
XX
PR 05-MAR-2001; 2001US-00799451.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;
PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;
PI Wehrman T, Wang J, Wang D, Drmanac RT;
XX
DR WPI; 2002-759812/82.
DR N-PSDB; AB211463.
XX
XX New polynucleotides comprising sequences assembled from expressed
PT sequence tags (ESTs), useful for treating cell-proliferative,
PT neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
PT or coagulation disorders.
XX
XX Claim 9; SEQ ID NO 1293; 1012pp + Sequence Listing; English.
PS
XX
XX The invention relates to an isolated polynucleotide (I) comprising a
CC nucleotide sequence selected from any of 948 sequences (AB211119-
CC AB212066) or their mature protein coding portion, active domain coding
CC protein or complementary sequences. The polynucleotides are useful for
CC identifying expressed genes or for physical mapping of human genome. The
CC encoded polypeptides (ABP6902-ABP6949) are useful as molecular weight
CC markers, as a food supplement, for generating antibodies, in medical
CC imaging, screening and diagnostic assays and for treating cell-
CC proliferative disorders (cancer), neurodegenerative diseases (Parkinson's
CC or Alzheimer's disease), autoimmune diseases (multiple sclerosis,
CC diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,
CC platelet or coagulation disorders, wound, burns, incision, ulcers, liver
CC or lung fibrosis, infections (bacterial, viral, fungal, parasitic),
CC arthritis, etc. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 702 AA;
Query Match 100.0%; Score 258; DB 5; Length 702;
Best Local Similarity 100.0%; Pred. No. 8.6e-28;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LQKQLSLPETGELDSATLKAMRTPCGVDPDLGRFOTFEGDLKWHHN 47
DB 74 LQKQLSLPETGELDSATLKAMRTPCGVDPDLGRFOTFEGDLKWHHN 120
RESULT 6
AAR07077
ID AAR07077 standard; protein; 707 AA.
XX
AC AAR07077;
XX
DT 25-MAR-2003 (revised)
DT 19-FEB-1991 (first entry)

```

XX DE 92-kDa human type IV collagenase gene product.
 XX KW Epidermal growth factor; EGF; interleukin 1; IL-1; tumour TPA.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT FT 20..707
 FT FT /label= Mature protein
 FT FT 38..40
 FT FT /label= Glycosylation site
 FT FT 120..122
 FT FT /label= Glycosylation site
 FT FT 127..129
 FT FT /label= Glycosylation site

XX EP39859-A.
 XX 22-NOV-1990.
 XX PF 14-MAY-1990; 90EP-00870069.
 XX PR 15-MAY-1989; 89US-00352078.
 XX (UNIV) UNIV WASHINGTON.
 XX PA Goldberg GI, Eisen AZ;
 XX PI WPI; 1990-350579/47.
 XX DR N-PSDB; AAQ06554.
 XX PT New 92-kD type IV collagenase and cDNA - from SV-40 transformed foetal
 PT lung fibroblasts.
 XX Claim 1; Fig 3; 2ipp; English.
 XX SV40 transformed foetal lung fibroblasts may be used to produce type IV
 CC collagenase, totally glycosylated at three sites. The enzyme is induced
 CC by EGF, IL-2 and the tumour promoter, 12-O-tetradecanoyl-phorbol acetate
 CC (TPA) and has therapeutic activity, being able to digest native type IV
 CC and V collagen. (Updated on 25-MAR-2003 to correct PA field.)
 XX SQ Sequence 707 AA;

Query Match 100.0%; Score 258; DB 2; Length 707;
 Best Local Similarity 100.0%; Pred. No. 8.7e-28;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LQKQLSLPETGELDSATLKAMRTPCGVPDLGRFQTFFGDLKWHHN 47
 DB 74 LQKQLSLPETGELDSATLKAMRTPCGVPDLGRFQTFFGDLKWHHN 120

RESULT 7
 AAY58015
 ID AAY58015 standard; protein; 707 AA.
 XX AC AAY58015;
 XX DT 28-FEB-2000 (first entry)
 XX DE Matrix metalloproteinase-9 (MMP-9) amino acid sequence.
 XX KW Matrix metalloproteinase-9; MMP-9; polymorphism; endopeptidase; detect;
 KW inflammatory disease; diagnose; atherosclerosis; tumour; metastasis;
 KW neurological disease; multiple sclerosis; arthritis; human.
 XX OS Homo sapiens.
 XX PN WO9957315-A2.
 XX PD 11-NOV-1999.

XX 07-MAY-1999; 99WO-GB001447.
 XX 07-MAY-1998; 98GB-00009764.
 XX (ISIS-) ISIS INNOVATION LTD.
 XX Zhang BP, Ye S, Henney A;
 XX WPI; 2000-052977/04.
 XX DR N-PSDB; AA245145.
 XX PT Detection of matrix metalloproteinase 9 gene polymorphisms for diagnosis or
 PT prognosis of diseases characterized by metalloproteinase mediated
 PT remodelling.
 XX Example 1; Fig 1; 29pp; English.
 XX This is the human matrix metalloproteinase-9 (MMP-9) amino acid sequence.
 CC MMP-9 is a zinc-dependent endopeptidase, and is located on chromosome 20.
 CC MMP activity is associated with inflammatory diseases and MMP-9 is
 CC implicated in the pathology of multiple sclerosis. Certain polymorphic
 CC sequences in the MMP-9 promoter, coding sequence and 3' untranslated
 CC region of the human MMP-9 gene can affect the severity of
 CC atherosclerosis. The invention relates to the presence or absence of one
 CC variant form of a MMP-9 gene polymorphism (-1562 Cytosine/Threonine),
 CC detection of this polymorphism using oligonucleotides AA245137-245140 can
 CC be used for disease prognosis. The invention shows that the MMP-9 C-1562T
 CC polymorphism is a regulatory functional polymorphism. The methods and
 CC oligonucleotides are used to detect polymorphisms in the MMP-9 gene. They
 CC are useful for the diagnosis and prognosis of diseases characterized by
 CC metalloproteinase mediated remodelling, such as atherosclerosis, tumour
 CC invasion and metastasis, inflammatory disease, and neurological diseases,
 CC particularly those involving demyelination such as multiple sclerosis,
 CC and arthritic disease. Proteins encoded by the MMP-9 gene variants may be
 CC used for screening compounds that bind specifically to a molecule encoded
 CC by one variant of a polymorphic sequence, thus identifying compounds
 CC which modulate the activity of the enzyme. Such compounds can then be
 CC used for rational drug design

SQ Sequence 707 AA;
 Query Match 100.0%; Score 258; DB 3; Length 707;
 Best Local Similarity 100.0%; Pred. No. 8.7e-28;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQKQLSLPETGELDSATLKAMRTPCGVPDLGRFQTFFGDLKWHHN 47
 DB 74 LQKQLSLPETGELDSATLKAMRTPCGVPDLGRFQTFFGDLKWHHN 120

RESULT 8
 AAB84611
 ID AAB84611 standard; protein; 707 AA.
 XX AC AAB84611;
 XX DT 05-SEP-2001 (first entry)

XX Amino acid sequence of matrix metalloproteinase-9.
 XX Growth factor; protein inhibitor; protease; damaged tissue;
 KW platelet-derived growth factor; PDGF; fibroblast growth factor; FGF;
 KW connective tissue derived growth factor; CTGF; chrysalin; VEGF;
 KW keratinocyte-derived growth factor; KGF; epidermal growth factor; EGF;
 KW transforming growth factor-beta; TGF-beta; matrix metalloproteinase; MMP;
 KW granulocyte macrophage colony stimulating factor; GM-CSF; UPA;
 KW vascular endothelial growth factor; urokinase plasminogen activator;
 KW dermal ulcer; wound.

XX OS Homo sapiens.
 XX PN WO200149309-A2.

XX 12-JUL-2001.
XX
XX
XX 21-DEC-2000; 2000WO-IB001935.
XX
XX
XX 29-DEC-1999; 99GB-00030768.
XX
XX (PFIZ) PRIZER LTD.
XX (PFIZ) PRIZER INC.
XX
XX Davies MJ, Huggins JP, McIntosh FS, Occleston NL;
XX WPI; 2001-418351/44.
XX DR N-PSDB; AAH28226.
XX
XX Composition for the treatment of damaged tissue i.e. chronic wounds and
XX dermal ulcers comprises an inhibitor agent i.e. a protease and a growth
XX factor.
XX
XX Disclosure; Page 557; 572pp; English.
XX
XX The specification describes a pharmaceutical composition, comprising a
XX growth factor, an inhibitor agent, i.e. a protease. The inhibitor agent
XX inhibits the action of at least one specific adverse protein, i.e. a
XX protease, that is upregulated in a damaged tissue such as a wound
XX environment. Growth factors which are included in the composition of the
XX invention are platelet-derived growth factor (PDGF), fibroblast growth
XX factor (FGF), connective tissue derived growth factor (CTGF),
XX keratinocyte-derived growth factor (KGF), transforming growth factor-beta
XX (TGF-beta), granulocyte macrophage colony stimulating factor (GM-CSF),
XX epidermal growth factor (EGF), vascular endothelial growth factor (VEGF),
XX and chrysalin. Inhibitors which are included in the composition of the
XX invention include inhibitors of urokinase-type plasminogen activator
XX (uPA) and matrix metalloproteinase (MMP). The composition is useful for
XX the treatment of chronic damaged tissue, i.e. wounds and dermal ulcers.
XX The present sequence represents a human MMP-9, and is used to produce the
XX composition of the invention
XX
XX Sequence 707 AA;
XX
XX Query Match 100.0%; Score 258; DB 4; Length 707;
XX Best Local Similarity 100.0%; Pred. No. 8.7e-28;
XX Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 LQQLSLPFTGELDSATLKAMRTPRCGVDPDLGRFTFEGDLKWHHN 47
XX 74 LQQLSLPFTGELDSATLKAMRTPRCGVDPDLGRFTFEGDLKWHHN 120
XX
XX RESULT 9
XX AAE10432
XX ID AAE10432 standard; protein; 707 AA.
XX AC AAE10432;
XX
XX DT 10-DEC-2001 (first entry)
XX
XX DE Human matrix metalloproteinase-9 (MMP-9) protein.
XX
XX Human; matrix metalloproteinase; MMP-9; hair growth; antisense therapy;
XX Human; matrix metalloproteinase; MMP-9; hair growth; antisense therapy;
XX Human; matrix metalloproteinase; MMP-9; hair growth; antisense therapy;
XX Human; matrix metalloproteinase; MMP-9; hair growth; antisense therapy;
XX Human; matrix metalloproteinase; MMP-9; hair growth; antisense therapy;
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..21
XX FT /label= Signal_peptide
XX FT 22..707
XX FT /label= Mature_MMP_2_protein
XX FT 97..103
XX FT /label= Cysteine_switch_domain
XX FT 168..192
XX FT /note= "Zinc and calcium binding domain"
XX FT

us-10-032-376a-8.rag

Mon Nov 15 13:54:00 2004

(SMIK) SMITHKLINE BEECHAM PLC.
Romanic Arnold A, Barone FC, Bingham S;
WPI: 2001-290654/30.
N-PSDB; AAF30808.
Polypeptide for the treatment of pain and the reduction of tissue damage
comprises an inhibitor of human matrix metalloproteinase.
Claim 1; Fig 4; 6lpp; English.
The present sequence is that of human matrix metalloproteinase-9 (MMP-9),
previously known as 92 kDa gelatinase and gelatinase B. MMP-9 is capable
of degrading the extracellular matrix components of the basement
membrane. The invention relates to methods for treating pain in a patient
by administering a dual inhibitor of MMP-9 and MMP-2 (see AAB20490). The
administration of an inhibitor of MMP-9 is useful for treating nerve
tissue damage (claimed), where the patient is suffering from a disease or
disorder selected from stroke, haemorrhage, reperfusion injury, cerebral
ischaemia and cerebral infarction (claimed). The method is useful for
treating a disease, disorder or nerve tissue damage selected from
enhanced or exaggerated sensitivity to acute pain, burn pain, atypical
facial pain, neuropathic pain, back pain, complex regional pain syndrome,
I and II, arthritic pain, sports injury pain, pain related to virus
infection, post-herpetic neuralgia, phantom limb pain, labour pain,
cancer pain, post-chemotherapy pain, post-operative pain, post-stroke
pain, physiological pain, inflammatory pain, acute inflammatory
conditions/visceral pain, neuralgia, painful diabetic retinopathy,
traumatic nerve injury, and tolerance to narcotics or withdrawal from
narcotics (claimed). MMP-9 polypeptides can also be used to screen for
agonist or antagonist (inhibitor) compounds
Sequence 707 AA;
Query Match 100.0%; Score 258; DB 4; Length 707;
Best Local Similarity 100.0%; Pred. No. 8.7e-28;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LOKQLSLPETGELDSATLKAMTPRCGVDPDLGRFOTFEGDLKWHHN 47
Db 74 LOKQLSLPETGELDSATLKAMTPRCGVDPDLGRFOTFEGDLKWHHN 120
RESULT 11
ABU56680 standard; protein; 707 AA.
AC ABU56680;
DT 02-APR-2003 (first entry)
DE Lung cancer-associated polypeptide #273.
KW Lung cancer-associated polypeptide; cytostatic; emphysema;
antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
OS Unidentified.
PN WO200286443-A2.
PD 31-OCT-2002.
PF 18-APR-2002; 2002WO-US012476.
PR 18-APR-2001; 2001US-0284770P.
PR 10-MAY-2001; 2001US-0290492P.
PR 09-NOV-2001; 2001US-0339245P.
PR 13-NOV-2001; 2001US-0350666P.
PR 29-NOV-2001; 2001US-0334370P.
PR 12-APR-2002; 2002US-0372246P.
(EOSB-) EOS BIOTECHNOLOGY INC.
Aziz N, Murray R;
WPI: 2003-093161/08.
N-PSDB; ABX76409.
Detecting a lung cancer-associated transcript in a cell from a patient
for treating lung cancer, by contacting a biological sample from the
patient with a polynucleotide that exhibits increased or decreased
expression in lung cancer.
Claim 27; Page 398; 453pp; English.
The invention relates to a method for detecting a lung cancer-associated
transcript in a cell from a patient, comprising contacting a biological
sample from the patient with a polynucleotide that selectively hybridises
to a sequence that is at least 80 % identical to a gene that exhibits
increased or decreased expression in lung cancer samples. Lung cancer-
associated polynucleotides and polypeptides are used for identifying a
compound that modulates a lung cancer-associated polypeptide, for
inhibiting proliferation of a lung cancer-associated cell to treat lung
cancer in a patient and for treating a mammal having lung cancer by
administering a modulatory compound identified. The methods are useful
for treating lung cancer, such as small cell lung cancer, non-small cell
lung cancer or other benign or precancerous lesions, e.g. atelectasis,
emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
bronchiectasis. The genes, polynucleotides and polypeptides are useful
for diagnostic purposes and as targets for screening for therapeutic
compounds that modulate lung cancer, such as antibodies. Sequences
ABU56408-ABU56745 represent lung cancer-associated polypeptides of the
invention
Sequence 707 AA;
Query Match 100.0%; Score 258; DB 6; Length 707;
Best Local Similarity 100.0%; Pred. No. 8.7e-28;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LOKQLSLPETGELDSATLKAMTPRCGVDPDLGRFOTFEGDLKWHHN 47
Db 74 LOKQLSLPETGELDSATLKAMTPRCGVDPDLGRFOTFEGDLKWHHN 120
RESULT 12
ABU56467
ID ABU56467 standard; protein; 707 AA.
AC ABU56467;
DT 02-APR-2003 (first entry)
DE Lung cancer-associated polypeptide #60.
KW Lung cancer-associated polypeptide; cytostatic; emphysema;
antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
OS Unidentified.
PN WO200286443-A2.
PD 31-OCT-2002.
PF 18-APR-2002; 2002WO-US012476.
PR 18-APR-2001; 2001US-0284770P.
PR 10-MAY-2001; 2001US-0290492P.
PR 09-NOV-2001; 2001US-0339245P.
PR 13-NOV-2001; 2001US-0350666P.
PR 29-NOV-2001; 2001US-0334370P.

PR 09-NOV-2001; 2001US-0339245P.
PR 13-NOV-2001; 2001US-0350666P.
PR 29-NOV-2001; 2001US-0334370P.
XX 12-APR-2002; 2002US-0372246P.
XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX
XX
XX Aziz N, Murray R;
XX WPI; 2003-093161/08.
XX N-PSDB; ABX76189.
XX
XX Detecting a lung cancer-associated transcript in a cell from a patient
XX for treating lung cancer, by contacting a biological sample from the
XX patient with a polynucleotide that exhibits increased or decreased
XX expression in lung cancer.
XX
XX
XX Claim 27; Page 236; 453pp; English.
XX
XX The invention relates to a method for detecting a lung cancer-associated
XX transcript in a cell from a patient, comprising contacting a biological
XX sample from the patient with a polynucleotide that selectively hybridizes
XX to a sequence that is at least 80 % identical to a gene that exhibits
XX increased or decreased expression in lung cancer samples. Lung cancer-
XX associated polynucleotides and polypeptides are used for identifying a
XX compound that modulates a lung cancer-associated polypeptide, for
XX inhibiting proliferation of a lung cancer-associated cell to treat lung
XX cancer in a patient and for treating a mammal having lung cancer by
XX administering a modulatory compound identified. The methods are useful
XX for treating lung cancer, such as small cell lung cancer, non-small cell
XX lung cancer or other benign or precancerous lesions, e.g. atelectasis,
XX emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
XX hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
XX bronchiectasis. The genes, polynucleotides and polypeptides are useful
XX for diagnostic purposes and as targets for screening for therapeutic
XX compounds that modulate lung cancer, such as antibodies. Sequences
XX ABUS6408-ABUS6745 represent lung cancer-associated polypeptides of the
XX invention
XX
XX Sequence 707 AA;
XX
XX Query Match 100.0%; Score 258; DB 6; Length 707;
XX Best Local Similarity 100.0%; Pred. No. 8.7e-28;
XX Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 LQKQLSPETGELDSATLKAMRTPCGVPDLGRFQTFFGDLKWHHN 47
XX 74 LQKQLSPETGELDSATLKAMRTPCGVPDLGRFQTFFGDLKWHHN 120
XX
XX
XX RESULT 13
XX AAO16609
XX ID AAO16609 standard; protein; 707 AA.
XX AC AAO16609;
XX XX
XX DT 08-MAY-2003 (first entry)
XX DE Human matrix metalloproteinase 9 (MMP9) gelatinase protein.
XX KW Human; enzyme; crystalline polypeptide; matrix metalloproteinase 9; MMP9;
XX gelatinase; metalloproteinase mediated disease; drug design; arthritis;
XX three-dimensional structure; MMP9 inhibitor; tumour growth;
XX cancer metastasis; osteoarthritis; atherosclerosis; restenosis;
XX periodontitis; multiple sclerosis; glomerulonephritis; MMP9 modulator;
XX Graft-versus-host disease; non-insulin dependent diabetes.
XX KW Homo sapiens.
XX OS
XX WO2003002729-A1.
XX PN
XX XX 09-JAN-2003.
XX PD
XX XX

PF 24-JUN-2002; 2002WO-SE001266.
XX
XX 27-JUN-2001; 2001SE-00002298.
XX
XX (ASTR) ASTRAZENECA AB.
XX
XX Jepsen H, Minshull C, Paupit R, Rowsell S;
XX WPI; 2003-201502/19.
XX
XX Novel crystalline form of a polypeptide corresponding to the catalytic
XX domain of matrix metalloproteinase 9 protein, useful for selecting or
XX designing chemical modulators which are used for treating diabetes,
XX cancer, arthritis.
XX
XX Disclosure; Fig 7; 227pp; English.
XX
XX The invention comprises a crystalline form of a polypeptide corresponding
XX to the catalytic domain of matrix metalloproteinase 9 (MMP9) protein - a
XX gelatinase. The crystalline polypeptide of the invention is useful for
XX treating a metalloproteinase mediated disease or condition in a warm-
XX blooded animal. The crystalline polypeptide is also useful for
XX determining the three-dimensional structure of the MMP9 catalytic domain
XX to high resolution. The three-dimensional structure of the MMP9 catalytic
XX domain is useful for rational drug design, and the atomic coordinates of
XX the catalytic domain of MMP9 are useful for selecting or designing
XX chemical modulators (preferably inhibitors) of MMP9. The crystalline
XX polypeptide of the invention is useful in the treatment of a
XX metalloproteinase mediated disease or condition, such as: tumour growth;
XX metastasis in cancer; arthritis; osteoarthritis; atherosclerosis;
XX restenosis; periodontitis; multiple sclerosis; glomerulonephritis; graft-
XX versus-host disease; and non-insulin dependent diabetes. The present
XX amino acid sequence represents a human matrix metalloproteinase 9 (MMP9)
XX protein
XX
XX Sequence 707 AA;
XX
XX Query Match 100.0%; Score 258; DB 6; Length 707;
XX Best Local Similarity 100.0%; Pred. No. 8.7e-28;
XX Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 LQKQLSPETGELDSATLKAMRTPCGVPDLGRFQTFFGDLKWHHN 47
XX 74 LQKQLSPETGELDSATLKAMRTPCGVPDLGRFQTFFGDLKWHHN 120
XX
XX
XX RESULT 14
XX ABR92116
XX ID ABR92116 standard; protein; 707 AA.
XX AC ABR92116;
XX XX
XX DT 10-SEP-2003 (first entry)
XX DE Human cervical cancer cell marker protein SEQ ID NO:142.
XX KW Human; cervical cancer; cervical cancer marker; cancer therapy;
XX detection; gene therapy; vaccine.
XX XX Homo sapiens.
XX OS
XX WO2002101075-A2.
XX PN
XX XX 19-DEC-2002.
XX PD
XX XX 12-JUN-2002; 2002WO-US018636.
XX PF
XX XX 13-JUN-2001; 2001US-0298155P.
XX PR
XX XX 13-JUN-2001; 2001US-0298159P.
XX PR
XX XX 14-NOV-2001; 2001US-0335936P.
XX PR
XX XX (MILL-) MILLENNIUM PHARM INC.
XX PA
XX XX

PI Schlegel R, Chen Y, Zhao X, Monahan JE, Kamatkar S;
 PI Gannavarapu M, Glatt K, Hoersch S;
 XX WPI; 2003-156967/15.
 DR N-PSDB; ACF12899.

XX New isolated nucleic acid molecule useful for detecting, characterizing,
 PT preventing and treating human cervical cancers, in various prognostic and
 PT diagnostic assays, in pharmacogenomics and in monitoring clinical trials.

XX Claim 4; Page 294-295; 386pp; English.

XX ACF12828 to ACF12947 encode the human cervical cancer marker proteins (I)
 CC given in ABR92047 to ABR92164. A higher level of expression of (I) than
 CC normal indicates the presence of cervical cancer. Also described: (1) a
 CC vector (II) containing (I); (2) a host cell (III) containing (I); and (3)
 CC assessing (M1) whether a patient is afflicted with cervical cancer,
 CC comprising comparing the level of expression of a marker in a patient's
 CC sample, and the normal level of expression of the marker in a control non
 CC -cervical cancer sample, where a significant increase in the level of
 CC expression of the marker in the patient's sample relative to that in the
 CC control sample is an indication that the patient is afflicted with
 CC cervical cancer. (I) has cytostatic activity, and can be used in gene
 CC therapy and in vaccines. (I) is useful in detecting, characterizing,
 CC preventing and treating human cervical cancers. (I) may also be used in
 CC various prognostic and diagnostic assays, pharmacogenomics and in
 CC monitoring clinical trials

XX Sequence 707 AA;

Query Match 100.0%; Score 258; DB 6; Length 707;
 Best Local Similarity 100.0%; Pred. No. 8.7e-28;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LOKQLSLPETGELDSATLKAMRTPCGVPDLGRFQTTFEGDLKWHHN 47
 Db 74 LOKQLSLPETGELDSATLKAMRTPCGVPDLGRFQTTFEGDLKWHHN 120

RESULT 15

ADL14993
 ID ADL14993 standard; protein; 707 AA.

XX ADL14993;

XX 06-MAY-2004 (first entry)

XX Human type IV collagenase protein for cancer treatment.

XX cytostatic; gene therapy; binding moiety; medicine; imaging; diagnosis;
 XX prognosis; mantle cell lymphoma; cancer.

XX Homo sapiens.

XX WO2003068268-A2.

XX 21-AUG-2003.

XX 13-FEB-2003; 2003WO-EP001461.

XX 14-FEB-2002; 2002GB-00003480.

XX 29-JUN-2002; 2002GB-00015095.

XX (BIOI-) BIOINVENT INT AB.

XX Ek S, Borrebaeck CAK, Ehinger M;

XX WPI; 2003-697496/66.

XX N-PSDB; ADL14994.

XX New compound for treating, imaging, diagnosing or prognosing mantle cell
 PT lymphoma, comprises a binding moiety (e.g. antibody) that binds to a
 PT protein (e.g. human autotaxin polypeptide), and a further moiety (e.g.

PT nucleic acid).
 XX Disclosure; SEQ ID NO 5; 342pp; English.

XX The invention relates to a compound comprising a binding moiety which
 CC selectively binds to a protein or polypeptide listed in the specification
 CC (e.g. human autotaxin polypeptide or human CD24 signal transducer
 CC polypeptide), and a further moiety. The compound is useful in medicine or
 CC in the treatment, imaging, diagnosis or prognosis of mantle cell
 CC lymphomas (MCL). It is used in preparing a medicament for treating MCL, a
 CC diagnostic or prognostic agent for MCL, or an agent for imaging MCL cells
 CC in the body of an individual. This sequence corresponds to one of the
 XX polypeptides of the invention.

XX Sequence 707 AA;

Query Match 100.0%; Score 258; DB 7; Length 707;
 Best Local Similarity 100.0%; Pred. No. 8.7e-28;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LOKQLSLPETGELDSATLKAMRTPCGVPDLGRFQTTFEGDLKWHHN 47
 Db 74 LOKQLSLPETGELDSATLKAMRTPCGVPDLGRFQTTFEGDLKWHHN 120

Search completed; October 13, 2004, 15:09:14
 Job time : 92.1795 secs

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OM protein - protein search, using sw model

Run on: October 13, 2004, 15:02:10 ; Search time 22.2949 Seconds
(without alignments)
139.806 Million cell updates/sec

Title: US-10-032-376A-8
Perfect score: 258
Sequence: 1 LQKLSLPETGELDSATLKA.....VPLDGRFQTPEGDLKWEHNN 47
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS.COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	258	100.0	707	3	US-08-704-711A-19
2	258	100.0	707	3	US-09-521-220-19
3	258	100.0	707	3	US-09-391-104-20
4	258	100.0	708	3	US-08-448-489-16
5	141	54.7	477	3	US-08-704-711A-20
6	141	54.7	477	3	US-08-448-489-15
7	141	54.7	477	3	US-08-281-313-1
8	141	54.7	477	3	US-09-521-220-20
9	141	54.7	477	3	US-09-391-104-21
10	133	51.6	476	3	US-08-704-711A-21
11	133	51.6	476	3	US-08-448-489-14
12	133	51.6	476	3	US-09-521-220-21
13	133	51.6	476	3	US-09-391-104-22
14	117	45.3	471	3	US-09-391-104-25
15	115	44.6	136	4	US-09-513-999C-4639
16	115	44.6	663	4	US-09-194-468A-30
17	114	44.2	631	3	US-08-448-489-17
18	114	44.2	660	3	US-08-704-711A-18
19	114	44.2	660	3	US-09-521-220-18
20	114	44.2	660	3	US-09-391-104-19
21	114	44.2	660	4	US-09-917-254-89
22	113	43.8	470	3	US-08-068-392-2
23	113	43.8	470	3	US-08-396-988-2
24	113	43.8	470	3	US-09-391-104-26
25	110	42.6	463	3	US-08-704-711A-16
26	110	42.6	463	3	US-08-448-489-12
27	110	42.6	469	3	US-09-521-220-16

28	110	42.6	469	3	US-09-391-104-23	Sequence 23, Appl
29	109	42.2	513	4	US-10-140-002-192	Sequence 192, App
30	109	42.2	513	4	US-09-862-631-4	Sequence 4, Appli
31	108	41.9	471	4	US-08-994-689C-1	Sequence 1, Appli
32	107	41.5	135	4	US-09-513-999C-4163	Sequence 4163, Ap
33	106	41.1	267	3	US-08-448-489-18	Sequence 18, Appl
34	106	41.1	267	3	US-09-391-104-27	Sequence 27, Appl
35	106	41.1	271	3	US-08-896-062-2	Sequence 2, Appli
36	105	40.7	264	3	US-09-009-156-6	Sequence 6, Appli
37	105	40.7	264	3	US-09-372-154-6	Sequence 6, Appli
38	101	39.1	471	4	US-08-994-689C-21	Sequence 21, Appl
39	100.5	39.0	582	3	US-08-704-711A-2	Sequence 2, Appli
40	100.5	39.0	582	3	US-08-448-489-1	Sequence 1, Appli
41	100.5	39.0	582	3	US-09-211-704A-9	Sequence 9, Appli
42	100.5	39.0	582	3	US-09-521-220-2	Sequence 2, Appli
43	100.5	39.0	582	3	US-09-391-104-28	Sequence 28, Appl
44	100.5	39.0	582	4	US-09-919-497-84	Sequence 84, Appl
45	100	38.8	444	1	US-09-178-002-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-704-711A-19
; Sequence 19, Application US/08704711A
; Patent No. 614159
; GENERAL INFORMATION:
; APPLICANT: WILZ, Horst
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,711A
; FILING DATE: 20-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/DE95/00357
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 707 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-704-711A-19

us-10-032-376a-8.ra1

Mon Nov 15 13:54:00 2004

Query Match 100.0%; Score 258; DB 3; Length 707;
Best Local Similarity 100.0%; Pred. No. 1.7e-29;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKQLSLPETGELDSATLKAMRTPRCGVPDLGRFOTFEGDLKWHHN 47
DB 74 LKQLSLPETGELDSATLKAMRTPRCGVPDLGRFOTFEGDLKWHHN 120

RESULT 2
US-09-521-220-19
Sequence 19, Application US/09521220
Patent No. 6399348
GENERAL INFORMATION:
APPLICANT: HINZMANN, Bernd
TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/521,220
FILING DATE: 08-Mar-2000
CLASSIFICATION: <Unknown>
21-OCT-1994
17-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/704,711
FILING DATE: <Unknown>
APPLICATION NUMBER: DE 4438838.1
FILING DATE: 21-OCT-1994
APPLICATION NUMBER: DE 4409663.1
FILING DATE: 17-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 26083/124
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 707 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 19:

US-09-521-220-19
Query Match 100.0%; Score 258; DB 3; Length 707;
Best Local Similarity 100.0%; Pred. No. 1.7e-29;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKQLSLPETGELDSATLKAMRTPRCGVPDLGRFOTFEGDLKWHHN 47
DB 74 LKQLSLPETGELDSATLKAMRTPRCGVPDLGRFOTFEGDLKWHHN 120

RESULT 3
US-09-391-104-20

; Sequence 20, Application US/09391104
; Patent No. 6399371
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Faiduto, Michael T.
; APPLICANT: Magnuson, Scott R.
; APPLICANT: Morgan, Douglas W.
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,
; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
; TITLE OF INVENTION: OF USING SAME
; FILE REFERENCE: 6073-US.P1
; CURRENT APPLICATION NUMBER: US/09/391,104
; CURRENT FILING DATE: 1999-09-07
; PRIOR APPLICATION NUMBER: US 08/814,394
; PRIOR FILING DATE: 1997-03-11
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 707
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-391-104-20

Query Match 100.0%; Score 258; DB 3; Length 707;
Best Local Similarity 100.0%; Pred. No. 1.7e-29;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKQLSLPETGELDSATLKAMRTPRCGVPDLGRFOTFEGDLKWHHN 47
DB 74 LKQLSLPETGELDSATLKAMRTPRCGVPDLGRFOTFEGDLKWHHN 120

RESULT 4
US-08-448-489-16
Sequence 16, Application US/08448489
Patent No. 6184022
GENERAL INFORMATION:
APPLICANT: SEIKI, Motoharu
APPLICANT: SAITO, Hiroshi
APPLICANT: SHINAGAWA, Akira
TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
FILE REFERENCE: 55-290P
CURRENT APPLICATION NUMBER: US/08/448,489
CURRENT FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 16
LENGTH: 708
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: X = UNKNOWN
OTHER INFORMATION: Description of Unknown Organism: Known Member of
OTHER INFORMATION: Matrix Metalloproteinase Family
US-08-448-489-16

Query Match 100.0%; Score 258; DB 3; Length 708;
Best Local Similarity 100.0%; Pred. No. 1.7e-29;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKQLSLPETGELDSATLKAMRTPRCGVPDLGRFOTFEGDLKWHHN 47
DB 74 LKQLSLPETGELDSATLKAMRTPRCGVPDLGRFOTFEGDLKWHHN 120

RESULT 5
US-08-704-711A-20
Sequence 20, Application US/08704711A
Patent No. 6114159
GENERAL INFORMATION:
APPLICANT: WILL, Horst
APPLICANT: HINZMANN, Bernd


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; OTHER INFORMATION: Matrix Metalloproteinase Family
US-08-448-489-15

Query Match          54.7%; Score 141; DB 3; Length 477;
Best Local Similarity 62.8%; Pred. No. 2.4e-12;
Matches 27; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

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Db 67 MQKFLGLEVTGKLSDTLEVMRKPRCGVPDVGHFRTFPGPWK 109

RESULT 7
US-08-281-313-1
; Sequence 9, Application US/09368169
; Patent No. 6284511
; GENERAL INFORMATION:
; APPLICANT: Tetsuya INAKA et al.
; TITLE OF INVENTION: HEAT-STABLE PROLYENDOPEPTIDASE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wengeroth, Lind & Ponack, L.L.P.
; STREET: 2033 K Street, N.W., Suite 800
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/368,169
; FILING DATE: August 5, 1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/750,816
; FILING DATE: January 8, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee Cheng
; REGISTRATION NUMBER: 40,949
; REFERENCE/DOCKET NUMBER: 99-0868/LC(WWC)49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-721-8200
; TELEFAX: 202-721-8250
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acid residues
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; ORIGINAL SOURCE:
; ORGANISM: Flavobacterium meningosepticum
; ORGANISM: Met Lys Tyr Asn Lys Leu Ser Val Ala Val Ala Phe Ala Phe Ala Val Ala V
; ORGANISM: 1
; Sequence 1, Application US/08281311
; Patent No. 6284513
; GENERAL INFORMATION:
; APPLICANT: Ye, Qi-Zhuang
; APPLICANT: Johnson, Linda L.
; APPLICANT: Hupe, Donald J.
; APPLICANT: Baragi, Vijaykumar
; TITLE OF INVENTION: Process for the Production of
; TITLE OF INVENTION: Stromelysin Catalytic Domain Protein
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Warner-Lambert Company
; STREET: 2800 Plymouth Rd.
; CITY: Ann Arbor
; STATE: MI
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COUNTRY: US
ZIP: 48105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/281,313
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/012,705
FILING DATE: 03-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Tinney, Francis J.
REGISTRATION NUMBER: 33,069
REFERENCE/DOCKET NUMBER: 4415-01-FJT
TELEPHONE: 313 996-7295
TELEFAX: 313 996-1553
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 477 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Protein
LOCATION: 100..273
OTHER INFORMATION: /note= "Mature stromelysin"
OTHER INFORMATION: catalytic domain protein"
FEATURE:
NAME/KEY: Region
LOCATION: 1..17
OTHER INFORMATION: /note= "Signal peptide"
FEATURE:
NAME/KEY: Region
LOCATION: 18..99
OTHER INFORMATION: /note= "Propeptide"
US-08-281-313-1
Query Match 54.7%; Score 141; DB 3; Length 477;
Best Local Similarity 62.8%; Pred. No. 2.4e-12;
Matches 27; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
QY 1 LOKQLSLPETGELDSATLKAMRTPCGVPDLGRFQTPEGDLKW 43
DB 67 MQKFLGLEVTGKLDSDTLEVMKRCGVPDVGHFRTFFGIPKW 109
RESULT 8
US-09-521-220-20
Sequence 20, Application US/09521220
Patent No. 6399348
GENERAL INFORMATION:
APPLICANT: WILL, Horst
HINZMANN, Bernd
TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/521,220
FILING DATE: 08-Mar-2000
CLASSIFICATION: <Unknown>
21-OCT-1994
17-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/704,711
FILING DATE: <Unknown>
APPLICATION NUMBER: DE 4438838.1
FILING DATE: 21-OCT-1994
APPLICATION NUMBER: DE 4409663.1
FILING DATE: 17-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 26083/124
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 477 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-521-220-20
Query Match 54.7%; Score 141; DB 3; Length 477;
Best Local Similarity 62.8%; Pred. No. 2.4e-12;
Matches 27; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
QY 1 LOKQLSLPETGELDSATLKAMRTPCGVPDLGRFQTPEGDLKW 43
DB 67 MQKFLGLEVTGKLDSDTLEVMKRCGVPDVGHFRTFFGIPKW 109
RESULT 9
US-09-391-104-21
Sequence 21, Application US/09391104
Patent No. 6399371
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Falduto, Michael T.
APPLICANT: Magnuson, Scott R.
APPLICANT: Morgan, Douglas W.
TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,
TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
TITLE OF INVENTION: OF USING SAME
FILE REFERENCE: 6073.US.P1
CURRENT APPLICATION NUMBER: US/09/391,104
CURRENT FILING DATE: 1999-09-07
PRIOR APPLICATION NUMBER: US 08/814,394
PRIOR FILING DATE: 1997-03-11
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 21
LENGTH: 477
TYPE: PRT
ORGANISM: Homo sapiens
US-09-391-104-21
Query Match 54.7%; Score 141; DB 3; Length 477;
Best Local Similarity 62.8%; Pred. No. 2.4e-12;
Matches 27; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
QY 1 LOKQLSLPETGELDSATLKAMRTPCGVPDLGRFQTPEGDLKW 43
DB 67 MQKFLGLEVTGKLDSDTLEVMKRCGVPDVGHFRTFFGIPKW 109

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RESULT 10
US-08-704-711A-21
; Sequence 21, Application US/08704711A
; Patent No. 6114159
; GENERAL INFORMATION:
; APPLICANT: HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,711A
; FILING DATE: 20-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/DE95/00357
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCES/DOCKET NUMBER: 26083/124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-704-711A-21
Query Match 51.6%; Score 133; DB 3; Length 476;
Best Local Similarity 58.1%; Pred. No. 3.6e-11;
Matches 25; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

Qy 1 LKQLSLPETGELDSATLKAMRTGCVDPDLGRFOTFEGDLKW 43
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Db 66 MOKFLGLEVTGKLDITLVMKRCRGVDPDVGHFSSFGMPKW 108
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RESULT 11
US-08-448-489-14
; Sequence 14, Application US/08448489
; Patent No. 6184022
; GENERAL INFORMATION:
; APPLICANT: SEIKI, Motoharu
; APPLICANT: SATO, Hiroshi
; APPLICANT: SHINAGAWA, Akira
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
; FILE REFERENCE: 55-290P
; CURRENT APPLICATION NUMBER: US/08/448,489
; CURRENT FILING DATE: 1995-06-07
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; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Known Member of
; OTHER INFORMATION: Matrix Metalloproteinase Family
US-08-448-489-14
Query Match 51.6%; Score 133; DB 3; Length 476;
Best Local Similarity 58.1%; Pred. No. 3.6e-11;
Matches 25; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

Qy 1 LKQLSLPETGELDSATLKAMRTGCVDPDLGRFOTFEGDLKW 43
;
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RESULT 12
US-09-521-220-21
; Sequence 21, Application US/09521220
; Patent No. 6393348
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/521,220
; FILING DATE: 08-Mar-2000
; CLASSIFICATION: <Unknown>
; 21-OCT-1994
; 17-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/704,711
; FILING DATE: <Unknown>
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCES/DOCKET NUMBER: 26083/124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-521-220-21
Query Match 51.6%; Score 133; DB 3; Length 476;
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GenCore version 5.1.6
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OM protein - protein search, using sw model

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Title: US-10-032-376A-8

Perfect score: 258

Sequence: 1 LQQLSLPTGELDSATLKAK.....VPDLGRFQTFFGDLKWHHN 47

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Minimum DB seq length: 0

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Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	258	100.0	47	16	US-10-219-561-16
5	258	100.0	47	16	US-10-032-376A-8
6	258	100.0	707	9	US-09-391-104-20
7	258	100.0	707	9	US-09-801-196-36
8	258	100.0	707	14	US-10-171-311-142
9	258	100.0	707	14	US-10-301-822-132
10	258	100.0	707	14	US-10-301-822-33
11	258	100.0	707	14	US-10-295-027-358
12	258	100.0	707	14	US-10-295-027-1253
13	258	100.0	707	15	US-10-440-464-66
14	258	100.0	707	15	US-10-447-315-7

15	258	100.0	707	16	US-10-480-621-2	Sequence 2, Appli
16	258	100.0	707	16	US-10-789-241-36	Sequence 36, Appl
17	228	88.4	43	14	US-10-219-329-16	Sequence 16, Appl
18	228	88.4	43	14	US-10-153-185-16	Sequence 16, Appl
19	228	88.4	43	14	US-10-219-561-16	Sequence 16, Appl
20	228	88.4	43	16	US-10-032-376A-16	Sequence 16, Appl
21	228	88.4	43	16	US-10-335-207-16	Sequence 16, Appl
22	150	58.1	171	14	US-10-050-216B-4	Sequence 4, Appli
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24	141	54.7	54	14	US-10-153-185-5	Sequence 5, Appli
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27	141	54.7	54	16	US-10-335-207-5	Sequence 5, Appli
28	141	54.7	267	14	US-10-133-797-73	Sequence 73, Appl
29	141	54.7	477	9	US-09-391-104-21	Sequence 21, Appl
30	141	54.7	477	9	US-09-801-196-24	Sequence 24, Appl
31	141	54.7	477	14	US-10-171-311-137	Sequence 137, App
32	141	54.7	477	14	US-10-301-822-127	Sequence 127, App
33	141	54.7	477	14	US-10-301-822-27	Sequence 27, Appl
34	141	54.7	477	14	US-10-131-985-27	Sequence 27, Appl
35	141	54.7	477	15	US-10-295-027-22	Sequence 22, Appl
36	141	54.7	477	15	US-10-115-479-44	Sequence 44, Appl
37	141	54.7	477	15	US-10-211-462-36	Sequence 36, Appl
38	135	52.3	173	15	US-10-447-315-5	Sequence 5, Appli
39	135	52.3	173	15	US-10-115-479-48	Sequence 48, Appl
40	133	51.6	477	15	US-10-115-479-48	Sequence 46, Appl
41	133	51.6	55	14	US-10-219-329-6	Sequence 6, Appli
42	133	51.6	55	14	US-10-153-185-6	Sequence 6, Appli
43	133	51.6	55	16	US-10-219-561-6	Sequence 6, Appli
44	133	51.6	55	16	US-10-032-376A-6	Sequence 6, Appli
45	133	51.6	475	14	US-10-335-207-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1

US-10-219-329-8
; Sequence 8, Application US/10219329
; Publication NO. US20030096757A1
; GENERAL INFORMATION:
; APPLICANT: Quirk, Stephen
; TITLE OF INVENTION: Anti-Cancer and Wound Healing Compounds
; FILE REFERENCE: 1443.035WO1
; CURRENT APPLICATION NUMBER: US/10/219,329
; PRIOR FILING DATE: 2002-08-15
; PRIOR FILING DATE: 2001-12-21
; PRIOR FILING DATE: 2001-12-21
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-219-329-8

Query Match 100.0%; Score 258; DB 14; Length 47;
Best Local Similarity 100.0%; Pred. No. 9.8e-28;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

7

★

QY

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Db

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US-10-153-185-8
; Sequence 8, Application US/10153185
; Publication NO. US20030148959A1
; GENERAL INFORMATION:

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; APPLICANT: Quirk, Stephen
; APPLICANT: Malik, Sohail
; TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds
; FILE REFERENCE: 1443.034US1
; CURRENT APPLICATION NUMBER: US/10/153,185
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 20
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; SEQ ID NO 8
; LENGTH: 47
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; ORGANISM: Homo sapiens
US-10-153-185-8

Query Match      100.0%; Score 258; DB 14; Length 47;
Best Local Similarity 100.0%; Pred. No. 9.8e-28;
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QY 1 LOKQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTPEGDLKWHHN 47
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DB 1 LOKQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTPEGDLKWHHN 47

RESULT 3
US-10-219-561-8
; Sequence 8, Application US/10219561
; Publication No. US20030166567A1
; GENERAL INFORMATION:
; APPLICANT: Quirk, Stephen
; APPLICANT: Malik, Sohail
; APPLICANT: Villanueva, Julie M.
; TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds
; FILE REFERENCE: 1443.008US2
; CURRENT APPLICATION NUMBER: US/10/219,561
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 10/153,185
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-219-561-8

Query Match      100.0%; Score 258; DB 14; Length 47;
Best Local Similarity 100.0%; Pred. No. 9.8e-28;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOKQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTPEGDLKWHHN 47
    |||||
DB 1 LOKQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTPEGDLKWHHN 47

RESULT 4
US-10-032-376A-8
; Sequence 8, Application US/10032376A
; Publication No. US20040127420A1
; GENERAL INFORMATION:
; APPLICANT: Quirk, Steven
; TITLE OF INVENTION: Metalloproteinase Inhibitors for Wound Healing
; FILE REFERENCE: 1443.008US1
; CURRENT APPLICATION NUMBER: US/10/032,376A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-376A-8

Query Match      100.0%; Score 258; DB 14; Length 47;
Best Local Similarity 100.0%; Pred. No. 9.8e-28;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOKQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTPEGDLKWHHN 47
    |||||
DB 1 LOKQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTPEGDLKWHHN 47

RESULT 5
US-10-335-207-8
; Sequence 8, Application US/10335207
; Publication No. US20040127421A1
; GENERAL INFORMATION:
; APPLICANT: Malik, Sohail
; APPLICANT: Quirk, Stephen
; TITLE OF INVENTION: Method to Increase Fibronectin
; FILE REFERENCE: 1443.047US1
; CURRENT APPLICATION NUMBER: US/10/335,207
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-335-207-8

Query Match      100.0%; Score 258; DB 16; Length 47;
Best Local Similarity 100.0%; Pred. No. 9.8e-28;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOKQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTPEGDLKWHHN 47
    |||||
DB 1 LOKQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTPEGDLKWHHN 47

RESULT 6
US-09-391-104-20
; Sequence 20, Application US/09391104
; Publication No. US20020031817A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Falduto, Michael T.
; APPLICANT: Magnuson, Scott R.
; APPLICANT: Morgan, Douglas W.
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEINASE GENE,
; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
; TITLE OF INVENTION: OF USING SAME
; FILE REFERENCE: 6073.US.P1
; CURRENT APPLICATION NUMBER: US/09/391,104
; CURRENT FILING DATE: 1999-09-07
; PRIOR APPLICATION NUMBER: US 08/814,394
; PRIOR FILING DATE: 1997-03-11
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 707
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-391-104-20

Query Match      100.0%; Score 258; DB 9; Length 707;
Best Local Similarity 100.0%; Pred. No. 2.2e-26;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOKQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTPEGDLKWHHN 47
    |||||
DB 1 LOKQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTPEGDLKWHHN 47
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Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQKQSLPTEGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 47
 |||||
 Db 74 LQKQSLPTEGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 120
 |||||

RESULT 7

US-09-801-196-36
 ; Sequence 36, Application US/09801196
 ; Patent No. US20020037827A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Kai
 ; APPLICANT: Smith, Ryan
 ; APPLICANT: Fajardo, Mark
 ; APPLICANT: Mcoss, Patrick
 ; TITLE OF INVENTION: A NOVEL MATRIX METALLOPROTEINASE (MMP-25)
 ; TITLE OF INVENTION: EXPRESSED IN SKIN CELLS
 ; FILE REFERENCE: 240083.509
 ; CURRENT APPLICATION NUMBER: US/09/801,196
 ; CURRENT FILING DATE: 2001-03-06
 ; NUMBER OF SEQ ID NOS: 37
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 36
 ; LENGTH: 707
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-801-196-36

Query Match 100.0%; Score 258; DB 9; Length 707;
 Best Local Similarity 100.0%; Pred. No. 2.2e-26;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQKQSLPTEGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 47
 |||||
 Db 74 LQKQSLPTEGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 120
 |||||

RESULT 8

US-10-171-311-142
 ; Sequence 142, Application US/10171311
 ; Publication No. US20030087270A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schlegel, Robert
 ; APPLICANT: Chen, Yan
 ; APPLICANT: Zhao, Xumei
 ; APPLICANT: Monahan, John
 ; APPLICANT: Kamatkar, Shubhangi
 ; APPLICANT: Glatt, Karen
 ; APPLICANT: Gannavarapu, Manjula
 ; APPLICANT: Hoersch, Sebastian
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
 ; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
 ; TITLE OF INVENTION: OF CERVICAL CANCER
 ; FILE REFERENCE: MRI-035
 ; CURRENT APPLICATION NUMBER: US/10/171,311
 ; CURRENT FILING DATE: 2002-06-12
 ; PRIOR APPLICATION NUMBER: US 60/298,159
 ; PRIOR FILING DATE: 2001-06-13
 ; PRIOR APPLICATION NUMBER: US 60/298,155
 ; PRIOR FILING DATE: 2001-06-13
 ; PRIOR APPLICATION NUMBER: US 60/335,936
 ; PRIOR FILING DATE: 2001-11-14
 ; NUMBER OF SEQ ID NOS: 238
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 142
 ; LENGTH: 707
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-171-311-142

Query Match 100.0%; Score 258; DB 14; Length 707;
 Best Local Similarity 100.0%; Pred. No. 2.2e-26;

Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQKQSLPTEGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 47
 |||||
 Db 74 LQKQSLPTEGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 120
 |||||

RESULT 9

US-10-301-822-132
 ; Sequence 132, Application US/10301822
 ; Publication No. US20030148410A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Millennium Pharmaceuticals, Inc.
 ; APPLICANT: Berger, Allison
 ; APPLICANT: Guillemette, Tracy L.
 ; APPLICANT: Kamatkar, Shubhangi
 ; APPLICANT: Schlegel, Robert
 ; APPLICANT: Monahan, John E.
 ; APPLICANT: Thibodeau, Stephen N.
 ; APPLICANT: BURGART, Lawrence J.
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
 ; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
 ; TITLE OF INVENTION: THERAPY OF COLON CANCER
 ; FILE REFERENCE: MEM01-029P2ERN
 ; CURRENT APPLICATION NUMBER: US/10/301,822
 ; CURRENT FILING DATE: 2002-11-21
 ; PRIOR APPLICATION NUMBER: US 60/339,971
 ; PRIOR FILING DATE: 2001-12-10
 ; PRIOR APPLICATION NUMBER: US 60/361,978
 ; PRIOR FILING DATE: 2002-03-05
 ; PRIOR APPLICATION NUMBER: US 60/381,988
 ; PRIOR FILING DATE: 2002-05-20
 ; NUMBER OF SEQ ID NOS: 228
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 132
 ; LENGTH: 707
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 US-10-301-822-132

Query Match 100.0%; Score 258; DB 14; Length 707;
 Best Local Similarity 100.0%; Pred. No. 2.2e-26;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQKQSLPTEGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 47
 |||||
 Db 74 LQKQSLPTEGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 120
 |||||

RESULT 10

US-10-131-985-33
 ; Sequence 33, Application US/10131985
 ; Publication No. US20030199440A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dack, Kevin N
 ; APPLICANT: Davies, Michael J
 ; APPLICANT: Fish, Paul V
 ; APPLICANT: Huggins, Jonathan P
 ; APPLICANT: McIntosh, Fraser S
 ; APPLICANT: Ocleston, Nicholas L
 ; TITLE OF INVENTION: Composition
 ; FILE REFERENCE: PCS 10391A
 ; CURRENT APPLICATION NUMBER: US/10/131,985
 ; CURRENT FILING DATE: 2002-04-25
 ; PRIOR APPLICATION NUMBER: US/09/726,295
 ; PRIOR FILING DATE: 2000-11-30
 ; PRIOR APPLICATION NUMBER: GB 9930768.8
 ; PRIOR FILING DATE: 1999-12-29
 ; NUMBER OF SEQ ID NOS: 60
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 33
 ; LENGTH: 707
 ; TYPE: PRT

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; ORGANISM: Homo sapiens
US-10-131-985-33

Query Match      100.0%; Score 258; DB 14; Length 707;
Best Local Similarity 100.0%; Pred. No. 2.2e-26;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 47
|||||
Db 74 LQQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 120

RESULT 11
US-10-295-027-358
; Sequence 358, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynnne, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 358
; LENGTH: 707
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-358

Query Match      100.0%; Score 258; DB 14; Length 707;
Best Local Similarity 100.0%; Pred. No. 2.2e-26;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 47
|||||
Db 74 LQQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 120

RESULT 12
US-10-295-027-1253
; Sequence 1253, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynnne, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 358
; LENGTH: 707
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-358

Query Match      100.0%; Score 258; DB 14; Length 707;
Best Local Similarity 100.0%; Pred. No. 2.2e-26;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 47
|||||
Db 74 LQQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 120

RESULT 13
US-10-440-464-66
; Sequence 66, Application US/10440464
; Publication No. US20040018528A1
; GENERAL INFORMATION:
; APPLICANT: DEPRIMO, SAMUEL
; APPLICANT: O'FARRELL, ANNE-MARIE
; APPLICANT: MORIMOTO, ALYSSA
; APPLICANT: SMOLICH, BEVERLY
; APPLICANT: MANNING, WILLIAM
; APPLICANT: WALTER, SARAH
; APPLICANT: CHERINGTON, JULIE
; APPLICANT: SCHILLING, JIM
; TITLE OF INVENTION: NOVEL BIOMARKERS OF TYROSINE KINASE INHIBITOR EXPOSURE
; FILE REFERENCE: 038602/1592
; CURRENT APPLICATION NUMBER: US/10/440,464
; CURRENT FILING DATE: 2003-05-19
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; PRIOR APPLICATION NUMBER: 60/380,872
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/448,922
; PRIOR FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: 60/448,874
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 707
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-440-464-66

Query Match 100.0%; Score 258; DB 15; Length 707;
Best Local Similarity 100.0%; Pred. No. 2.2e-26;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQKQLSPETGELDSATLKAMRTPRCGVPDLGRFQTFEGDLKWHHN 47
DB 74 LQKQLSPETGELDSATLKAMRTPRCGVPDLGRFQTFEGDLKWHHN 120

RESULT 14

US-10-447-315-7
; Sequence 7, Application US/10447315
; Publication No. US20040071687A1
; GENERAL INFORMATION:
; APPLICANT: Rafii, Shahin
; APPLICANT: Heissig, Beate
; APPLICANT: Hattori, Koichi
; APPLICANT: Cornell Research Foundation, Inc.
; TITLE OF INVENTION: Adult Stem Cell Recruitment
; FILE REFERENCE: 1676.006US1
; CURRENT APPLICATION NUMBER: US/10/447,315
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: US 60/383,658
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 707
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-447-315-7

Query Match 100.0%; Score 258; DB 15; Length 707;
Best Local Similarity 100.0%; Pred. No. 2.2e-26;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQKQLSPETGELDSATLKAMRTPRCGVPDLGRFQTFEGDLKWHHN 47
DB 74 LQKQLSPETGELDSATLKAMRTPRCGVPDLGRFQTFEGDLKWHHN 120

RESULT 15

US-10-480-621-2
; Sequence 2, Application US/10480621
; Publication No. US20040175817A1
; GENERAL INFORMATION:
; APPLICANT: Jepson, Holly
; APPLICANT: Minshull, Claire
; APPLICANT: Pauptit, Richard
; APPLICANT: Rowse, Sian
; TITLE OF INVENTION: A CRYSTALLISED CATALYTIC DOMAIN OF MATRIX
; TITLE OF INVENTION: METALLOPROTEINASE 9 (MMP9) AND THE USE OF
; TITLE OF INVENTION: ITS THREE DIMENSIONAL STRUCTURE TO DESIGN
; TITLE OF INVENTION: MMP9 MODULATORS
; FILE REFERENCE: 06275-377US1
; CURRENT APPLICATION NUMBER: US/10/480,621
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: PCT/SE02/01266
; PRIOR FILING DATE: 2002-06-24

; PRIOR APPLICATION NUMBER: SE 0102298-7
; PRIOR FILING DATE: 2001-06-27
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 707
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-480-621-2

Query Match 100.0%; Score 258; DB 16; Length 707;
Best Local Similarity 100.0%; Pred. No. 2.2e-26;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQKQLSPETGELDSATLKAMRTPRCGVPDLGRFQTFEGDLKWHHN 47
DB 74 LQKQLSPETGELDSATLKAMRTPRCGVPDLGRFQTFEGDLKWHHN 120

Search completed: October 13, 2004, 15:35:39
Job time : 66.8846 secs

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A:Molecule type: protein
 A:Residues: 20-25,'X',27-37 <VAR>
 A:Experimental source: monocytic cell line THP-1
 A>Note: sequence extracted from NCBI backbone (NCBIP:63812) and corrected to correspond
 R:Opdenakker, G.; Masure, S.; Grillet, B.; Van Damme, J.
 A:Title: Cytokine-mediated regulation of human leukocyte gelatinases and role in arthritis
 A:Reference number: A61385; MUID:92032113; PMID:1932376
 A:Accession: A61385
 A:Molecule type: protein
 A:Residues: 28-37 <OPD>
 R:Masure, S.; Proost, P.; van Damme, J.; Opdenakker, G.
 Eur. J. Biochem. 198, 391-398, 1991
 A:Title: Purification and identification of 91-kDa neutrophil gelatinase. Release by the
 A:Reference number: S16097; MUID:91249834; PMID:1645657
 A:Accession: S16097
 A:Molecule type: protein
 A:Residues: 28-42,'X',44-60,'XX',63 <WAS>
 R:Sang, O.X.; Birkedal-Hansen, H.; van Wart, H.E.
 Biochim. Biophys. Acta 1251, 99-108, 1995
 A:Title: Proteolytic and non-proteolytic activation of human neutrophil progelatinase B.
 A:Reference number: S59488; MUID:95399447; PMID:7669817
 A:Accession: S59488
 A:Molecule type: protein
 A:Residues: 20-27;60-87;94-98,'X',100-101,107-114 <SAR>
 A:Comment: Gelatinase B hydrolyzes peptide bonds in plasminogen to yield a fragment with
 C:Genetics:
 A:Gene: GDB:MPP9; CLG4B
 A:Cross-references: GDB:125224; OMIM:120361
 A:Map position: 20c12-20c13
 A:Introns: 46/3; 124/2; 174/1; 217/1; 275/1; 333/1; 392/1; 444/1; 537/2; 584/1; 634/2; 6
 C:Function:
 A:Description: hydrolyzes type IV collagen
 C:Superfamily: gelatinase A; fibronectin type II repeat homology; hemopexin repeat homol
 C:Keywords: glycoprotein; hydrolase; metalloproteinase; zinc; zymogen
 F:1-15/Domain: signal sequence #status predicted <SIG>
 F:20-707/Product: gelatinase B proenzyme #status predicted <PRE>
 F:20-106/Domain: activation peptide #status predicted <ACT>
 F:28-707/Product: 91K neutrophil gelatinase B proenzyme #status predicted <PR>
 F:107-707/Product: 91K neutrophil gelatinase B #status predicted <MAT>
 F:230-271/Domain: fibronectin type II repeat homology <2F9>
 F:288-329/Domain: fibronectin type II repeat homology <2F8>
 F:347-388/Domain: fibronectin type II repeat homology <2F1>
 F:445-497/Region: proline-rich
 F:509-704/Domain: hemopexin repeat homology <PXN>
 F:58,120,127/Binding site: carboxydrate (Asn) (covalent) #status predicted
 F:99,401,405,411/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status
 F:401,405,411/Binding site: zinc, catalytic (His) (active) #status predicted
 F:402/Active site: Glu #status predicted
 Query Match 100.0%; Score 258; DB 1; Length 707;
 Best Local Similarity 100.0%; Pred. No. 1.8e-26;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LQKQSLPPTGELDSATLKAMTPRCGVDPDLGRFOTFGDLKWHHN 47
 DB 74 LQKQSLPPTGELDSATLKAMTPRCGVDPDLGRFOTFGDLKWHHN 120
 RESULT 2
 JC4364
 Gelatinase B (EC 3.4.24.35) precursor - rat
 N:Alternate names: 92-kDa type IV collagenase; matrix metalloproteinase 9 (MMP9)
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 10-Jan-1996 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
 C:Accession: JC4364
 R:Okada, A.; Santavica, M.; Basset, P.
 Gene 164, 317-321, 1995
 A:Title: The cDNA cloning and expression of the gene encoding rat gelatinase B.
 A:Reference number: JC4364; MUID:96069602; PMID:7590350
 A:Accession: JC4364
 A:Molecule type: mRNA
 A:Residues: 1-708 <OKA>

A:Cross-references: UNIPROT:P50282; GB:U24441; NID:91173505; PIDN:AAA90911.1; PID:911735
 A:Experimental source: skin wounds
 C:Comment: This enzyme belongs to the matrix metalloproteinase family, proteolytic enzym
 ogression.
 C:Genetics:
 A:Gene: gelB
 C:Superfamily: gelatinase A; fibronectin type II repeat homology; hemopexin repeat homol
 C:Keywords: extracellular matrix; fibroblast; glycoprotein; hydrolase; metalloproteinase
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-708/Product: progelatinase B #status predicted <PRO>
 F:25-107/Domain: activation peptide #status predicted <ACT>
 F:108-708/Product: gelatinase B #status predicted <MAT>
 F:214-389/Region: collagen binding #status predicted
 F:231-272/Domain: fibronectin type II repeat homology <2F1>
 F:289-330/Domain: fibronectin type II repeat homology <2F2>
 F:348-389/Domain: fibronectin type II repeat homology <2F3>
 F:514-707/Domain: hemopexin repeat homology <PXN>
 F:39,121/Binding site: carboxydrate (Asn) (covalent) #status predicted
 F:100,402,406,412/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status
 F:402,406,412/Binding site: zinc, catalytic (His) (active) #status predicted
 F:403/Active site: Glu #status predicted
 F:519-707/Disulfide bonds: #status predicted
 Query Match 91.5%; Score 236; DB 2; Length 708;
 Best Local Similarity 87.2%; Pred. No. 1.6e-23;
 Matches 41; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LQKQSLPPTGELDSATLKAMTPRCGVDPDLGRFOTFGDLKWHHN 47
 DB 75 LQKQSLPPTGELDSATLKAMTPRCGVDPDLGRFOTFGDLKWHHN 121
 RESULT 3
 A53796
 Gelatinase B (EC 3.4.24.35) precursor - rabbit
 N:Alternate names: 92K matrix metalloproteinase; 92K type IV collagenase; matrix metallo
 C:Species: Oryctolagus cuniculus (Domestic rabbit)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C:Accession: A53796; A55398
 R:Tezuka, K.; Nemoto, K.; Tezuka, Y.; Sato, T.; Ikeda, Y.; Kobori, M.; Kawashima, H.; Eg
 J. Biol. Chem. 269, 15006-15009, 1994
 A:Title: Identification of matrix metalloproteinase 9 in rabbit osteoclasts.
 A:Reference number: A53796; MUID:94253056; PMID:8195136
 A:Accession: A53796
 A:Molecule type: mRNA
 A:Residues: 1-707 <TEZ>
 A:Cross-references: UNIPROT:P41246; GB:D26514; NID:G499372; PIDN:BAA05520.1; PID:G499373
 A:Experimental source: osteoclasts
 R:Finli, M.E.; Bartlett, J.D.; Matsubara, M.; Rinehart, W.B.; Mody, M.K.; Girard, M.T.; R
 J. Biol. Chem. 269, 28620-28628, 1994
 A:Title: The rabbit gene for 92-kDa matrix metalloproteinase. Role of AP1 and AP2 in cel
 A:Reference number: A55398; MUID:95050662; PMID:7961810
 A:Accession: A55398
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-75,'P',77-99,'ASR',103-171 <FIN>
 A:Cross-references: GB:U36050; NID:9535714; PIDN:AAA64358.1; PID:9535715
 C:Genetics:
 A:Introns: 46/3; 124/2
 C:Superfamily: gelatinase A; fibronectin type II repeat homology; hemopexin repeat homol
 C:Keywords: glycoprotein; hydrolase; metalloproteinase; zinc; zymogen
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-106/Domain: activation peptide #status predicted <ACT>
 F:107-707/Product: 91K neutrophil gelatinase B #status predicted <PRO>
 F:230-271/Domain: fibronectin type II repeat homology <2F9>
 F:288-329/Domain: fibronectin type II repeat homology <2F8>
 F:347-388/Domain: fibronectin type II repeat homology <2F1>
 F:510-704/Domain: hemopexin repeat homology <PXN>
 F:88,120,127/Binding site: carboxydrate (Asn) (covalent) #status predicted
 F:99,401,405,411/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status
 F:401,405,411/Binding site: zinc, catalytic (His) (active) #status predicted
 F:402/Active site: Glu #status predicted

```
Query Match      91.1%; Score 235; DB 1; Length 707;
Best Local Similarity 87.2%; Pred. No. 2.2e-23;
Matches 40; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 LQKLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 47
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 74 LQKLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 120

RESULT 4
Gelatinase B (EC 3.4.24.35) precursor - rat
N/Alternate names: collagenase type IV
C/Species: Rattus norvegicus (Norway rat)
C/Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C/Accession: S62307, S72371
R/Xia, Y.; Garcia, G.; Chen, S.; Wilson, C.B.; Feng, L.
FEBS Lett. 387, 285-288, 1996
A/Title: Cloning of rat 92-kDa type IV collagenase and expression of an active recombinant
A/Reference number: S62307; MUID:96184505; PMID:8605986
A/Accession: S62307
A/Status: preliminary; nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-708 <XIA>
A/Cross-references: UNIPROT:P50282; EMBL:U36476
R/Feng, L.
submitted to the EMBL Data Library, September 1995
A/Reference number: S72371
A/Accession: S72371
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-127, 'S', 129-708 <FEN>
A/Cross-references: EMBL:U36476; NID:G1022783; PIDN:AAB01721.1; PID:G1022784
C/Superfamily: gelatinase A; fibronectin type II repeat homology; hemopexin repeat homol
C/Keywords: extracellular matrix; fibroblast; glycoprotein; hydrolase; metalloproteinase
F:1-19/Domain: signal sequence #status predicted <SIG>
F:25-107/Domain: propeptide #status predicted <PRO>
F:108-708/Domain: activation peptide #status predicted <ACT>
F:214-389/Region: collagen binding #status predicted <MAT>
F:231-272/Domain: fibronectin type II repeat homology <2F1>
F:289-330/Domain: fibronectin type II repeat homology <2F2>
F:348-389/Domain: fibronectin type II repeat homology <2F3>
F:514-707/Domain: hemopexin repeat homology <PXN>
F:100,402,406,412/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status
F:402,406,412/Binding site: zinc, catalytic (His) (active) #status predicted
F:403/Active site: Glu #status predicted
F:519-707/Disulfide bonds: #status predicted

Query Match      90.3%; Score 233; DB 2; Length 708;
Best Local Similarity 85.1%; Pred. No. 4.2e-23;
Matches 40; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 LQKLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 47
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 75 LQKLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 121

RESULT 5
Gelatinase B (EC 3.4.24.35) - bovine
N/Alternate names: matrix metalloproteinase 9 (MMP9)
C/Species: Bos primigenius taurus (cattle)
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C/Accession: I46031; S43112
R/Baylis, H.A.; Megson, A.; Hall, R.
Mol. Biochem. Parasitol. 69, 211-222, 1995
A/Title: Infection with Theileria annulata induces expression of matrix metalloproteinase
A/Reference number: I46031; MUID:95287902; PMID:7770085
A/Accession: I46031
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: mRNA
```

```
A/Residues: 1-712 <BAY>
A/Cross-references: UNIPROT:P52176; EMBL:X78324; NID:G467620; PIDN:CAA55127.1; PID:G467
A/Note: submitted to the EMBL Data Library, March 1994
C/Genetics:
A/Gene: mmp9
C/Superfamily: gelatinase A; fibronectin type II repeat homology; hemopexin repeat homo
C/Keywords: hydrolase; metalloproteinase; zinc; zymogen
F:67-216,392-444/Domain: matrix metalloproteinase homology #status atypical <MMP>
F:230-271/Domain: fibronectin type II repeat homology <2F1>
F:288-329/Domain: fibronectin type II repeat homology <2F2>
F:347-388/Domain: fibronectin type II repeat homology <2F3>
F:515-709/Domain: hemopexin repeat homology <PXN>
F:99,401,405,411/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status
F:401,405,411/Binding site: zinc, catalytic (His) (active) #status predicted
F:402/Active site: Glu #status predicted

Query Match      87.6%; Score 226; DB 1; Length 712;
Best Local Similarity 84.8%; Pred. No. 3.7e-22;
Matches 39; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 QKQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 47
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 75 QRRLSLPETGELDTTLNMRAPRCGVPDVGFRFQTFEGELKWHHN 120

RESULT 6
Gelatinase B (EC 3.4.24.35) precursor - mouse
N/Alternate names: collagenase type IV
C/Species: Mus sp. (mouse)
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C/Accession: I52580
R/Graubert, T.; Johnston, J.; Berliner, N.
Blood 82, 3192-3197, 1993
A/Title: Cloning and expression of the cDNA encoding mouse neutrophil gelatinase: demon
A/Reference number: I52580; MUID:94033534; PMID:8219207
A/Accession: I52580
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-730 <RES>
A/Cross-references: GB:S67830; NID:G460863; PIDN:AAB28942.1; PID:G460864
C/Superfamily: Gelatinase A; fibronectin type II repeat homology; hemopexin repeat homo
C/Keywords: hydrolase; metalloproteinase; zinc; zymogen
F:230-271/Domain: fibronectin type II repeat homology <2F1>
F:288-329/Domain: fibronectin type II repeat homology <2F2>
F:347-388/Domain: fibronectin type II repeat homology <2F3>
F:523-729/Domain: hemopexin repeat homology <PXN>
F:100,401,405,411/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status
F:401,405,411/Binding site: zinc, catalytic (His) (active) #status predicted
F:402/Active site: Glu #status predicted

Query Match      82.8%; Score 213.5; DB 1; Length 730;
Best Local Similarity 85.1%; Pred. No. 1.8e-20;
Matches 40; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

QY 1 LQKLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 47
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 75 LQKLSLPETGELDSOTLKAITRPRCGVDPDVGFRFQTFKG-LKWDHNN 120

RESULT 7
JC1456
Gelatinase B (EC 3.4.24.35) precursor - mouse
N/Alternate names: 92K gelatinase; 92K type IV collagenase; matrix metalloproteinase 9
C/Species: Mus musculus (house mouse)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C/Accession: JC1456; S39525; S39526; I48296; S38654
R/Tanaka, H.; Hojo, K.; Yoshida, H.; Yoshika, T.; Sugita, K.
Biochem. Biophys. Res. Commun. 190, 732-740, 1993
A/Title: Molecular cloning and expression of the mouse 105-kDa gelatinase cDNA.
A/Reference number: JC1456; MUID:93176173; PMID:8382489
A/Accession: JC1456
A/Molecule type: mRNA
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A;Residues: 1-730 <TAN>
A;Cross-references: UNIPROT:P41245; DDBJ:D12712; NID:G286079; PIDN:BA02208.1; PID:G286079
R;Masure, S.; Nys, G.; Fiten, P.; van Damme, J.; Opdenakker, G.
Eur. J. Biochem. 218, 129-141, 1993
A;Title: Mouse gelatinase B. cDNA cloning, regulation of expression and glycosylation in
A;Reference number: S39525; MUID:94062823; PMID:8243459
A;Accession: S39525
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-638, 'L', '640-730 <MAS>
A;Cross-references: EMBL:X72794; NID:G433432; PIDN:CAA51314.1; PID:G433433
A;Accession: S39526
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 133-513, 'A', '515-710, 'P', '712-730 <MA2>
A;Cross-references: EMBL:X72795; NID:G433434; PIDN:CAA51315.1; PID:G433435
R;Reponen, P.; Sahiberg, C.; Munat, C.; Thesleff, I.; Tryggvason, K.
J. Cell Biol. 124, 1091-1102, 1994
A;Title: High expression of 92-kD type IV collagenase (gelatinase B) in the osteoclast
A;Reference number: A54476; MUID:94179406; PMID:8132709
A;Accession: I48296
A;Molecule type: mRNA
A;Residues: 1-513, 'A', '515-710, 'P', '712-730 <RES>
A;Cross-references: EMBL:X72731; NID:G415980; PIDN:CAA81745.1; PID:G415981
C;Genetics:
A;Gene: CLG4B
A;Introns: 47/3; 124/2; 174/1; 217/1; 275/1; 333/1; 392/1; 444/1; 555/2; 602/1; 652/2; 6
C;Superfamily: gelatinase A; fibronectin type II repeat homology; hemopexin repeat homol
C;Keywords: extracellular matrix; fibroblast; glycoprotein; hydrolase; metalloproteinase
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-730/Domain: activation peptide #status predicted <ACT>
F;108-730/Product: gelatinase A #status predicted <MAT>
F;213-388/Region: collagen binding #status predicted
F;230-271/Domain: fibronectin type II repeat homology <2F1>
F;288-329/Domain: fibronectin type II repeat homology <2F2>
F;347-388/Domain: fibronectin type II repeat homology <2F3>
F;453-549/Region: PEST sequence
F;529-729/Domain: hemopexin repeat homology <PXN>
F;100-401, 405, 411/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status
F;401, 405, 411/Binding site: zinc, catalytic (His) (active) #status predicted
F;402/Active site: Glu #status predicted
F;534-729/Disulfide bonds: #status predicted
Query Match 82.8%; Score 213.5; DB 2; Length 730;
Best Local Similarity 85.1%; Pred. No. 1.8e-20;
Matches 40; Conservative 4; Mismatches 2; Indels 1; Gaps 1;
QY 1 LQKLSLPTGELDSATLXAMTPTGCVDPDLGRFOTFEGLKWHHN 47
DB 75 LQKLSLPTGELDSATLXAMTPTGCVDPDLGRFOTFEGLKWHHN 120
RESULT 8
KCHU1
stromelysin 1 (EC 3.4.24.17) precursor [validated] - human
N;Alternate names: angiotensin-converting enzyme; collagenase activating protein; matrix
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1992 #sequence revision 08-May-1998 #text change 09-Jul-2004
C;Accession: A28156; C29157; A28399; A60964; S15427
R;Saus, J.; Quinones, S.; Otani, Y.; Nagase, H.; Harris Jr., E.D.; Kurkiren, M.
J. Biol. Chem. 263, 6742-6745, 1988
A;Title: The complete primary structure of human matrix metalloproteinase-3. Identity wi
A;Reference number: A28156; MUID:88198243; PMID:3360803
A;Accession: A28156
A;Molecule type: mRNA
A;Residues: 1-44, 'E', '46-477 <SAU>
A;Cross-references: UNIPROT:P08254; GB:J03209; NID:G188618; PIDN:AAA36321.1; PID:G188619
R;Whitham, S.E.; Murphy, G.; Angel, P.; Rahmsdorf, H.J.; Smith, B.J.; Lyons, A.; Harris,
Biochem. J. 240, 913-916, 1986
A;Title: Comparison of human stromelysin and collagenase by cloning and sequence analysi
A;Reference number: A90336; MUID:87156645; PMID:3030290
A;Accession: C29157
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-477 <WHI>
A;Cross-references: EMBL:X05232; NID:G36632; PIDN:CAA28859.1; PID:G36633
R;Wilhelm, S.M.; Collier, I.E.; Kronberger, A.; Eisen, B.L.; Grant, G.A.;
Proc. Natl. Acad. Sci. U.S.A. 84, 6725-6729, 1987
A;Title: Human skin fibroblast stromelysin: structure, glycosylation, substrate specific
A;Reference number: A28399; MUID:88016164; PMID:3477804
A;Accession: A28399
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-49, 'G', '51-419, 'L', '421-477 <WIL>
A;Cross-references: GB:U78045; NID:G1688257; PIDN:AAB36942.1; PID:G1688259
A;Note: part of the sequence, including the amino end of the proenzyme, was confirmed by
R;Lark, M.W.; Walakovic, L.A.; Shah, T.K.; Vanmiddlesworth, J.; Cameron, P.M.; Lin, T.Y.
Connect. Tissue Res. 25, 49-65, 1990
A;Title: Production and purification of prostromelysin and procollagenase from IL-1 beta
A;Reference number: A60964; MUID:91059606; PMID:2173990
A;Accession: A60964
A;Molecule type: protein
A;Residues: 18-29;100-108 <LAR>
R;Koklitis, P.A.; Murphy, G.; Sutton, C.; Angal, S.
Biochem. J. 276, 217-221, 1991
A;Title: Purification of recombinant human prostromelysin. Studies on heat activation to
A;Reference number: S15427; MUID:91248150; PMID:2039471
A;Accession: S15427
A;Status: preliminary
A;Molecule type: protein
A;Residues: 18-23 <BIO>
R;Lijnen, H.R.; Ugwu, F.; Bini, A.; Collen, D.
Biochemistry 37, 4699-4702, 1998
A;Title: Generation of an angiotensin-like fragment from plasminogen by stromelysin-1 (M
A;Reference number: A58812; MUID:9548733; PMID:9548733
A;Contents: annotation
R;Becker, J.W.
submitted to the Brookhaven Protein Data Bank, February 1997
A;Reference number: A68466; PDB:1HFS
A;Contents: annotation; X-ray crystallography, 1.70 angstroms, residues 105-160
R;Becker, J.W.; Marcy, A.I.; Rokosz, L.L.; Axel, M.G.; Burbaum, J.J.; Fitzgerald, P.M.D.
Protein Sci. 4, 1966-1976, 1995
A;Title: Stromelysin-1: three-dimensional structure of the inhibited catalytic domain an
A;Reference number: A58814; MUID:96117647; PMID:8535233
A;Contents: annotation; X-ray crystallography, 1.70 angstroms
R;Marcy, A.I.; Eiberger, L.L.; Harrison, R.; Chan, H.K.; Hutchinson, N.I.; Hagmann, W.K.
Biochemistry 30, 6476-6483, 1991
A;Title: Human fibroblast stromelysin catalytic domain: expression, purification, and ch
A;Reference number: A39589; MUID:91274298; PMID:1647201
A;Contents: annotation
R;Becker, J.W.
submitted to the Brookhaven Protein Data Bank, August 1995
A;Reference number: A66337; PDB:1SLM
A;Contents: annotation; X-ray crystallography, 1.90 angstroms, residues 33-47;57-267
R;Gooley, P.R.; O'Connell, J.F.
submitted to the Brookhaven Protein Data Bank, March 1995
A;Reference number: A67284; PDB:2SRT
A;Contents: annotation; conformation by (1)H-NMR, residues 100-272
R;Gooley, P.R.; Johnson, B.A.; Marcy, A.I.; Cuca, G.C.; Salowe, S.P.; Hagmann, W.K.; Ess
Biochemistry 32, 13098-14008, 1993
A;Title: Secondary structure and zinc ligation of human recombinant short-form stromelys
A;Reference number: A58815; MUID:94059987; PMID:8241164
A;Contents: annotation; conformation by (1)H-NMR
C;Comment: Stromelysin 1 activates its proenzyme after cleavage(s) within the activation
C;Comment: Stromelysin 1 is found in glycosylated and unglycosylated forms, both of whi
C;Genetics:
A;Gene: GDB:MMP3; STMY; STMY1
A;Cross-references: GDB:I20727; OMIM:185250
A;Map position: 11q23-11q23
C;Function:
A;Description: endopeptidase preferentially hydrolyzing peptide bonds on the carboxyl si
A;Note: degrades various extracellular matrix proteins, including fibronectin, plasminog
plasminogen to yield a fragment with angiostatin activity
C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotei

DB 68 MQKFLGLEVTCKLDSNTLEIVKRCGVDPDVGHFSTFPSTPKW 110

RESULT 10

KCRTLH

stromelysin 1 (EC 3.4.24.17) precursor - rat

N:Alternate names: collagenase activating protein; matrix metalloproteinase 3 (MMP3);

C:Species: Rattus norvegicus (Norway rat)

C>Date: 13-Aug-1986 #sequence revision 13-Aug-1986 #text_change 09-Jul-2004

C:Accession: A00997; PS0150; S22767

R:Matrisian, L.M.; Glaichenhaus, N.; Gesnel, M.C.; Breathnach, R.

EMBO J. 4, 1435-1440, 1985

A:Title: Epidermal growth factor and oncogenes induce transcription of the same cellula

A:Reference number: A00997; MUID:85284930; PMID:3875482

A:Accession: A00997

A:Molecule type: mRNA

A:Residues: 1-475 <VAL>

A:Cross-references: UNIPROT:P03957; GB:X02601; NID:G57460; PIDN:CAA26448.1; PID:G57461

R:Umenishi, F.; Yasumitsu, H.; Ashida, Y.; Yamauti, J.; Umeda, M.; Miyazaki, K.

J. Biochem. 108, 537-543, 1990

A:Title: Purification and properties of extracellular matrix-degrading metallo-proteina

A:Reference number: PS0150; MUID:91154156; PMID:1963430

A:Accession: PS0150

A:Molecule type: Protein

A:Residues: 19-207; X, 22-28; 110-112, X', 114-115, X', 117, X', 119; 309-325 <UME>

R:Breathnach, R.; Matrisian, L.M.; Gesnel, M.C.; Staub, A.; Leroy, P.

Nucleic Acids Res. 15, 1139-1151, 1987

A:Title: Sequences coding for part of oncogene-induced transin are highly conserved in

A:Reference number: A26403; MUID:87146421; PMID:3547333

A:Contents: annotation; introns

A>Note: intron positions were determined by comparison of the previously reported cDNA

R:Sanchez-Lopez, R.; Nicholson, R.; Gesnel, M.C.; Matrisian, L.M.; Breathnach, R.

J. Biol. Chem. 263, 11892-11899, 1988

A:Title: Structure-function relationships in the collagenase family member transin.

A:Reference number: S22767; MUID:88298869; PMID:2841336

A:Contents: annotation; active site; activation

A>Note: molecules with mutations in the autoinhibitory region showed a much increased t

R:Park, A.J.; Matrisian, L.M.; Kells, A.F.; Pearson, R.; Yuan, Z.; Navre, M.

J. Biol. Chem. 266, 1584-1590, 1991

A:Title: Mutational analysis of the transin (rat stromelysin) autoinhibitor region demo

A:Reference number: A43028; MUID:91107652; PMID:1938438

A:Contents: annotation; autoinhibitory region

C>Note: Arg-89 and Cys-92 are essential for maintaining latency

C:Comment: Stromelysin 1 hydrolyzes various extracellular matrix proteins, including fibron

C:Comment: Stromelysin 1 activates its proenzyme after cleavage(s) within the activatio

C:Comment: Prostromelysin 1 is found in glycosylated and unglycosylated forms, both of wh

C:Genetics:

A:Introns: 33/3; 115/2; 165/1; 207/1; 262/1; 310/2; 355/1; 408/2; 443/1

C:Function:

A:Description: endopeptidase preferentially hydrolyzing peptide bonds on the carboxyl s

C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprote

C:Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo

F:1-17/Domain: signal sequence #status predicted <SIG>

F:18-475/Product: prostromelysin 1 #status predicted <PRO>

F:18-97/Domain: activation peptide #status predicted <ACT>

F:58-262/Domain: matrix metalloproteinase homology <MMP>

F:88-95/Region: autoinhibitory

F:88-475/Product: stromelysin 1 #status predicted <MAT>

F:282-475/Domain: hemopexin repeat homology <PXN>

F:90,216,220,226/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status

F:118/Binding site: carboxylate (Asn) (covalent) #status predicted

F:216,220,226/Binding site: zinc, catalytic (His) (active) #status predicted

F:217/Active site: Glu #status experimental

F:288-475/Disulfide bonds: #status predicted

Query Match 51.9%; Score 134; DB 1; Length 475;
Best Local Similarity 53.2%; Pred. No. 5.4e-10;
Matches 25; Conservative 7; Mismatches 15; Indels

QY 1 LQQLSLPETGELDSATLKAMRTPRCGVPLGRFQTFEGDLKWHHN 47

DB 65 MQKFLGLKMTGKLDNTMLMKPCGVPDVGGFSTFGSPKRWKH 111

RESULT 11

JC6505

stromelysin 2 (EC 3.4.24.22) precursor - mouse

N;Alternate names: matrix metalloproteinase 10

C;Species: Mus musculus (house mouse)

C;Date: 16-Oct-1998 #sequence_revision 16-Oct-1998 #text_change 09-Jul-2004

C;Accession: J06505

R;Madlener, M.; Werner, S.

Gene 202, 75-81, 1997

A;Title: cDNA cloning and expression of the gene encoding murine stromelysin-2 (MMP-10).

A;Reference number: JC6505; MUID:98087420; PMID:9427548

A;Accession: JC6505

A;Molecule type: mRNA

A;Residues: 1-476 <MAT>

A;Cross-references: UNIPROT:O55123; GB:Y13185; NID:G2791311; PIDN:CRA73641.1; PID:G27913

C;Comment: This enzyme degrades various extracellular matrix proteins, including fibronectin

C;Genetics:

A;Gene: MMP-10

C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloproteinase

C;Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metalloproteinase

F;1-17/Domain: signal sequence #status predicted <SIG>

F;18-476/Product: prostromelysin 2 #status predicted <PRO>

F;18-99/Domain: activation peptide #status predicted <ACT>

F;60-264/Domain: matrix metalloproteinase homology <MMP>

F;90-97/Region: autoinhibitory

F;100-476/Product: stromelysin 2 #status predicted <MAT>

F;283-476/Domain: hemopexin repeat homology <PXN>

F;92,218,222,228/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status predicted

F;120/Binding site: carboxylate (Asn) (covalent) #status predicted

F;218,222,228/Binding site: zinc, catalytic (His) (active) #status predicted

F;219/Active site: Glu #status predicted

F;289-476/Disulfide bonds: #status predicted

Query Match 51.6%; Score 133; DB 1; Length 476;

Best Local Similarity 58.1%; Pred. No. 7.4e-10;

Matches 25; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

Cy 1 LKQSLPTEGELDSATLKAMRTPCGVDPDLGRFTQTEGDLKW 43

Db 67 MQKFLGLKMTGKLDNTMLMKPCGVPDVGGFSTFGSPKRW 109

RESULT 12

KCHUS2

stromelysin 2 (EC 3.4.24.22) precursor [validated] - human

N;Alternate names: matrix metalloproteinase 10 (MMP10); transin-2

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004

C;Accession: A28816; A47496

R;Miller, D.; Quantin, B.; Gesnel, M.C.; Millon-Collard, R.; Abecassis, J.; Breathnach, Biochem. J. 253, 187-192, 1988

A;Title: The collagenase gene family in humans consists of at least four members.

A;Reference number: A90339; MUID:88339885; PMID:2844164

A;Accession: A28816

A;Molecule type: mRNA

A;Residues: 1-476 <MVL>

A;Cross-references: UNIPROT:P09238; EMBL:X07820; NID:G36628; PIDN:CAA30679.1; PID:G36628

A;Note: mRNA for this protein was detected in several human tumors

R;Windor, L.J.; Grenett, R.; Birkedal-Hansen, B.; Bodden, M.K.; Engler, J.A.; Birkedal-J. Biol. Chem. 268, 17341-17347, 1993

A;Title: Cell type-specific regulation of SL-1 and SL-2 genes. Induction of the SL-2 gene

A;Reference number: A47496; MUID:93352520; PMID:8349617

A;Accession: A47496

A;Molecule type: protein

A;Residues: 17-33 <WIN>

C;Comment: This enzyme degrades various extracellular matrix proteins, including fibronectin

C;Genetics:

A;Gene: GDB:MMP10; STWY2

A;Cross-references: GDB:120392; OMIM:185260

A;Map position: 11q22.3-11q23

C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloproteinase

C;Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metalloproteinase

F;1-16/Domain: signal sequence #status predicted <SIG>

F;17-476/Product: prostromelysin 2 #status experimental <PRO>

F;17-98/Domain: activation peptide #status predicted <ACT>

F;59-263/Domain: matrix metalloproteinase homology <MMP>

F;89-96/Region: autoinhibitory

F;99-476/Product: stromelysin 2 #status predicted <MAT>

F;283-476/Domain: hemopexin repeat homology <PXN>

F;91,217,221,227/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status predicted

F;119/Binding site: carboxylate (Asn) (covalent) #status predicted

F;217,221,227/Binding site: zinc, catalytic (His) (active) #status predicted

F;218/Active site: Glu #status predicted

F;289-476/Disulfide bonds: #status predicted

Query Match 51.6%; Score 133; DB 1; Length 476;

Best Local Similarity 58.1%; Pred. No. 7.4e-10;

Matches 25; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

Cy 1 LKQSLPTEGELDSATLKAMRTPCGVDPDLGRFTQTEGDLKW 43

Db 66 MQKFLGLKMTGKLDNTMLMKPCGVPDVGGFSTFGSPKRW 108

RESULT 13

KCHUS2

stromelysin 2 (EC 3.4.24.22) precursor - rat

N;Alternate names: matrix metalloproteinase 10 (MMP10); transin-2

C;Species: Rattus norvegicus (Norway rat)

C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004

C;Accession: B26403; A41775; S26498

R;Breathnach, R.; Matrisian, L.M.; Gesnel, M.C.; Staub, A.; Leroy, P. Nucleic Acids Res. 15, 1139-1151, 1987

A;Title: Sequences coding for part of oncogene-induced transin are highly conserved in a

A;Reference number: A26403; MUID:87146421; PMID:3547333

A;Accession: B26403

A;Molecule type: mRNA

A;Residues: 1-476 <BRE>

A;Cross-references: UNIPROT:P07152; EMBL:X05083; NID:G57388; PIDN:CAA28739.1; PID:G57389

A;Note: Intron positions were determined by comparison of the cDNA sequence to genomic s

R;Chan, J.C.; Scanlon, M.; Zhang, H.Z.; Jia, L.B.; Yu, D.H.; Hung, M.C.; French, M.; Es J. Biol. Chem. 267, 1099-1103, 1992

A;Title: Molecular cloning and characterization of v-mos-activated transformation-associ

A;Reference number: A41775; MUID:92112748; PMID:1370458

A;Accession: A41775

A;Molecule type: mRNA

A;Residues: 1-476 <CHA>

A;Cross-references: GB:M65253; NID:G207150; PIDN:AAA42202.1; PID:G207151

A;Note: sequence extracted from NCBI backbone (NCBIP:76184)

R;de Vries, M.W.; Mukherjee, B.B. Oncogene 7, 109-119, 1992

A;Title: Transformation of normal rat kidney cells by v-K-ras enhances expression of tra

A;Reference number: S26496; MUID:92158347; PMID:1741158

A;Accession: S26498

A;Status: preliminary; translation not shown

A;Molecule type: mRNA

A;Residues: 31-103, 'L', 241-242, 'TQMEKPH', 251, 'L', 253-254, 'CE', 293-294, 'L', 296 <DEV>

A;Cross-references: EMBL:X64020

C;Genetics:

A;Introns: 35/3; 117/1; 167/1; 209/1; 264/1; 311/2; 356/1; 409/2; 444/1

C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloproteinase

C;Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metalloproteinase

F;1-17/Domain: signal sequence #status predicted <SIG>

F;18-476/Product: prostromelysin 2 #status predicted <PRO>

F;18-99/Domain: activation peptide #status predicted <ACT>

F;60-264/Domain: matrix metalloproteinase homology <MMP>

F;90-97/Region: autoinhibitory

F;100-476/Product: stromelysin 2 #status predicted <MAT>

F;283-476/Domain: hemopexin repeat homology <PXN>

F;92,218,222,228/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status predicted

F;120/Binding site: carboxylate (Asn) (covalent) #status predicted

F;218,222,228/Binding site: zinc, catalytic (His) (active) #status predicted

Search completed: October 13, 2004, 15:15:44
Job time : 18.7756 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 13, 2004, 15:00:44 ; Search time 96.4103 Seconds
(without alignments)
280.495 Million cell updates/sec

Title: US-10-032-376A-8

Perfect score: 258

Sequence: 1 LQKQLSLPTGELDSATLKA.....VPLGLRFOTPGDLKWHHNN 47

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Uniprot_02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	258	100.0	707	1 MM03_HUMAN	P14780 homo sapien
2	235	91.1	707	1 MM03_RABIT	P41246 ocyctolagus
3	233	90.3	708	1 MM03_RAT	P50282 rattus norv
4	226	87.6	324	2 Q9N282	Q9N282 bos taurus
5	226	87.6	712	1 MM09_BOVIN	P52176 bos taurus
6	216	83.7	149	2 Q9TVB4	Q9TVB4 canis famil
7	216	83.7	704	1 MM09_CANFA	O18733 canis famil
8	216	83.7	704	2 O19130	O19130 canis famil
9	216	83.7	704	2 Q71U09	Q71U09 canis famil
10	216	83.7	704	2 AA050275	AA050275 canis fam
11	213.5	82.8	730	1 MM03_MOUSE	P41245 mus musculu
12	213.5	82.8	730	2 Q80X18	Q80X18 mus musculu
13	193	74.8	679	2 Q98856	Q98856 cynops pyrr
14	185	71.7	686	2 Q9DE15	Q9DE15 gallus gall
15	177	68.6	673	2 Q90YB3	Q90YB3 paralicichy
16	176	68.2	671	2 Q6PF33	Q6PF33 xenopus lae
17	176	68.2	671	2 Q9W7L6	Q9W7L6 xenopus lae
18	176	68.2	671	2 AA057745	AA057745 xenopus l
19	172	66.7	675	2 Q8QFQ6	Q8QFQ6 oncorhynch
20	170	65.9	674	2 Q98TC6	Q98TC6 cyprinus ca
21	168	65.1	690	2 Q9PYM5	Q9PYM5 oryzias lat
22	167	64.7	670	2 Q6DF16	Q6DF16 xenopus tro
23	160	62.0	680	2 Q7T317	Q7T317 brachydania
24	141	54.7	477	1 MM03_HUMAN	P08254 homo sapien
25	141	54.7	477	2 AAH53676	AAH53676 homo sapi
26	141	54.7	477	2 AAH59716	AAH59716 homo sapi
27	138	53.5	478	1 MM03_RABIT	P28863 ocyctolagus
28	135	52.3	145	2 Q9N283	Q9N283 bos taurus
29	134	51.9	475	1 MM03_RAT	P03957 rattus norv
30	133	51.6	139	2 Q9GM68	Q9GM68 sus scrofa
31	133	51.6	476	1 MM10_HUMAN	P03238 homo sapien

RESULT 1

ID	MM03_HUMAN	STANDARD;	PRT;	707 AA.
AC	P14780; Q8N725; Q9H421;			
DT	01-APR-1990 (Rel. 14, Last sequence update)			
DT	01-APR-1990 (Rel. 14, Last sequence update)			
DT	01-OCT-2004 (Rel. 45, Last annotation update)			
DE	92 kDa type IV collagenase precursor (EC 3.4.24.35) (92 kDa			
DE	gelatinase) (Matrix metalloproteinase-9) (MMP-9) (Gelatinase B)			
DE	(GELS)			
GN	Name=MMP9; Synonyms=CLG4B;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 20-37.			
RX	MEDLINE=90008879; PubMed=22551898;			
RA	Wilhelm S.M., Collier I.E., Marmer B.L., Eisen A.Z., Grant G.A.,			
RA	Goldberg G.I.;			
RT	"SV40-transformed human lung fibroblasts secrete a 92-kDa type IV			
RT	collagenase which is identical to that secreted by normal human			
RT	macrophages.";			
RL	J. Biol. Chem. 264:17213-17221(1989).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91358433; PubMed=1653238;			
RA	Huhtala P., Tuuttila A., Chow L.T., Lohi J., Keski-Oja J.,			
RA	Tryggvason K.;			
RT	"Complete structure of the human gene for 92-kDa type IV collagenase.			
RT	Divergent regulation of expression for the 92- and 72-kilodalton			
RT	enzyme genes in Ht-1080 cells.";			
RL	J. Biol. Chem. 266:16485-16490(1991).			
RN	[3]			
RP	SEQUENCE FROM N.A., AND VARIANT GLN-279.			
RA	Rieder M.J., Armet T.Z., Carrington D.P., Ozuna M., Kuldane S.A.,			
RA	Rajkumar N.R., Toth E.J., Yi Q., Nickerson D.A.;			
RT	"SeattlesNP. NLEI HL6682 program for genomic applications, UN-			
RT	PHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";			
RL	Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A., AND VARIANT GLN-279.			
RX	MEDLINE=21638749; PubMed=11780052; DOI=10.1039/414865a;			
RA	Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,			
RA	Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,			
RA	Bailey J., Barlow K.F., Bates K.N., Bead L.M., Beare D.M.,			
RA	Beasley O.P., Bird C.P., Blakey S.E., Bridgman A.M., Brown A.J.,			
RA	Buckley D., Burrill W.D., Butler A.P., Carder C., Carter N.P., Clee C.M.,			
RA	Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clegg S.,			
RA	Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,			
RA	Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,			
RA	Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,			
RA	Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,			
RA	Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,			

ALIGNMENTS

32	133	51.6	476	1	MM10_MOUSE	O55123 mus musculu
33	133	51.6	476	1	MM10_RAT	P07152 rattus norv
34	133	51.6	476	2	AA036110	AA036110 homo sapi
35	133	51.6	477	1	MM03_MOUSE	P28862 mus musculu
36	133	51.6	477	2	Q922W6	Q922W6 mus musculu
37	131	50.8	478	2	Q6Y4Q5	Q6Y4Q5 canis famil
38	131	50.8	478	2	AA063580	AA063580 canis fam
39	128	49.6	167	2	Q7ZWD0	Q7ZWD0 brachydania
40	128	49.6	465	1	MM08_MOUSE	Q70138 mus musculu
41	128	49.6	465	2	Q8C209	Q8C209 mus musculu
42	128	49.6	465	2	Q8C230	Q8C230 mus musculu
43	128	49.6	465	2	AAH42742	AAH42742 mus muscu
44	128	49.6	465	2	BAC40805	BAC40805 mus muscu
45	128	49.6	466	1	MM08_RAT	O88765 rattus norv

RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Leivaeslahti M.H., Leverisa M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConachie L.J., McLay K., McMurray A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S.,
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann R.M., Syamcore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.,
 RT "The DNA sequence and comparative analysis of human chromosome 20";
 RL Nature 414:865-871(2001).
 RN [5]
 RN SEQUENCE FROM N.A.
 RC TISSUE=B-cell;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Schaefer C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzyzinski M.J., Skalska U., Smailus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [6]
 RN SEQUENCE OF 1-11 FROM N.A.
 RX MEDLINE=93149601; PubMed=8426746;
 RA Sato H., Seiki M.,
 RT "Regulatory mechanism of 92 kDa type IV collagenase gene expression
 RT which is associated with invasiveness of tumor cells.";
 RL Oncogene 8:395-405(1993).
 RN [7]
 RN SEQUENCE OF 20-37.
 RX MEDLINE=91355647; PubMed=1653055;
 RA van Ranst M., Norga K., Masure S., Proost P., Vandekerckhove F.,
 RA Auerx J., van Damme J., Opdenakker G.,
 RT "The cytokine-protease connection: identification of a 96-kD THP-1
 RT gelatinase and regulation by interleukin-1 and cytokine inducers.";
 RL Cytokine 3:231-239(1991).
 RN [8]
 RN SEQUENCE OF 28-60.
 RX TISSUE=Neutrophils;
 RC MEDLINE=91249834; PubMed=1645657;
 RA Masure S., Proost P., van Damme J., Opdenakker G.,
 RT "Purification and identification of 91-kDa neutrophil gelatinase.
 RT Release by the activating peptide interleukin-8.";
 RL Eur. J. Biochem. 198:391-398(1991).
 RN [9]
 RN CHARACTERIZATION.
 RA Kang K., Lee D.-H.,
 RT "Purification and characterization of human 92-kDa type IV collagenase
 RT (gelatinase B).";
 RL Exp. Mol. Med. 28:161-165(1996).
 RN [10]
 RN 3D-STRUCTURE MODELING.
 RA Mallena S.C., Sagarikar R.D.,
 RT "Theoretical model of human type IV collagenase precursor.";
 RT

RL Submitted (APR-2002) to the PDB data bank.
 RN [11]
 RN VARIANTS VAL-20; LYS-82 AND GLN-279.
 RX MEDLINE=20065865; PubMed=1059806;
 RA Zhang B., Henney A., Eriksson P., Hamsten A., Watkins H., Ye S.,
 RT "Genetic variation at the matrix metalloproteinase-9 locus on
 RT chromosome 20q12.2-13.1.";
 RL Hum. Genet. 105:418-423(1999).
 CC -!- FUNCTION: Could play a role in bone osteoclastic resorption.
 CC -!- CATALYTIC ACTIVITY: Cleavage of gelatin types I and V and collagen
 CC types IV and V.
 CC -!- COFACTOR: Binds 2 zinc ions per subunit, calcium (By similarity).
 CC -!- SUBUNIT: Exists as monomer, disulfide-linked homodimer, and as a
 CC heterodimer with a 25 kDa protein. Macrophages and transformed
 CC cell lines produce only the monomeric form.
 CC -!- TISSUE SPECIFICITY: Produced by normal alveolar macrophages and
 CC granulocytes.
 CC -!- SIMILARITY: Belongs to peptidase family M10A.
 CC -!- SIMILARITY: Contains 3 fibronectin type II domains.
 CC -!- SIMILARITY: Contains 1 hemopexin-like domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC -----
 CC EMBL: J05070; AA51539.1; -
 CC EMBL: D10051; BAA20967.1; -
 CC EMBL: AF538844; AAM97934.1; -
 CC EMBL: AL162458; CAC10459.1; -
 CC EMBL: BC060693; AAH06093.1; -
 CC FIR: A34458; A34458;
 CC PDB: 1GKC; X-ray; A/B=106-443.
 CC PDB: 1GKD; X-ray; A/B=106-443.
 CC PDB: 1LTV; X-ray; A/B=513-707.
 CC PDB: 1L6J; X-ray; A=20-444.
 CC PDB: 1LKG; Model; A=1-707.
 CC MEROPS: M10.004; -
 CC GlycoSuiteDB: P14780; -
 CC Genew: HGNC:7176; MMEP9.
 CC MIM: 120361; -
 CC GO: GO:0005615; C:extracellular space; TAS.
 CC GO: GO:0008133; F:collagenase activity; TAS.
 CC GO: GO:0008270; F:zinc ion binding; TAS.
 CC GO: GO:0006508; P:proteolysis and peptidolysis; TAS.
 CC InterPro: IPR000562; FN Type II.
 CC InterPro: IPR000585; Hemopexin.
 CC InterPro: IPR001818; Pept_M10A_M12B.
 CC InterPro: IPR006025; Pept_M_Zn_BS.
 CC InterPro: IPR009070; PGSD_Like.
 CC InterPro: IPR006970; PT.
 CC Pfam: PF00040; fn2; 3.
 CC Pfam: PF00045; Hemopexin; 4.
 CC Pfam: PF00413; Peptidase M10; 1.
 CC Pfam: PF03933; Peptidase M10_N; 1.
 CC Pfam: PF04886; PT; 1.
 CC PRINTS: PR00013; FNTPBII.
 CC PRINTS: PR00138; MATRXIN.
 CC ProDom: PD000995; FN_Type_II; 3.
 CC PROSITE: PS00546; CYSTEINE_SWITCH; 1.
 CC PROSITE: PS00023; FIBRONECTIN_2; 3.
 CC PROSITE: PS00024; HEMOPEXIN; 1.
 CC PROSITE: PS00142; ZINC_PROTEASE; 1.
 CC 3D-structure; Calcium; Collagen degradation;
 KW Direct protein sequencing; Extracellular matrix; Glycoprotein;
 KW Hydrolase; Metalloprotease; Polymorphism; Repeat; Signal; Zinc;
 KW Zymogen.
 FT SIGNAL
 FT PROPEP 1 19
 FT CHAIN 20 707
 FT 92 kDa type IV collagenase.

```

FT DOMAIN 223 280 Fibronection type-II 1.
FT DOMAIN 281 339 Fibronection type-II 2.

Query Match 100.0%; Score 258; DB 1; Length 707;
Best Local Similarity 100.0%; Pred. No. 2.9e-26;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKQLSLPTGELDSATLKAMETPCGVPDLCGRFOTFEGDLKWHHN 47
Db .74 LKQLSLPTGELDSATLKAMETPCGVPDLCGRFOTFEGDLKWHHN 120

RESULT 2
MM09 RABBIT
ID MM09 RABBIT STANDARD; PRT; 707 AA.
AC P1476;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE 92 kDa type IV collagenase precursor (EC 3.4.24.35) (92 kDa
DE (gelatinase) (Matrix metalloproteinase-9) (MMP-9) (Gelatinase B)
DE (GELB).
GN Name=MMP9;
OS Oryctolagus cuniculus (Rabbit);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Japanese White; TISSUE=Bone;
RX MEDLINE=94253056; PubMed=8195136;
RA Tezuka K.I., Nemoto K., Tezuka Y., Sato T., Ikeda Y., Kobori M.,
RA Kawashima H., Eguchi H., Hakeda Y., Kumegawa M.;
RT "Identification of matrix metalloproteinase 9 in rabbit osteoclasts.";
RL J. Biol. Chem. 269:15006-15009(1994).
RN [2]
RP SEQUENCE OF 1-171 FROM N.A.
RC STRAIN=New Zealand white; TISSUE=Liver;
RX MEDLINE=95050662; PubMed=7961810;
RA Fini M.E., Bartlett J.D., Matsubara M., Rinehart W.B., Mody M.K.,
RA Girard M.T., Rainville M.;
RT "The rabbit gene for 92-kDa matrix metalloproteinase. Role of AP1 and
RT AP2 in cell type-specific transcription.";
RL J. Biol. Chem. 269:28620-28628(1994).
CC -!- FUNCTION: Could play a role in bone osteoclastic resorption.
CC -!- CATALYTIC ACTIVITY: Cleavage of gelatin types I and V and collagen
CC types IV and V.
CC -!- COFACTOR: Binds 2 zinc ions per subunit, calcium (By similarity).
CC -!- TISSUE SPECIFICITY: Osteoclasts.
CC -!- SIMILARITY: Belongs to peptidase family M10A.
CC -!- SIMILARITY: Contains 3 fibronection type II domains.
CC -!- SIMILARITY: Contains 1 hemopexin-like domain.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; D26514; BAA03520.1; -
DR EMBL; L36050; AAA64358.1; -
DR PIR; A53796; A53796.
DR HSSP; P14780; 1GKC.
DR MEROPS; M10.004; -.
DR InterPro; IPR000562; FN Type II.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR006026; Peptidase M.
DR InterPro; IPR018181; Pept M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR009070; PGSD_Like.
DR InterPro; IPR006970; PT.

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DR Pfam; PF00040; fn2; 3.
DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF00413; Peptidase M10; 1.
DR Pfam; PF03933; Peptidase_M10_N; 1.
DR Pfam; PF04886; PT; 1.
DR PRINTS; PR00013; FNTYPEII.
DR PRINTS; PR00138; MAIRIXIN.
DR PRODOM; PD000995; FN_Type_II; 3.
DR SMART; SM00059; FN2; 3.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZnMc; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
DR PROSITE; PS00023; FIBRONECTIN_2; 3.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Calcium; Collagen degradation; Extracellular matrix; Glycoprotein;
KW Hydrolyase; Metalloprotease; Repeat; Signal; Zinc; Zymogen.
FT SIGNAL 1 19 By similarity.
FT PROPEP 20 106 Activation peptide (By similarity).
FT CHAIN 107 707 92 kDa type IV collagenase.
FT DOMAIN 223 280 Fibronection type-II 1.
FT DOMAIN 281 339 Fibronection type-II 2.
FT DOMAIN 340 397 Fibronection type-II 3.
FT DOMAIN 513 707 Hemopexin-like.
FT SITE 99 99 Cysteine switch (By similarity).
FT METAL 401 401 Zinc (catalytic) (By similarity).
FT ACT_SITE 402 402 By similarity.
FT METAL 405 405 Zinc (catalytic) (By similarity).
FT METAL 411 411 Zinc (catalytic) (By similarity).
FT CARBOHYD 88 88 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 120 120 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 127 127 N-linked (GlcNAc...) (Potential).
FT DISULFID 516 704 By similarity.
FT CONFLICT 76 76 K->P (in Ref. 2).
FT CONFLICT 100 102 GVP->ASR (in Ref. 2).
SQ SEQUENCE 707 AA; 78307 MW; 053BCE8DC4D4758F CRC64;

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Query Match 91.1%; Score 235; DB 1; Length 707;
Best Local Similarity 87.2%; Pred. No. 4.1e-23;
Matches 41; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

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QY 1 LKQLSLPTGELDSATLKAMETPCGVPDLCGRFOTFEGDLKWHHN 47
Db .74 LKQLSLPTGELDSATLKAMETPCGVPDLCGRFOTFEGDLKWHHN 120

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RESULT 3
MM09 RAT
ID MM09 RAT STANDARD; PRT; 708 AA.
AC P50282;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE 92 kDa type IV collagenase precursor (EC 3.4.24.35) (92 kDa
DE gelatinase) (Matrix metalloproteinase-9) (MMP-9) (Gelatinase B)
DE (GELB).
GN Name=Mmp9;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]_TaxID=10116;
RP SEQUENCE FROM N.A.
RC STRAIN=Fischer 344;
RX MEDLINE=96184505; PubMed=8605986;
RA Xia Y., Garcia G., Chen S., Wilson C.B., Feng L.;
RT "Cloning of rat 92-kDa type IV collagenase and expression of an active
RT recombinant catalytic domain.";
RL FEBS Lett. 382:285-288(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar;
RX MEDLINE=96069602; PubMed=7590350;

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(GELB).
 Name=WWP9;
 Bos taurus (Bovine).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leukocyte;
 RX MEDLINE=95287902; PubMed=7770085;
 RA Baylis H.A., Megson A., Hall R.;
 RT "Infection with Theileria annulata induces expression of matrix
 metalloproteinase 9 and transcription factor Ap-1 in bovine
 leucocytes";
 RL Mol. Biochem. Parasitol. 69:211-222(1995).
 CC -!- FUNCTION: Could play a role in bone osteoclastic resorption.
 CC -!- CATALYTIC ACTIVITY: Cleavage of gelatin types I and V and collagen
 CC types IV and V.
 CC -!- COFACTOR: Binds 2 zinc ions per subunit, calcium (By similarity).
 CC -!- SIMILARITY: Belongs to peptidase family M10A.
 CC -!- SIMILARITY: Contains 3 fibronectin type II domains.
 CC -!- SIMILARITY: Contains 1 hemopexin-like domain.
 CC
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 CC
 CC EMBL; X78324; CAA55127.1; -.
 CC PIR; I46031; I46031.
 CC HSSP; P14780; 1GKD.
 CC
 CC MEROPS; M10.004; -.
 CC InterPro; IPR000562; FN_Type_II.
 CC InterPro; IPR000585; Hemopexin.
 CC InterPro; IPR006026; Peptidase M.
 CC InterPro; IPR001818; Pept_M10A_M12B.
 CC InterPro; IPR006025; Pept_M_Zn_BS.
 CC InterPro; IPR009070; PGSD_like.
 CC InterPro; IPR006970; PT.
 CC Pfam; PF00040; fn2; 3.
 CC Pfam; PF00045; Hemopexin; 4.
 CC Pfam; PF00413; Peptidase M10; 1.
 CC Pfam; PF03933; Peptidase M10_N; 1.
 CC Pfam; PF04886; PT; 1.
 CC PRINTS; PR00013; ENTPEII.
 CC PRINTS; PR00138; MATRXIN.
 CC ProDom; PD000951; FN_Type_II; 3.
 CC SMART; SM00059; FN2; 3.
 CC SMART; SM00120; HX; 4.
 CC SMART; SM00235; ZtMC; 1.
 CC PROSITE; PS00546; CYSTEINE_SWITCH; 1.
 CC PROSITE; PS00023; FIBRONECTIN_2; 3.
 CC PROSITE; PS00024; HEMOPEXIN; FALSE_NEG.
 CC PROSITE; PS00142; ZINC_PROTEASE; 1.
 CC Calcium; Collagen degradation; Extracellular matrix; Glycoprotein;
 CC Hydrolyase; Metalloprotease; Repeat; Signal; Zinc; Zymogen.
 CC SIGNAL
 CC 1 19
 CC By similarity.
 CC PROPEP 20 106 Activation peptide.
 CC CHAIN 107 712 92 kDa type IV collagenase.
 CC DOMAIN 223 280 Fibronectin type-II 1.
 CC DOMAIN 281 339 Fibronectin type-II 2.
 CC DOMAIN 340 397 Fibronectin type-II 3.
 CC DOMAIN 518 712 Hemopexin-like.
 CC SITE 99 99 Cysteine switch (By similarity).
 CC METAL 401 401 Zinc (catalytic) (By similarity).
 CC ACT_SITE 402 402 Zinc (catalytic) (By similarity).
 CC METAL 405 405 Zinc (catalytic) (By similarity).
 CC METAL 411 709 Zinc (catalytic) (By similarity).
 CC DISULFID 521

FT CARBOHYD 38 38 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 120 120 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 127 127 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 712 AA; 79087 MW; E7FDA28372AE0CE CRC64;
 Query Match 87.6%; Score 226; DB 1; Length 712;
 Best Local Similarity 84.8%; Pred. No. 7e-22; Indels 0; Gaps 0;
 Matches 39; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 QY 2 QKQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 47
 DB 75 QRRLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 120
 RESULT 6
 QYTVB4 PRELIMINARY; PRT; 149 AA.
 ID Q9TVB4 AC Q9TVB4;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Type IV collagenase MMP-9 (Fragment).
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fibrosarcoma;
 RA Paria B.C., Kitchell B.E.;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF147104; AAD31323.1; -.
 DR GO; GO:0005578; C:extracellular matrix; IEA.
 DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001818; Pept_M10A_M12B.
 DR InterPro; IPR009070; PGSD_like.
 DR Pfam; PF00413; Peptidase M10; 1.
 DR Pfam; PF03933; Peptidase M10_N; 1.
 DR PRINTS; PR00138; MATRXIN.
 DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
 KW Collagen.
 FT NON_TER 149 149
 SQ SEQUENCE 149 AA; 17025 MW; CA6A5062EFD0CBFF CRC64;
 Query Match 83.7%; Score 216; DB 2; Length 149;
 Best Local Similarity 78.7%; Pred. No. 2.7e-21; Indels 0; Gaps 0;
 Matches 37; Conservative 7; Mismatches 3; Indels 0; Gaps 0;
 QY 1 LQQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 47
 DB 74 LQRLALPETGELDKTTLEAMRAPRCGVDPDLGRFQTFEGDLKWHND 120
 RESULT 7
 MM09 CANFA STANDARD; PRT; 704 AA.
 ID MM09 CANFA AC O18733;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE 92 kDa type IV collagenase precursor (EC 3.4.24.35) (92 kDa
 DE gelatinase) (Matrix metalloproteinase-9) (MMP-9) (Gelatinase B)
 DE (GELB).
 GN Name=WWP9;
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Mongrel;
 RX MEDLINE=21587576; PubMed=11731079; DOI=10.1016/S0304-4165(01)00192-1;

RA Yokota H., Kumata T., Takekaba S., Kobayashi T., Moue H., Taniyama H.,
RA Hirayama K., Kagawa Y., Itoh N., Fujita O., Nakade T., Yuasa A.;
RT "High expression of 92 kDa type IV collagenase (matrix
RT metalloproteinase-9) in canine mammary adenocarcinoma.";
RL Biochim. Biophys. Acta 1569:7-12(2001).
CC -!- FUNCTION: Could play a role in bone osteoclastic resorption.
CC -!- CATALYTIC ACTIVITY: Cleavage of gelatin types I and V and collagen
CC types IV and V.
CC -!- COFACTOR: Binds 2 zinc ions per subunit, calcium (By similarity).
CC -!- SIMILARITY: Belongs to peptidase family M10A.
CC -!- SIMILARITY: Contains 3 fibronectin type II domains.
CC -!- SIMILARITY: Contains 1 hemopexin-like domain.
CC -----
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CC -----
CC EMBL; AB06421; BAA22087.3; --
CC HSSP; P14780; IGKC.
CC MEROPS; M10.004; --
CC InterPro; IPR000562; FN_Type_II.
CC InterPro; IPR000585; Hemopexin.
CC InterPro; IPR006026; Peptidase M.
CC InterPro; IPR001818; Pept_M10A_M12B.
CC InterPro; IPR006025; Pept_M_Zn_BS.
CC InterPro; IPR009070; PGSD_like.
CC InterPro; IPR006970; PT.
CC Pfam; PF00040; fn2; 3.
CC Pfam; PF00045; Hemopexin; 4.
CC Pfam; PF00413; Peptidase_M10; 1.
CC Pfam; PF03933; Peptidase_M10_N; 1.
CC Pfam; PF04886; PT; 1.
CC PRINTS; PR00013; FNTYPEII.
CC PRINTS; PR00138; MATRIXIN.
CC ProDom; PD000995; FN_Type_II; 3.
CC SMART; SM00059; FN2; 3.
CC SMART; SM00120; HX; 4.
CC SMART; SM00235; ZMC; 1.
CC PROSITE; PS00546; CYSTEINE_SWITCH; 1.
CC PROSITE; PS00023; FIBRONECTIN_2; 3.
CC PROSITE; PS00024; HEMOPEXIN; FALSE NEG.
CC PROSITE; PS00142; ZINC_PROTEASE; 1.
CC Calcium; Collagen degradation; Extracellular matrix; Glycoprotein;
KW Hydrolase; Metalloprotease; Repeat; Signal; Zinc; Zymogen.
FT SIGNAL 1 19
FT PROPEP 20 106 Activation peptide (By similarity).
FT CHAIN 107 704 92 kDa type IV collagenase.
FT DOMAIN 223 280 Fibronectin type-II 1.
FT DOMAIN 281 339 Fibronectin type-II 2.
FT DOMAIN 340 397 Fibronectin type-II 3.
FT DOMAIN 445 508 Pro-rich.
FT DOMAIN 510 704 Hemopexin-like.
FT METAL 401 401 Zinc (catalytic) (By similarity).
FT ACT_SITE 402 402 By similarity.
FT METAL 405 405 Zinc (catalytic) (By similarity).
FT METAL 411 411 Zinc (catalytic) (By similarity).
FT CARBOHYD 38 38 N-linked (GlcNAc...) (Potential).
FT DISULFID 127 127 N-linked (GlcNAc...) (Potential).
FT SIGNAL 513 701 By similarity.
SQ SEQUENCE 704 AA; 78123 MW; 0D3394D26256391 CRC64;
Query Match 83.7%; Score 216; DB 1; Length 704;
Best Local Similarity 78.7%; Pred. No. 1.6e-20;
Matches 37; Conservative 7; Mismatches 3; Indels 0; Gaps 0;
QY 1 LKQLSLPETGELDSATLKXMTPECGVDPDLGRFOTFEGDLKWHHN 47
DB 74 LQRLALPETGELDKTTLEAMRAPCGVDPDLGRFOTFEGDLKWHND 120

RESULT 8
O19130 PRELIMINARY; PRT; 704 AA.
ID O19130;
AC O19130;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Gelatinase B.
DE Canis familiaris (Dog).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97467354; PubMed=9325284;
RA Fang K.C., Raymond W.W., Blount J.L., Caughey G.H.;
RT "Dog mast cell alpha-chymase activates progelatinase B by cleaving the
RT Phe88-Gln89 and Phe91-Glu92 bonds of the catalytic domain.";
RL J. Biol. Chem. 272:25628-25635(1997).
DR EMBL; U9842; AAB81681.1; --
DR HSSP; P14780; IGKC.
DR GO; GO:0005578; C:extracellular matrix; IEA.
DR GO; GO:004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:000508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000562; FN_Type_II.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR006026; Peptidase M.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR009070; PGSD_like.
DR InterPro; IPR006970; PT.
DR Pfam; PF00040; fn2; 3.
DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF00413; Peptidase_M10; 1.
DR Pfam; PF03933; Peptidase_M10_N; 1.
DR Pfam; PF04886; PT; 1.
DR PRINTS; PR00013; FNTYPEII.
DR PRINTS; PR00138; MATRIXIN.
DR ProDom; PD000995; FN_Type_II; 2.
DR SMART; SM00059; FN2; 3.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZMC; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
DR PROSITE; PS00023; FIBRONECTIN_2; 3.
DR PROSITE; PS00024; HEMOPEXIN; UNKNOWN_1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
DR Calcium; Collagen degradation; Extracellular matrix; Glycoprotein;
SQ SEQUENCE 704 AA; 78259 MW; AF9999247E463318 CRC64;
Query Match 83.7%; Score 216; DB 2; Length 704;
Best Local Similarity 78.7%; Pred. No. 1.6e-20;
Matches 37; Conservative 7; Mismatches 3; Indels 0; Gaps 0;
QY 1 LKQLSLPETGELDSATLKXMTPECGVDPDLGRFOTFEGDLKWHHN 47
DB 74 LQRLALPETGELDKTTLEAMRAPCGVDPDLGRFOTFEGDLKWHND 120

RESULT 9
Q71U09 PRELIMINARY; PRT; 704 AA.
ID Q71U09;
AC Q71U09;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Matrix metalloproteinase-9.
DE Canis familiaris (Dog).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fibroscroma;

```

RA Paria B.C., Balkin R.G., Kitchell B.E.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF169244; AAD50275.1; -
DR InterPro; IPR000562; FN_Type II.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR006036; Peptidase M.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR009070; FGBD_like.
DR InterPro; IPR006970; PT.
DR Pfam; PF00040; fn2; 3.
DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF00413; Peptidase M10; 1.
DR Pfam; PF03933; Peptidase_M10_N; 1.
DR Pfam; PF04886; PT_1.
DR PRINTS; PR00013; FNTYPEII.
DR PRINTS; PR00138; MATRIXIN.
DR ProDom; PD000995; FN_Type II; 2.
DR SMART; SM00059; FN2; 3.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZnMc; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
DR PROSITE; PS00023; FIBRONECTIN_2; 3.
DR PROSITE; PS00024; HEMOPEXIN; UNKNOWN_1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SQ SEQUENCE 704 AA; 78198 MW; A3935A2C8F85CDD7 CRC64;

Query Match      83.7%; Score 216; DB 2; Length 704;
Best Local Similarity 78.7%; Pred. No. 1.6e-20;
Matches 37; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 LQKQLSLPTGELDSATLKAMTRPGVDPDLGRFQTFEGDLKWHHN 47
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 74 LQRLALPTGELDKTTLKAMRAPRCGVDPDLGKFTFEGDLKWHND 120

RESULT 10
ID AAD50275 PRELIMINARY; PRT; 704 AA.
AC AAD50275;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Matrix metalloproteinase-9.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OC NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fibrosarcoma;
RA Paria B.C., Balkin R.G., Kitchell B.E.;
RT "Partial cloning of canine type-IV (MMP-9) from canine fibrosarcoma.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF169244; AAD50275.1; -
SQ SEQUENCE 704 AA; 78198 MW; A3935A2C8F85CDD7 CRC64;

Query Match      83.7%; Score 216; DB 2; Length 704;
Best Local Similarity 78.7%; Pred. No. 1.6e-20;
Matches 37; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 LQKQLSLPTGELDSATLKAMTRPGVDPDLGRFQTFEGDLKWHHN 47
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 74 LQRLALPTGELDKTTLKAMRAPRCGVDPDLGKFTFEGDLKWHND 120

RESULT 11
MM09 MOUSE
ID MM09 MOUSE STANDARD; PRT; 730 AA.
AC P41345; Q06788; Q9DC02;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)

```

```

DE 92 kDa type IV collagenase precursor (EC 3.4.24.35) (92 kDa
DE gelatinase) (Matrix metalloproteinase-9) (MMP-9) (Gelatinase B)
DE (GELB).
GN Name=Mmp9; Synonyms=C1g4b;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone;
RA MEDLINE=94179406; PubMed=8132709;
RX Reponen P., Sahlberg C., Munaut C., Thesleff I., Tryggvason K.;
RT "High expression of 92-kD type IV collagenase (gelatinase B) in the
RT osteoclast lineage during mouse development.";
RL J. Cell Biol. 124:1091-1102(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=93176173; PubMed=8382489;
RX Tanaka H., Hojo K., Yoshida H., Yoshioka T., Sugita K.;
RT "Molecular cloning and expression of the mouse 105-kDa gelatinase
RT cDNA.";
RL Biochem. Biophys. Res. Commun. 190:732-740(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Liver;
RX MEDLINE=94062823; PubMed=8243459;
RA Masure S., Nys G., Fiten P., van Damme J., Odenakker G.;
RT "Mouse gelatinase B. cDNA cloning, regulation of expression and
RT glycosylation in WH1-3 macrophages and gene organisation.";
RL Eur. J. Biochem. 218:129-141(1993).
RN [4]
RP SEQUENCE FROM N.A.
RA MEDLINE=94033534; PubMed=8219207;
RX Graubert T., Johnston J., Berliner N.;
RT "Cloning and expression of the cDNA encoding mouse neutrophil
RT gelatinase: demonstration of coordinate secondary granule protein gene
RT expression during terminal neutrophil maturation.";
RL Blood 82:3192-3197(1993).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Clothia C., Corbani L.B., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.P., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Naglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilmink L.G., Wynshaw-Boris A., Yanagisawa M., Yang L., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Binney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
CC -!- FUNCTION: Could play a role in bone osteoclastic resorption.

```


DR PRINTS; PR00013; FNTYPEII.
DR PRINTS; PR00138; MATRINXIN.
DR PRODOM; PD00095; FN_Type_II; 2.
DR SMART; SM00059; FN2; 3.
DR SMART; SM00120; FN2; 3.
DR SMART; SM00120; FN2; 3.
DR SMART; SM00235; ZINC; 1.
DR PROSITE; PS00546; CYSTEINE SWITCH; 1.
DR PROSITE; PS00023; FIBROECTIN_2; 3.
DR PROSITE; PS00024; HEMOPEXIN; UNKNOWN 1.
DR PROSITE; PS00142; ZINC PROTEASE; UNKNOWN 1.
SQ SEQUENCE 730 AA; 80535 MW; E16F45C24B4D1024 CRC64;
Query Match 82.8%; Score 213.5; DB 2; Length 730;
Best Local Similarity 85.1%; Pred. No. 3.7e-20;
Matches 40; Conservative 4; Mismatches 2; Indels 1; Gaps 1;
OY 1 LQKSLPPTGELDSATLKAMTPRCGVPDLGRFQTFEGDLKWHHN 47
DB 75 MQKXGLNETGELDSQTLKAMTPRCGVPDVGDFQTFEGDLKWHND 120
RESULT 13
Q98856 PRELIMINARY; PRT; 679 AA.
ID Q98856
AC Q98856
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Gelatinase-b.
OS Cynops pyrrhogaster (Japanese common newt).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandridae; Cynops.
OX NCBI_TaxID=8330;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Limb;
RX MEDLINE=96270627; PubMed=8692902;
RA Miyazaki K, Uchiyama K, Imokawa Y, Yoshizato K.
RT "Cloning and characterization of cDNAs for matrix metalloproteinases
of regenerating newt limbs.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:6819-6824 (1996).
DR EMBL; D82052; BA011523.1; -.
DR HSSP; P08253; 1J7M.
DR MEROPS; M10.004; -.
DR GO; GO:0005578; C:extracellular matrix; IEA.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000562; FN_Type_II.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR006026; Peptidase M.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR009070; PGSD_like.
DR Pfam; PF00040; FN2; 3.
DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF00413; Peptidase M10; 1.
DR Pfam; PF03933; Peptidase M10_N; 1.
DR PRINTS; PR00013; FNTYPEII.
DR PRODOM; PD00095; FN_Type_II; 3.
DR SMART; SM00059; FN2; 3.
DR SMART; SM00120; FN2; 3.
DR SMART; SM00235; ZINC; 1.
DR PROSITE; PS00546; CYSTEINE SWITCH; 1.
DR PROSITE; PS00023; FIBROECTIN_2; 3.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC PROTEASE; UNKNOWN 1.
SQ SEQUENCE 679 AA; 75581 MW; 573CDB9DBF85524 CRC64;

Query Match 74.8%; Score 193; DB 2; Length 679;
Best Local Similarity 70.2%; Pred. No. 2.2e-17;
Matches 33; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

OY 1 LQKSLPPTGELDSATLKAMTPRCGVPDLGRFQTFEGDLKWHHN 47
DB 75 MQKXGLNETGELDSQTLKAMTPRCGVPDVGDFQTFEGDLKWHND 121
RESULT 14
Q9DE15 PRELIMINARY; PRT; 686 AA.
ID Q9DE15
AC Q9DE15
DT 01-MAR-2001 (TREMBlrel. 15, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE 75 kDa gelatinase.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20576236; PubMed=11010969;
RA Hahn-Dantona E.A., Aimes R.T., Quigley J.P.;
RT "The isolation, characterization, and molecular cloning of a 75-kDa
gelatinase B-like enzyme, a member of the matrix metalloproteinase
(MMP) family. An avian enzyme that is MMP-9-like in its cell
expression pattern but diverges from mammalian gelatinase B in
sequence and biochemical properties.";
RL J. Biol. Chem. 275:40827-40838 (2000).
DR EMBL; AF222690; AAG47650.1; -.
DR HSSP; P33435; 1CXV.
DR MEROPS; M10.004; -.
DR GO; GO:0005578; C:extracellular matrix; IEA.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000562; FN_Type_II.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR006025; Peptidase M.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR009070; PGSD_like.
DR Pfam; PF00040; FN2; 3.
DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF00413; Peptidase M10; 1.
DR Pfam; PF03933; Peptidase M10_N; 1.
DR PRINTS; PR00013; FNTYPEII.
DR PRODOM; PD00095; FN_Type_II; 2.
DR SMART; SM00059; FN2; 3.
DR SMART; SM00120; FN2; 3.
DR SMART; SM00235; ZINC; 1.
DR PROSITE; PS00546; CYSTEINE SWITCH; 1.
DR PROSITE; PS00023; FIBROECTIN_2; 2.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC PROTEASE; UNKNOWN 1.
SQ SEQUENCE 686 AA; 76679 MW; 9E9AB59F96A497CE CRC64;
Query Match 71.7%; Score 185; DB 2; Length 686;
Best Local Similarity 73.3%; Pred. No. 2.8e-16;
Matches 33; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

OY 1 LQKSLPPTGELDSATLKAMTPRCGVPDLGRFQTFEGDLKWHH 45
DB 74 MQKXGLNETGELDSQTLKAMTPRCGVPDVGDFQTFEGDLKWH 118
RESULT 15
Q90YB3 PRELIMINARY; PRT; 673 AA.
ID Q90YB3
AC Q90YB3
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Gelatinase.

Search completed: October 13, 2004, 15:14:40
Job time : 98.4103 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 13, 2004, 14:57:16 ; Search time 102.462 Seconds
(without alignments)
189.060 Million cell updates/sec

Title: US-10-032-376A-9
Perfect score: 292
Sequence: 1 MOEFFGLKVTGRDAETLKV.....VLTEGNPRWEQTHLVYRIEN 54

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : A Geneseq 23Sep04:*
- 1: Geneseqp1980s:*
 - 2: Geneseqp1990s:*
 - 3: Geneseqp2000s:*
 - 4: Geneseqp2001s:*
 - 5: Geneseqp2002s:*
 - 6: Geneseqp2003as:*
 - 7: Geneseqp2003bs:*
 - 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	292	100.0	54	6	ABP97131 Human mat
2	292	100.0	54	6	ABG76317 Human mat
3	292	100.0	54	8	ADQ17092 Human mat
4	292	100.0	454	7	ADL16002 G-coupled
5	292	100.0	454	7	ADL16004 G-coupled
6	292	100.0	454	7	ADL16006 G-coupled
7	292	100.0	454	7	ADL16008 G-coupled
8	292	100.0	454	8	ADL93945 Human G-C
9	292	100.0	454	8	ADL93943 Human G-C
10	292	100.0	455	8	ADL93941 Human G-C
11	292	100.0	469	4	AB84606 Amino aci
12	292	100.0	469	4	ABE10415 Human mat
13	292	100.0	469	4	ABU03466 Angiogene
14	292	100.0	469	6	ABR58543 Human can
15	292	100.0	469	6	ABR58542 Human can
16	292	100.0	469	6	ABR48148 Human bla
17	292	100.0	469	6	ABU56596 Lung canc
18	292	100.0	469	6	ABU56597 Lung canc
19	292	100.0	469	6	ABU07454 Protein d
20	292	100.0	469	6	ABP54454 Matrix me
21	292	100.0	469	7	ABD79176 Matrix me
22	292	100.0	469	7	ABE34550 Human ski
23	292	100.0	469	7	ABE16000 G-coupled
24	292	100.0	469	7	ABE16010 G-coupled
25	292	100.0	469	7	ADN39849 Cancer/an

26	292	100.0	469	7	ADN38694 Cancer/an
27	292	100.0	469	7	ADN38696 Cancer/an
28	292	100.0	469	7	ADN39850 Cancer/an
29	292	100.0	469	7	ADN95538 Human BEC
30	292	100.0	469	8	ADL93949 Human G-C
31	292	100.0	469	8	ADL93939 Human G-C
32	292	100.0	470	8	ADN07695 Human mat
33	292	100.0	490	7	ADN07892 Novel pro
34	292	100.0	496	4	AAAG75509 Human col
35	286	97.9	457	1	AAAP93628 Sequence
36	286	97.9	469	1	AAAP70611 Sequence
37	286	97.9	469	8	ADQ18359 Human sof
38	285	97.6	454	8	ADL93947 Human G-C
39	233	79.8	43	6	ABP97139 Human mat
40	233	79.8	43	6	ABG76325 Partial s
41	233	79.8	43	8	ADQ17100 Human mat
42	214	73.3	55	6	ABP97132 Human mat
43	214	73.3	55	6	ABG76318 Human mat
44	214	73.3	55	8	ADQ17093 Human mat
45	214	73.3	444	4	AAAG5357 Human MMP

ALIGNMENTS

RESULT 1
ABP97131
ID ABP97131 standard; peptide; 54 AA.
XX
AC ABP97131;
XX
DT 24-JUN-2003 (first entry)
XX
DE Human matrix metalloproteinase 1 cleavage region peptide SEQ ID NO:9.
XX
KW Human; matrix metalloproteinase; MMP; anticancer; wound healing;
KW matrix metalloproteinase inhibitor; antitumor; antiangiogenic; cardiant;
KW vascular endothelial growth factor inhibitor; VEGF inhibitor; cytostatic;
KW vulnary; cerebroprotective; antidiabetic; ophthalmological; tumour;
KW dermatological; metastatic; non-metastatic; vascularised; heart disease;
KW non-vascularised; surgical incision; chronic wound; stroke; angiogenesis;
KW macular degeneration; diabetic retinopathy; cleavage region.
XX
OS Homo sapiens.
XX
FN WO2003018748-A2.
XX
PD 06-MAR-2003.
XX
PF 15-AUG-2002; 2002WO-US026319.
XX
PR 16-AUG-2001; 2001US-0312726P.
PR 21-DEC-2001; 2001US-00032376.
PR 21-MAY-2002; 2002US-00153185.
XX
PA (KIMB) KIMBERLY-CLARK WORLDWIDE INC.
XX
PI Quirk S, Weart IF;
XX
WP 2003-381408/36.
XX
DR Anti-angiogenic composition comprising peptide inhibitor of matrix
XX metalloproteinase, useful for decreasing the expression of vascular
XX endothelial growth factor and treating cancers and tissue injuries.
XX
PS Claim 17; Page 16; 103pp; English.
XX
CC The present invention describes an anti-angiogenic composition (I) for
XX inhibiting expression of vascular endothelial growth factor (VEGF). (I)
XX comprises an effective amount of a peptide inhibitor of matrix
XX metalloproteinase (MMP), where the peptide can inhibit the expression of
XX VEGF. (I) has cytostatic, vulnary, cardiant, cerebroprotective,
XX antidiabetic, ophthalmological and dermatological activities. (I) can be

CC used for inhibiting expression of VEGF, and so can be used for inhibiting
 CC growth of tumours and diminishing tumours size. The tumour can be
 CC metastatic, non-metastatic, vascularised, non-vascularised, hard or soft.
 CC (I) is also useful for treating injuries including wounds, surgical
 CC incisions, chronic wounds, heart diseases and stroke. (I) is also useful
 CC for treating disorders characterised by excessive angiogenesis e.g.
 CC macular degeneration and diabetic retinopathy. The present sequence
 CC represents a human MMP cleavage region peptide, which is used in the
 CC exemplification of the present invention
 SQ Sequence 54 AA;

Query Match 100.0%; Score 292; DB 6; Length 54;
 Best Local Similarity 100.0%; Pred. No. 1.4e-32;
 Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGPNRWQTHLTYYRIEN 54
 Db 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGPNRWQTHLTYYRIEN 54

RESULT 2
 ABG76317
 ID ABG76317 standard; protein; 54 AA.

AC ABG76317;
 DT 10-MAY-2003 (first entry)
 DE Human matrix metalloproteinase (MMP) peptide inhibitor #9.
 KW Human; peptide inhibitor; matrix metalloproteinase-1; MMP-1;
 KW cleavage region; proenzyme form; cellular proliferation; fibroblast;
 KW keratinocyte; healthy skin development; wound healing; scarring;
 KW skin tone; wrinkle; anti-aging; vulnary.
 OS Homo sapiens.

XX WO2003016520-A1.
 XX 27-FEB-2003.
 XX 15-AUG-2002; 2002WO-US026198.
 XX 16-AUG-2001; 2001US-0312726P.
 XX 21-DEC-2001; 2001US-00032376.
 XX 21-MAY-2002; 2002US-00153185.
 XX (KIMB) KIMBERLY-CLARK WORLDWIDE INC.

XX Quirk S, Malik S, Villanueva JM;
 XX WPI; 2003-289980/26.
 XX Novel peptide inhibitor of proteinase activity of matrix
 XX metalloproteinases, e.g. matrix metalloproteinase-2, useful for
 XX stimulating cellular proliferation of fibroblasts or keratinocytes.
 XX Claim 1; Page 15; 120pp; English.

XX The present invention relates to peptide inhibitors of metalloproteinases
 CC (MMPs), particularly metalloproteinase-2 (MMP-2). The inhibitors have
 CC peptide sequences related to the cleavage regions of the proenzyme forms
 CC of the MMPs. The peptide inhibitors are useful for stimulating cellular
 CC proliferation of fibroblasts or keratinocytes, promoting healthy skin
 CC development, treating wounds, preventing scarring, improving skin tone,
 CC reducing wrinkling and for stimulating the development of smooth, healthy
 CC skin. The peptide inhibitors are useful as anti-aging and wound healing
 CC compounds. ABG76309-ABG76321 represent peptide inhibitors of MMPs
 XX
 SQ Sequence 54 AA;

Query Match 100.0%; Score 292; DB 6; Length 54;

Best Local Similarity 100.0%; Pred. No. 1.4e-32;
 Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGPNRWQTHLTYYRIEN 54
 Db 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGPNRWQTHLTYYRIEN 54

RESULT 3
 ADQ17092
 ID ADQ17092 standard; peptide; 54 AA.

AC ADQ17092;
 DT 23-SEP-2004 (first entry)
 DE Human matrix metalloproteinase-1 (MMP1) cleavage region peptide.
 KW Fibronectin; healthy skin; wrinkle; wound; vulnary; dermatological;
 KW human; matrix metalloproteinase; MMP.

OS Homo sapiens.
 XX US2004127421-A1.
 XX 01-JUL-2004.

XX 30-DEC-2002; 2002US-00335207.
 XX 30-DEC-2002; 2002US-00335207.

XX (MALI/) MALIK S.
 XX (QUIR/) QUIRK S.
 XX Malik S, Quirk S;
 XX WPI; 2004-S06456/48.

XX Composition used for preventing and treating wrinkles and treating wounds
 XX comprises peptide having sequence related to matrix metalloproteinase
 XX proenzyme.

XX Example 1; SEQ ID NO 9; 60pp; English.

XX The present invention provides peptides and compositions containing such
 CC peptides that are useful as agents to maintain healthy skin and to
 CC promote the condition of the skin. The invention is useful for increasing
 CC the amount of fibronectin in tissue. The invention is also useful for
 CC encouraging the maintenance and development of healthy skin, preventing
 CC and treating wrinkles and for treating wounds. The invention acts as
 CC vulnary and dermatological agents. The present sequence is human matrix
 CC metalloproteinase (MMP) cleavage region peptide. This sequence is used in
 CC the exemplification of the invention.

XX Sequence 54 AA;

Query Match 100.0%; Score 292; DB 8; Length 54;
 Best Local Similarity 100.0%; Pred. No. 1.4e-32;
 Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGPNRWQTHLTYYRIEN 54
 Db 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGPNRWQTHLTYYRIEN 54

RESULT 4
 ADE16002
 ID ADE16002 standard; protein; 454 AA.

XX ADE16002;
 XX 29-JAN-2004 (first entry)
 XX

DE G-coupled protein receptor related polypeptide, SEQ ID No 32.
 XX G-coupled protein receptor; antidiabetic; anorectic; antibacterial;
 KW virucide; fungicide; cytostatic; neurotropic; neuroprotective;
 KW antiparkinsonian; haemostatic; antilipaeamic; neurogenesis;
 KW cell differentiation; cell proliferation; hematopoiesis; wound healing;
 KW angiogenesis; gene therapy; chromosome mapping; tissue typing;
 KW preventive medicine; pharmacogenomics; human.
 XX Homo sapiens.
 OS
 XX
 XX W0200283841-A2.
 XX
 XX 24-OCT-2002.
 XX
 XX 03-APR-2002; 2002WO-US010713.
 XX
 XX 03-APR-2001; 2001US-0281136P.
 PR 05-APR-2001; 2001US-0281863P.
 PR 08-APR-2001; 2001US-0281906P.
 PR 10-APR-2001; 2001US-0282934P.
 PR 13-APR-2001; 2001US-0283657P.
 PR 13-APR-2001; 2001US-0283578P.
 PR 13-APR-2001; 2001US-0283587P.
 PR 13-APR-2001; 2001US-0283710P.
 PR 17-APR-2001; 2001US-0284234P.
 PR 19-APR-2001; 2001US-0285325P.
 PR 20-APR-2001; 2001US-0285609P.
 PR 23-APR-2001; 2001US-0285748P.
 PR 24-APR-2001; 2001US-0285890P.
 PR 24-APR-2001; 2001US-0286068P.
 PR 27-APR-2001; 2001US-0287213P.
 PR 03-MAY-2001; 2001US-0288509P.
 PR 30-MAY-2001; 2001US-0294495P.
 PR 31-JUL-2001; 2001US-0294801P.
 PR 31-JUL-2001; 2001US-0309216P.
 PR 28-SEP-2001; 2001US-0324775P.
 PR 28-NOV-2001; 2001US-0333900P.
 PR 02-APR-2002; 2002US-00115479.
 XX
 XX (CURA-) CURAGEN CORP.
 XX
 XX Li L, Gerlach V, Liu X, Miller CE, Spytek KA, Zerhusen BD;
 PI Pena CEA, Shenoy SG, Zhong H, Smithson G, Casman SJ, Boldog FL;
 PI Voss EZ, Vernet CAM, Macdougall JR, Rastelli L, Anderson DW;
 PI Zhong M, Mezes PB, Furtak K, Patturajan M, Burgess CE, Malyankar UM;
 PI Shinkets RA, Taupier RJ, Edinger SR, Mazur A;
 XX
 DR WPI; 2003-067574/06.
 DR N-PSDB; ADE16001.
 XX
 XX New isolated NOVX polypeptides and polynucleotides, useful for
 PT preventing, diagnosing or treating NOVX-associated disorders e.g.
 PT diabetes, obesity, dyslipidaemias, cancer, Parkinson's disease,
 PT Alzheimer's disease, infections.
 XX
 PS Claim 1; SEQ ID NO 32; 320pp; English.
 XX
 XX The invention relates to a novel isolated G-coupled protein receptor
 CC related polypeptides. The novel polypeptide comprise any of the 22 fully
 CC defined sequences of 87-1780 amino acids, given in the specification;
 CC their mature forms; and possible variants. The novel polypeptides have
 CC the following activities: antidiabetic, anorectic, antibacterial,
 CC virucide, fungicide, cytostatic, neurotropic, neuroprotective,
 CC antiparkinsonian, haemostatic, and antilipaeamic. The G-coupled protein
 CC receptor related polypeptides are useful in a method of treating or
 CC preventing in a human, a pathology associated with the G-coupled protein
 CC receptor related polypeptides. The polypeptides are useful in the
 CC manufacture of a medicament for treating a syndrome associated with a
 CC human disease, preferably a NOVX-associated disorder. The novel
 CC polypeptides are useful for treating, preventing or diagnosing diseases,
 CC such as metabolic disorders, diabetes, obesity, infectious diseases,
 CC anorexia, cancer-associated diseases, neurodegenerative disorders,
 CC

CC Alzheimer's disease, Parkinson's disease, immune disorders, hematopoietic
 CC disorders, and various dyslipidaemias, metabolic disturbances associated
 CC with obesity, metabolic X syndrome and wasting disorders associated with
 CC chronic diseases and various cancers. The nucleic acids and polypeptides
 CC may also be used as targets for the identification of small molecules
 CC that modulate or inhibit e.g. neurogenesis, cell differentiation, cell
 CC proliferation, hematopoiesis, wound healing and angiogenesis, in gene
 CC therapy, in generation of antibodies that bind immunospecifically to NOVX
 CC substances for use in therapeutic or diagnostic methods. The nucleic
 CC acids are further used as hybridization probes, in chromosome mapping.
 CC tissue typing, preventive medicine, and pharmacogenomics. This sequence
 CC represents one of the novel G-coupled protein receptor related
 CC polypeptides of the invention.
 XX
 XX Sequence 454 AA;
 SQ

Query Match 100.0%; Score 292; DB 7; Length 454;
 Best Local Similarity 100.0%; Pred. No. 2e-31;
 Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MQEFGGLKVTGKPDATLKVWKQRCGVPDVAQFVLTEGPNRWQTHLYRIEN 54
 DB 50 MQEFGGLKVTGKPDATLKVWKQRCGVPDVAQFVLTEGPNRWQTHLYRIEN 103

RESULT 5
 ADE16004
 ID ADE16004 standard; protein; 454 AA.
 XX
 AC ADE16004;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE G-coupled protein receptor related polypeptide, SEQ ID No 34.
 KW G-coupled protein receptor; antidiabetic; anorectic; antibacterial;
 KW virucide; fungicide; cytostatic; neurotropic; neuroprotective;
 KW antiparkinsonian; haemostatic; antilipaeamic; neurogenesis;
 KW cell differentiation; cell proliferation; hematopoiesis; wound healing;
 KW angiogenesis; gene therapy; chromosome mapping; tissue typing;
 KW preventive medicine; pharmacogenomics; human.
 XX Homo sapiens.
 OS
 XX W0200283841-A2.
 XX
 XX 24-OCT-2002.
 XX
 XX 03-APR-2002; 2002WO-US010713.
 XX
 XX 03-APR-2001; 2001US-0281136P.
 PR 05-APR-2001; 2001US-0281863P.
 PR 05-APR-2001; 2001US-0281906P.
 PR 10-APR-2001; 2001US-0282934P.
 PR 13-APR-2001; 2001US-0283657P.
 PR 13-APR-2001; 2001US-0283578P.
 PR 13-APR-2001; 2001US-0283678P.
 PR 13-APR-2001; 2001US-0283687P.
 PR 13-APR-2001; 2001US-0283710P.
 PR 19-APR-2001; 2001US-0284234P.
 PR 19-APR-2001; 2001US-0285325P.
 PR 20-APR-2001; 2001US-0285609P.
 PR 23-APR-2001; 2001US-0285748P.
 PR 23-APR-2001; 2001US-0285890P.
 PR 24-APR-2001; 2001US-0286068P.
 PR 27-APR-2001; 2001US-0287213P.
 PR 27-APR-2001; 2001US-0288509P.
 PR 30-MAY-2001; 2001US-0294495P.
 PR 30-MAY-2001; 2001US-0294801P.
 PR 31-JUL-2001; 2001US-0294801P.
 PR 31-JUL-2001; 2001US-0309216P.
 PR 28-SEP-2001; 2001US-0324775P.
 PR 28-NOV-2001; 2001US-0333900P.
 PR 02-APR-2002; 2002US-00115479.
 XX
 XX (CURA-) CURAGEN CORP.
 XX
 XX Li L, Gerlach V, Liu X, Miller CE, Spytek KA, Zerhusen BD;
 PI Pena CEA, Shenoy SG, Zhong H, Smithson G, Casman SJ, Boldog FL;
 PI Voss EZ, Vernet CAM, Macdougall JR, Rastelli L, Anderson DW;
 PI Zhong M, Mezes PB, Furtak K, Patturajan M, Burgess CE, Malyankar UM;
 PI Shinkets RA, Taupier RJ, Edinger SR, Mazur A;
 XX
 DR WPI; 2003-067574/06.
 DR N-PSDB; ADE16001.
 XX
 XX New isolated NOVX polypeptides and polynucleotides, useful for
 PT preventing, diagnosing or treating NOVX-associated disorders e.g.
 PT diabetes, obesity, dyslipidaemias, cancer, Parkinson's disease,
 PT Alzheimer's disease, infections.
 XX
 PS Claim 1; SEQ ID NO 32; 320pp; English.
 XX
 XX The invention relates to a novel isolated G-coupled protein receptor
 CC related polypeptides. The novel polypeptide comprise any of the 22 fully
 CC defined sequences of 87-1780 amino acids, given in the specification;
 CC their mature forms; and possible variants. The novel polypeptides have
 CC the following activities: antidiabetic, anorectic, antibacterial,
 CC virucide, fungicide, cytostatic, neurotropic, neuroprotective,
 CC antiparkinsonian, haemostatic, and antilipaeamic. The G-coupled protein
 CC receptor related polypeptides are useful in a method of treating or
 CC preventing in a human, a pathology associated with the G-coupled protein
 CC receptor related polypeptides. The polypeptides are useful in the
 CC manufacture of a medicament for treating a syndrome associated with a
 CC human disease, preferably a NOVX-associated disorder. The novel
 CC polypeptides are useful for treating, preventing or diagnosing diseases,
 CC such as metabolic disorders, diabetes, obesity, infectious diseases,
 CC anorexia, cancer-associated diseases, neurodegenerative disorders,
 CC

us-10-032-376a-9.rag

Mon Nov 15 13:54:01 2004

PA (CURA-) CURAGEN CORP.
XX Li L, Gerlach V, Liu X, Miller CE, Spytek KA, Zethusen BD;
PI Pena CEA, Shenoy SG, Zhong H, Smithson G, Casman SJ, Boldog FL;
PI Voss EZ, Vernet CAM, MacDougall JR, Rastelli L, Anderson DW;
PI Zhong M, Mezes PD, Furtak K, Patturajan M, Burgess CE, Malyankar UM;
PI Shimkets RA, Taupier RJ, Edinger SR, Mazur A;
XX WPI; 2003-067574/06.
DR N-PSDB; ADE16008.
XX
XX New isolated NOVX polypeptides and polynucleotides, useful for
PT preventing, diagnosing or treating NOVX-associated disorders e.g.
PT diabetes, obesity, dyslipidemias, cancer, Parkinson's disease,
PT Alzheimer's disease, infections.
XX
XX Claim 1; SEQ ID NO 34; 320pp; English.
XX
XX The invention relates to a novel isolated G-coupled protein receptor
CC related polypeptides. The novel polypeptide comprise any of the 22 fully
CC defined sequences of 87-1780 amino acids, given in the specification;
CC their mature forms; and possible variants. The novel polypeptides have
CC the following activities: antidiabetic, anorectic, antibacterial,
CC virucide, fungicide, cytostatic, nootropic, neuroprotective,
CC antiparkinsonian, haemostatic, and antilipaeamic. The G-coupled protein
CC receptor related polypeptides are useful in a method of treating or
CC preventing in a human, a pathology associated with the G-coupled protein
CC receptor related polypeptides. The polypeptides are useful in the
CC manufacture of a medicament for treating a syndrome associated with a
CC human disease, preferably a NOVX-associated disorder. The novel
CC polypeptides are useful for treating, preventing or diagnosing diseases,
CC such as metabolic disorders, diabetes, obesity, infectious diseases,
CC anorexia, cancer-associated diseases, neurodegenerative disorders,
CC Alzheimer's disease, Parkinson's disease, immune disorders, hematopoietic
CC disorders, and various dyslipidemias, metabolic disturbances associated
CC with obesity, metabolic X syndrome and wasting disorders associated
CC chronic diseases and various cancers. The nucleic acids and polypeptides
CC may also be used as targets for the identification of small molecules
CC that modulate or inhibit e.g. neurogenesis, cell differentiation, cell
CC proliferation, hematopoiesis, wound healing and angiogenesis, in gene
CC therapy, in generation of antibodies that bind immunospecifically to NOVX
CC substances for use in therapeutic or diagnostic methods. The nucleic
CC acids are further used as hybridization probes, in chromosome mapping,
CC tissue typing, preventive medicine, and pharmacogenomics. This sequence
CC represents one of the novel G-coupled protein receptor related
CC polypeptides of the invention.
XX
XX Sequence 454 AA;
XX
XX Query Match 100.0%; Score 232; DB 7; Length 454;
XX Best Local Similarity 100.0%; Pred. No. 2e-31;
XX Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MQEFFGLKVTGKDAETLKVMKPCRCGVPDVAQFVLTEGNPRWEQHLTYRIEN 54
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 50 MQEFFGLKVTGKDAETLKVMKPCRCGVPDVAQFVLTEGNPRWEQHLTYRIEN 103
XX
XX RESULT 6
XX ADE16008
XX ID ADE16008 standard; protein; 454 AA.
XX
XX AC ADE16008;
XX
XX 29-JAN-2004 (first entry)
XX
XX G-coupled protein receptor related polypeptide, SEQ ID NO 38.
XX
XX G-coupled protein receptor; antidiabetic; anorectic; antibacterial;
XX virucide; fungicide; cytostatic; nootropic; neuroprotective;
XX antiparkinsonian; haemostatic; antilipaeamic; neurogenesis;
XX cell differentiation; cell proliferation; hematopoiesis; wound healing;
XX angiogenesis; gene therapy; chromosome mapping; tissue typing;

preventive medicine; pharmacogenomics; human.
XX Homo sapiens.
XX WO200283841-A2.
XX 24-OCT-2002.
XX
XX 03-APR-2002; 2002WO-US010713.
XX
XX 03-APR-2001; 2001US-0281136P.
XX 05-APR-2001; 2001US-0281863P.
XX 05-APR-2001; 2001US-0281906P.
XX 10-APR-2001; 2001US-0282934P.
XX 13-APR-2001; 2001US-0283657P.
XX 13-APR-2001; 2001US-0283678P.
XX 13-APR-2001; 2001US-0283687P.
XX 13-APR-2001; 2001US-0283710P.
XX 17-APR-2001; 2001US-0284234P.
XX 19-APR-2001; 2001US-0285325P.
XX 20-APR-2001; 2001US-0285609P.
XX 23-APR-2001; 2001US-0285748P.
XX 23-APR-2001; 2001US-0285890P.
XX 24-APR-2001; 2001US-0286068P.
XX 27-APR-2001; 2001US-0287213P.
XX 03-MAY-2001; 2001US-0288509P.
XX 30-MAY-2001; 2001US-0294495P.
XX 31-MAY-2001; 2001US-0294801P.
XX 31-JUL-2001; 2001US-0309216P.
XX 25-SEP-2001; 2001US-0324775P.
XX 28-NOV-2001; 2001US-0333900P.
XX 02-APR-2002; 2002US-00115479.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Li L, Gerlach V, Liu X, Miller CE, Spytek KA, Zethusen BD;
XX Pena CEA, Shenoy SG, Zhong H, Smithson G, Casman SJ, Boldog FL;
XX Voss EZ, Vernet CAM, MacDougall JR, Rastelli L, Anderson DW;
XX Zhong M, Mezes PD, Furtak K, Patturajan M, Burgess CE, Malyankar UM;
XX Shimkets RA, Taupier RJ, Edinger SR, Mazur A;
XX WPI; 2003-067574/06.
XX N-PSDB; ADE16007.
XX
XX New isolated NOVX polypeptides and polynucleotides, useful for
XX preventing, diagnosing or treating NOVX-associated disorders e.g.
XX diabetes, obesity, dyslipidemias, cancer, Parkinson's disease,
XX Alzheimer's disease, infections.
XX
XX Claim 1; SEQ ID NO 38; 320pp; English.
XX
XX The invention relates to a novel isolated G-coupled protein receptor
XX related polypeptides. The novel polypeptide comprise any of the 22 fully
XX defined sequences of 87-1780 amino acids, given in the specification;
XX their mature forms; and possible variants. The novel polypeptides have
XX the following activities: antidiabetic, anorectic, antibacterial,
XX virucide, fungicide, cytostatic, nootropic, neuroprotective,
XX antiparkinsonian, haemostatic, and antilipaeamic. The G-coupled protein
XX receptor related polypeptides are useful in a method of treating or
XX preventing in a human, a pathology associated with the G-coupled protein
XX receptor related polypeptides. The polypeptides are useful in the
XX manufacture of a medicament for treating a syndrome associated with a
XX human disease, preferably a NOVX-associated disorder. The novel
XX polypeptides are useful for treating, preventing or diagnosing diseases,
XX such as metabolic disorders, diabetes, obesity, infectious diseases,
XX anorexia, cancer-associated diseases, neurodegenerative disorders,
XX Alzheimer's disease, Parkinson's disease, immune disorders, hematopoietic
XX disorders, and various dyslipidemias, metabolic disturbances associated
XX with obesity, metabolic X syndrome and wasting disorders associated
XX chronic diseases and various cancers. The nucleic acids and polypeptides
XX may also be used as targets for the identification of small molecules
XX that modulate or inhibit e.g. neurogenesis, cell differentiation, cell
XX proliferation, hematopoiesis, wound healing and angiogenesis, in gene
XX therapy, in generation of antibodies that bind immunospecifically to NOVX
XX substances for use in therapeutic or diagnostic methods. The nucleic
XX acids are further used as hybridization probes, in chromosome mapping,
XX tissue typing, preventive medicine, and pharmacogenomics. This sequence
XX represents one of the novel G-coupled protein receptor related
XX polypeptides of the invention.

CC therapy, in generation of antibodies that bind immunospecifically to NOVX
 CC substances for use in therapeutic or diagnostic methods. The nucleic
 CC acids are further used as hybridization probes, in chromosome mapping,
 CC tissue typing, preventive medicine, and pharmacogenomics. This sequence
 CC represents one of the novel G-coupled protein receptor related
 CC polypeptides of the invention.

XX Sequence 454 AA;

Query Match 100.0%; Score 292; DB 7; Length 454;

Best Local Similarity 100.0%; Pred. No. 2e-31; Indels 0; Gaps 0;
 Matches 54; Conservative 0; Mismatches 0;

Qy 1 MQEFFGLKVTGKDPDAETLKVMKQPCGVPDVAQFVLTEGNPRWEQHTLYRIEN 54

Db 50 MQEFFGLKVTGKDPDAETLKVMKQPCGVPDVAQFVLTEGNPRWEQHTLYRIEN 103

RESULT 7

ADL16006

ID ADE16006 standard; protein; 454 AA.

AC ADE16006;

XX

DT 29-JAN-2004 (first entry)

XX

DE G-coupled protein receptor related polypeptide, SEQ ID No 36.

XX

KW G-coupled protein receptor; anidiabetic; anorectic; antibacterial;

KW virucide; fungicide; cytostatic; nootropic; neuroprotective;

KW antiparkinsonian; haemostatic; antilipaeamic; neurogenesis;

KW cell differentiation; cell proliferation; hematopoiesis; wound healing;

KW angiogenesis; gene therapy; chromosome mapping; tissue typing;

KW preventive medicine; pharmacogenomics; human.

XX Homo sapiens.

OS

XX

PN WO200283841-A2.

XX

PD 24-OCT-2002.

XX

XX 03-APR-2002; 2002WO-US010713.

XX

PR 03-APR-2001; 2001US-0281136P.

PR 05-APR-2001; 2001US-0281863P.

PR 05-APR-2001; 2001US-0281906P.

PR 10-APR-2001; 2001US-0282934P.

PR 13-APR-2001; 2001US-0283657P.

PR 13-APR-2001; 2001US-0283678P.

PR 13-APR-2001; 2001US-0283687P.

PR 17-APR-2001; 2001US-0283710P.

PR 19-APR-2001; 2001US-0284234P.

PR 20-APR-2001; 2001US-0285325P.

PR 23-APR-2001; 2001US-0285609P.

PR 23-APR-2001; 2001US-0285748P.

PR 24-APR-2001; 2001US-0285890P.

PR 24-APR-2001; 2001US-0286068P.

PR 27-APR-2001; 2001US-0287213P.

PR 03-MAY-2001; 2001US-0288509P.

PR 30-MAY-2001; 2001US-0294495P.

PR 31-MAY-2001; 2001US-0294801P.

PR 31-JUL-2001; 2001US-0309216P.

PR 25-SEP-2001; 2001US-0324775P.

PR 28-NOV-2001; 2001US-0333908P.

PR 02-APR-2002; 2002US-00115479.

XX (CURA-) CURAGEN CORP.

XX

PI Li L, Gerlach V, Liu X, Miller CE, Spytek KA, Zerhusen BD;

PI Pena CE, Shenoy SG, Zhong H, Smithson G, Casman SJ, Boldog FL;

PI Voss EZ, Vernet CM, Macdougall JR, Rastelli L, Anderson DW;

PI Zhong M, Mezes PD, Furtak K, Patturajan M, Burgess CE, Malyankar UM;

PI Shinkets RA, Taupier RJ, Edinger SR, Mazur A;

PI

XX

DR WPI; 2003-067574/06.

DR N-PSDB; ADE16005.

XX

PT New isolated NOVX polypeptides and polynucleotides, useful for
 PT preventing, diagnosing or treating NOVX-associated disorders e.g.
 PT diabetes, obesity, dyslipidemias, cancer, Parkinson's disease,
 PT Alzheimer's disease, infections.

XX

PS Claim 1; SEQ ID NO 36; 320pp; English.

XX

CC The invention relates to a novel isolated G-coupled protein receptor
 CC related polypeptides. The novel polypeptide comprise any of the 22 fully
 CC defined sequences of 87-1780 amino acids, given in the specification;
 CC their mature forms; and possible variants. The novel polypeptides have
 CC the following activities: antidiabetic, anorectic, antibacterial,
 CC virucide, fungicide, cytostatic, nootropic, neuroprotective,
 CC antiparkinsonian, haemostatic, and antilipaeamic. The G-coupled protein
 CC receptor related polypeptides are useful in a method of treating or
 CC preventing in a human, a pathology associated with the G-coupled protein
 CC receptor related polypeptides. The polypeptides are useful in the
 CC manufacture of a medicament for treating a syndrome associated with a
 CC human disease, preferably a NOVX-associated disorder. The novel
 CC polypeptides are useful for treating, preventing or diagnosing diseases,
 CC such as metabolic disorders, diabetes, obesity, infectious diseases,
 CC anorexia, cancer-associated diseases, neurodegenerative disorders,
 CC Alzheimer's disease, Parkinson's disease, immune disorders, hematopoietic
 CC disorders, and various dyslipidemias, metabolic disturbances associated
 CC with obesity, metabolic X syndrome and wasting disorders associated with
 CC chronic diseases and various cancers. The nucleic acids and polypeptides
 CC may also be used as targets for the identification of small molecules
 CC that modulate or inhibit e.g. neurogenesis, cell differentiation, cell
 CC proliferation, hematopoiesis, wound healing and angiogenesis, in gene
 CC therapy, in generation of antibodies that bind immunospecifically to NOVX
 CC substances for use in therapeutic or diagnostic methods. The nucleic
 CC acids are further used as hybridization probes, in chromosome mapping,
 CC tissue typing, preventive medicine, and pharmacogenomics. This sequence
 CC represents one of the novel G-coupled protein receptor related
 CC polypeptides of the invention.

XX

SQ Sequence 454 AA;

XX

Query Match 100.0%; Score 292; DB 7; Length 454;

Best Local Similarity 100.0%; Pred. No. 2e-31;

Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQEFFGLKVTGKDPDAETLKVMKQPCGVPDVAQFVLTEGNPRWEQHTLYRIEN 54

Db 50 MQEFFGLKVTGKDPDAETLKVMKQPCGVPDVAQFVLTEGNPRWEQHTLYRIEN 103

RESULT 8

ADL93945

ID ADL93945 standard; protein; 454 AA.

XX

AC ADL93945;

XX

DT 20-MAY-2004 (first entry)

XX

DE Human G-coupled protein receptor-related protein #18.

XX

KW human; transgenic; Gene Therapy; Protein Therapy; cardiomyopathy;

KW atherosclerosis; hypertension; congenital heart defect; aortic stenosis;

KW atrial septal defect; atrioventricular canal defect; ductus arteriosus;

KW pulmonary stenosis; subaortic stenosis; ventricular septal defect;

KW valve disease; tuberosus sclerosis; scleroderma; obesity; transplantation;

KW adrenoleukodystrophy; congenital adrenal hyperplasia; prostate cancer;

KW neoplasia; adenocarcinoma; lymphoma; uterus cancer; fertility;

KW haemophilia; hypercoagulation; idiopathic thrombocytopenic purpura;

KW immunodeficiency; graft versus host disease; AIDS; bronchial asthma;

KW Crohn's disease; G-coupled protein receptor; metabolic disorder;

KW neurodegenerative disorder; receptor.

XX

PR 27-APR-2001; 2001US-0287213P.
PR 03-MAY-2001; 2001US-0288509P.
PR 30-MAY-2001; 2001US-0294495P.
PR 31-MAY-2001; 2001US-0294801P.
PR 31-JUL-2001; 2001US-0309216P.
PR 25-SEP-2001; 2001US-0324775P.
PR 28-NOV-2001; 2001US-0333900P.
XX
PA (LILL/) LI L.
PA (GERL/) GERLACH V.
PA (LIUX/) LIU X.
PA (MILL/) MILLER C E.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PENA/) PENNA C E A.
PA (SHEN/) SHENOY S G.
PA (ZHON/) ZHONG H.
PA (SMIT/) SMITHSON G.
PA (CASM/) CASMAN S J.
PA (BOLD/) BOLDOGF F L.
PA (VOSS/) VOSS E Z.
PA (VERN/) VERNET C A.
PA (MACD/) MACDOUGALL J R.
PA (RAST/) RASTELLI L.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (MEZE/) MEZES P S.
PA (FURT/) FURTA K.
PA (PATI/) PATTURAJAN M.
PA (BURG/) BURGESS C E.
PA (MALY/) MALYANKAR U M.
PA (SHIM/) SHIMKETS R A.
PA (TAUP/) TAUPIER R J.
PA (EDIN/) EDINGER S.
PA (MAZU/) MAZUR A.
XX
PI Li L, Gerlach V, Liu X, Miller CE, Spytek KA, Zerhusen BD;
PI Pena CER, Shenoy SG, Zhong H, Smithson G, Casman SJ, Boldog FL;
PI Voss EZ, Vernet CA, Macdougall JR, Rastelli L, Anderson DW, Zhong M;
PI Mezes PS, Furtak K, Patturajan M, Burgess CE, Malyankar UM;
PI Shinkets RA, Taupier RJ, Edinger S, Mazur A;
XX
XX WPI; 2004-224146/21.
DR N-PSDB; ADL93942.
XX
PT New G-coupled protein-receptor related polypeptides, for preventing
PT treating or ameliorating, e.g. acquired immunodeficiency syndrome,
PT bronchial asthma, Crohn's disease, prostate cancer, hemophilia,
PT scleroderma or obesity.
XX
PS Claim 1; Page 67; 220pp; English.
XX
CC The invention relates to isolated human G-coupled protein receptor-
CC related polypeptides and polynucleotides. The proteins are useful for
CC preventing, treating or ameliorating medical disorders by protein or gene
CC therapy. Disorders include cardiomyopathy, atherosclerosis, hypertension,
CC congenital heart defects, aortic stenosis, atrial septal defect,
CC atrioventricular canal defect, ductus arteriosus, pulmonary stenosis,
CC subaortic stenosis, ventricular septal defect, valve diseases, tuberos
CC sclerosis, scleroderma, obesity, transplantation, adrenoleukodystrophy,
CC congenital adrenal hyperplasia, prostate cancer, fertility, neoplasm,
CC adenocarcinoma, lymphoma, uterus cancer, cancer, hemophilia,
CC hypercoagulation, idiopathic thrombocytopenic purpura,
CC immunodeficiencies, graft versus host disease, AIDS, bronchial asthma,
CC metabolic disorders, neurodegenerative disorders or Crohn's disease. They
CC are also useful as diagnostic or research tools. The present sequence
CC represents a human G-coupled protein receptor-related protein of the
CC invention.
XX
SQ Sequence 454 AA;
Query Match 100.0%; Score 292; DB 8; Length 454;
Best Local Similarity 100.0%; Pred. No. 2e-31;

Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQEFGGLKVTGKPDATILKWKQPCGVPDVAQFVLTEGPRWEQTHLYRIEN 54
|||||
DB 50 MQEFGGLKVTGKPDATILKWKQPCGVPDVAQFVLTEGPRWEQTHLYRIEN 103
|||||
RESULT 10
ADL93941
ID ADL93941 standard; protein; 455 AA.
XX
AC ADL93941;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human G-coupled protein receptor-related protein #16.
XX
DE human; transgenic; Gene Therapy; Protein Therapy; cardiomyopathy;
KW atherosclerosis; hypertension; congenital heart defect; aortic stenosis;
KW atrial septal defect; atrioventricular canal defect; ductus arteriosus;
KW pulmonary stenosis; subaortic stenosis; ventricular septal defect;
KW valve disease; tuberos sclerosis; scleroderma; obesity; transplantation;
KW adrenoleukodystrophy; congenital adrenal hyperplasia; prostate cancer;
KW neoplasm; adenocarcinoma; lymphoma; uterus cancer; fertility;
KW haemophilia; hypercoagulation; idiopathic thrombocytopenic purpura;
KW immunodeficiency; graft versus host disease; AIDS; bronchial asthma;
KW Crohn's disease; G-coupled protein receptor; metabolic disorder;
KW neurodegenerative disorder; receptor.
XX
OS Homo sapiens.
OS
PN US2004006205-A1.
XX
PD 08-JAN-2004.
XX
PF 02-APR-2002; 2002US-00115479.
XX
PR 03-APR-2001; 2001US-0281136P.
PR 05-APR-2001; 2001US-0281863P.
PR 05-APR-2001; 2001US-0281906P.
PR 10-APR-2001; 2001US-0282934P.
PR 13-APR-2001; 2001US-0283657P.
PR 13-APR-2001; 2001US-0283678P.
PR 13-APR-2001; 2001US-0283687P.
PR 13-APR-2001; 2001US-0283710P.
PR 17-APR-2001; 2001US-0284234P.
PR 19-APR-2001; 2001US-0285325P.
PR 20-APR-2001; 2001US-0285609P.
PR 23-APR-2001; 2001US-0285748P.
PR 24-APR-2001; 2001US-0285890P.
PR 27-APR-2001; 2001US-0287213P.
PR 03-MAY-2001; 2001US-0288509P.
PR 30-MAY-2001; 2001US-0294495P.
PR 31-MAY-2001; 2001US-0294801P.
PR 31-JUL-2001; 2001US-0309216P.
PR 25-SEP-2001; 2001US-0324775P.
PR 28-NOV-2001; 2001US-0333900P.
XX
PA (LILL/) LI L.
PA (GERL/) GERLACH V.
PA (LIUX/) LIU X.
PA (MILL/) MILLER C E.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PENA/) PENNA C E A.
PA (SHEN/) SHENOY S G.
PA (ZHON/) ZHONG H.
PA (SMIT/) SMITHSON G.
PA (CASM/) CASMAN S J.
PA (BOLD/) BOLDOGF F L.
PA (VOSS/) VOSS E Z.
PA (VERN/) VERNET C A.

KW (MACD/) MACDOUGALL J R.
KW (RST/) RASTELLI L.
KW (ANDE/) ANDERSON D W.
XX (ZHON/) ZHONG M.
XX (MEZE/) MEZES P S.
XX (FURT/) FURTAK K.
XX (PATT/) PATTURAJAN M.
XX (BURG/) BURGESS C E.
XX (MALY/) MALYANKAR U M.
XX (SHIM/) SHIMKETS R A.
XX (TAUP/) TAUPIER R J.
XX (EDIN/) EDINGER S.
XX (MAZU/) MAZUR A.
XX Li L, Gerlach V, Liu X, Miller CE, Spytek KA, Zerkhusen BD;
PI Pena CEA, Shenoy SG, Zhong H, Smithson G, Casman SJ, Boldog FL;
PI Voss EZ, Vernet CA, Macdougall JR, Rastelli L, Anderson DW, Zhong M;
PI Mezes PS, Furtak K, Patturajan M, Burgess CE, Malyankar UM;
PI Shimkets RA, Taupier RJ, Edinger S, Mazur A;
XX WPI; 2004-224146/21.
DR N-PSDB; ADL93940.
XX
XX New G-coupled protein-receptor related polypeptides, for preventing
PT treating or ameliorating, e.g. acquired immunodeficiency syndrome,
PT bronchial asthma, Crohn's disease, prostate cancer, hemophilia,
PT scleroderma or obesity.
XX
XX Claim 1; Page 67; 220pp; English.
XX
XX The invention relates to isolated human G-coupled protein receptor-
CC related polypeptides and polynucleotides. The proteins are useful for
CC preventing, treating or ameliorating medical disorders by protein or gene
CC therapy. Disorders include cardiomyopathy, atherosclerosis, hypertension,
CC congenital heart defects, aortic stenosis, atrial septal defect,
CC atrioventricular canal defect, ductus arteriosus, pulmonary stenosis,
CC subaortic stenosis, ventricular septal defect, valve diseases, tuberos
CC sclerosis, scleroderma, obesity, transplantation, adrenoleukodystrophy,
CC congenital adrenal hyperplasia, prostate cancer, neoplasia,
CC adenocarcinoma, lymphoma, uterus cancer, fertility, haemophilia,
CC hypercoagulation, idiopathic thrombocytopenic purpura,
CC immunodeficiencies, graft versus host disease, AIDS, bronchial asthma,
CC metabolic disorders, neurodegenerative disorders or Crohn's disease. They
CC are also useful as diagnostic or research tools. The present sequence
CC represents a human G-coupled protein receptor-related protein of the
CC invention.
XX
XX Sequence 455 AA;
SQ
Query Match 100.0%; Score 292; DB 8; Length 455;
Best Local Similarity 100.0%; Pred. No. 2e-31;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 50 MQEFFGLKVTGKPDATLTKVMQKPRGCVDPDVAQFVLTGPNRWEQTHLYRIEN 103
RESULT 11
AAB84606
ID AAB84606 standard; protein; 469 AA.
XX
XX AAB84606;
XX
XX 05-SEP-2001 (first entry)
XX
XX Amino acid sequence of matrix metalloproteinase collagenase 1.
XX
XX Growth factor; protein inhibitor; protease; damaged tissue;
XX platelet-derived growth factor; PDGF; fibroblast growth factor; FGF;
XX connective tissue derived growth factor; CTGF; chrysalin; VEGF;
XX keratinocyte-derived growth factor; KGF; epidermal growth factor; EGF;
XX transforming growth factor-beta; TGF-beta; matrix metalloproteinase; MMP;

KW granulocyte macrophage colony stimulating factor; GM-CSF; uPA;
KW vascular endothelial growth factor; urokinase plasminogen activator;
KW dermal ulcer; wound.
XX Homo sapiens.
XX WO200149309-A2.
XX 12-JUL-2001.
XX 21-DEC-2000; 2000WO-1B001935.
XX 29-DEC-1999; 99GB-00030768.
XX (PFIZ) PFIZER LTD.
XX (PFIZ) PFIZER INC.
XX Davies MJ, Huggins JP, McIntosh FS, Occleston NL;
XX WPI; 2001-418351/44.
XX N-PSDB; AAH28221.
XX
XX Composition for the treatment of damaged tissue i.e. chronic wounds and
PT dermal ulcers comprises an inhibitor agent i.e. a protease and a growth
PT factor.
XX
XX Disclosure; Page 551; 572pp; English.
XX
XX The specification describes a pharmaceutical composition, comprising a
CC growth factor, an inhibitor agent, i.e. a protease. The inhibitor agent
CC inhibits the action of at least one specific adverse protein, i.e. a
CC protease, that is upregulated in a damaged tissue such as a wound
CC environment. Growth factors which are included in the composition of the
CC invention are platelet-derived growth factor (PDGF), fibroblast growth
CC factor (FGF), connective tissue derived growth factor (CTGF), transforming growth factor-beta
CC (TGF-beta), granulocyte macrophage colony stimulating factor (GM-CSF),
CC keratinocyte-derived growth factor (KGF), vascular endothelial growth factor (VEGF),
CC and chrysalin. Inhibitors which are included in the composition of the
CC invention include inhibitors of urokinase-type plasminogen activator
CC (uPA) and matrix metalloproteinase (MMP). The composition is useful for
CC the treatment of chronic damaged tissue, i.e. wounds and dermal ulcers.
CC The present sequence represents a human MMP-1, and is used to produce the
CC composition of the invention
XX
XX Sequence 469 AA;
SQ
Query Match 100.0%; Score 292; DB 4; Length 469;
Best Local Similarity 100.0%; Pred. No. 2.1e-31;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQEFFGLKVTGKPDATLTKVMQKPRGCVDPDVAQFVLTGPNRWEQTHLYRIEN 54
Db 67 MQEFFGLKVTGKPDATLTKVMQKPRGCVDPDVAQFVLTGPNRWEQTHLYRIEN 120
RESULT 12
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ID AAE10415 standard; protein; 469 AA.
XX
XX AAE10415;
XX
XX 10-DEC-2001 (first entry)
XX
XX Human matrix metalloproteinase-1 (MMP-1) protein.
XX
XX Human; matrix metalloproteinase; MMP-1; hair growth; antisense therapy;
XX endopeptidase; skin cell; breast cancer; hair follicle; chromosome 11q22.
XX Homo sapiens.
XX Key Location/Qualifiers
XX Peptide 1. .19
FT

PR 13-NOV-2001; 2001US-0350666P.
PR 08-FEB-2002; 2002US-0355145P.
PR 08-FEB-2002; 2002US-0355257P.
PR 12-APR-2002; 2002US-0372246P.
XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;
XX Zlotnik A;
XX WPI; 2003-354600/33.
XX N-PSDB; ACC72663.
XX New genes that are up-regulated or down-regulated in cancers, useful as
XX markers for diagnosing e.g. cancer, ischemia or heart diseases, or as
XX therapeutic targets for screening drugs for treating these diseases.
XX Claim 12; Page 735; 767pp; English.
XX The present invention describes an isolated nucleic acid molecule, which
XX comprises the sequence of any of the genes that are up-regulated or down-
XX regulated in specific cancers (e.g. about 1031 genes up-regulated in
XX acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer
XX related gene nucleotide sequences which encode the proteins given in
XX ABR58521 to ABR58709. Also described: (1) determining the presence or
XX absence of a pathological cell in a patient; (2) an expression vector
XX comprising a nucleic acid molecule described above; (3) a host cell
XX comprising the vector; (4) an isolated polypeptide, which is encoded by
XX the nucleic acid; (5) an antibody that specifically binds the polypeptide
XX of (4); (6) specifically targeting a compound to a pathological cell in a
XX patient by administering to the patient the antibody above; and (7) a
XX drug screening assay. The nucleic acid is useful as diagnostic markers or
XX therapeutic targets. In particular, the nucleic acid is useful for
XX diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,
XX bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,
XX pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases,
XX atherosclerosis and endometriosis. The nucleic acid is also useful in
XX drug screening, particularly for identifying agents for treating these
XX pathologies
XX SQ Sequence 469 AA;
Query Match 100.0%; Score 292; DB 6; Length 469;
Best Local Similarity 100.0%; Pred. No. 2.1e-31;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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PR 13-NOV-2001; 2001US-0350666P.
PR 08-FEB-2002; 2002US-0355145P.
PR 08-FEB-2002; 2002US-0355257P.
PR 12-APR-2002; 2002US-0372246P.
XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;
XX Zlotnik A;
XX WPI; 2003-354600/33.
XX N-PSDB; ACC72663.
XX New genes that are up-regulated or down-regulated in cancers, useful as
XX markers for diagnosing e.g. cancer, ischemia or heart diseases, or as
XX therapeutic targets for screening drugs for treating these diseases.
XX Claim 12; Page 735; 767pp; English.
XX The present invention describes an isolated nucleic acid molecule, which
XX comprises the sequence of any of the genes that are up-regulated or down-
XX regulated in specific cancers (e.g. about 1031 genes up-regulated in
XX acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer
XX related gene nucleotide sequences which encode the proteins given in
XX ABR58521 to ABR58709. Also described: (1) determining the presence or
XX absence of a pathological cell in a patient; (2) an expression vector
XX comprising a nucleic acid molecule described above; (3) a host cell
XX comprising the vector; (4) an isolated polypeptide, which is encoded by
XX the nucleic acid; (5) an antibody that specifically binds the polypeptide
XX of (4); (6) specifically targeting a compound to a pathological cell in a
XX patient by administering to the patient the antibody above; and (7) a
XX drug screening assay. The nucleic acid is useful as diagnostic markers or
XX therapeutic targets. In particular, the nucleic acid is useful for
XX diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,
XX bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,
XX pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases,
XX atherosclerosis and endometriosis. The nucleic acid is also useful in
XX drug screening, particularly for identifying agents for treating these
XX pathologies
XX SQ Sequence 469 AA;
Query Match 100.0%; Score 292; DB 6; Length 469;
Best Local Similarity 100.0%; Pred. No. 2.1e-31;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQEFFGLKVTGKPDATLTKVMKQPRCGVDPVDAQFVLTGPNRWEQTHLYRIEN 54
Db 67 MQEFFGLKVTGKPDATLTKVMKQPRCGVDPVDAQFVLTGPNRWEQTHLYRIEN 120
RESULT 15
ABR58542
ID ABR58542 standard; protein; 469 AA.
XX ABR58542;
XX ABR58542;
DT 09-JUL-2003 (first entry)
XX Human cancer related protein SEQ ID NO:199.
XX Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;
XX heart disease; atherosclerosis; endometriosis.
XX Homo sapiens.
XX WO2003025138-A2.
XX 27-MAR-2003.
XX 17-SEP-2002; 2002WO-US029560.
XX 17-SEP-2001; 2001US-0323469P.
PR

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Run on: October 13, 2004, 15:02:10 ; Search time 25.6154 Seconds
(without alignments)
139.806 Million cell updates/sec

Title: US-10-032-376A-9

Perfect score: 292

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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	292	100.0	469	3	US-08-704-711A-16
2	292	100.0	469	3	US-08-448-489-12
3	292	100.0	469	3	US-09-521-220-16
4	292	100.0	469	3	US-09-391-104-23
5	214	73.3	444	1	US-09-178-002-2
6	214	73.3	466	3	US-08-704-711A-17
7	214	73.3	466	3	US-09-521-220-17
8	214	73.3	467	1	US-09-178-002-4
9	214	73.3	467	3	US-09-391-104-24
10	214	73.3	468	3	US-08-448-489-13
11	189	64.7	476	3	US-08-704-711A-21
12	189	64.7	476	3	US-08-448-489-14
13	189	64.7	476	3	US-09-521-220-21
14	189	64.7	476	3	US-09-391-104-22
15	189	64.7	477	3	US-08-704-711A-20
16	189	64.7	477	3	US-08-448-489-15
17	189	64.7	477	3	US-08-281-313-1
18	189	64.7	477	3	US-09-521-220-20
19	189	64.7	477	3	US-09-391-104-21
20	163	55.8	471	3	US-09-391-104-25
21	163	55.8	513	4	US-10-140-002-192
22	163	55.8	513	4	US-09-862-631-4
23	159	54.5	470	3	US-08-068-392-2
24	159	54.5	470	3	US-08-398-988-2
25	159	54.5	470	3	US-09-391-104-26
26	158	54.1	663	4	US-09-194-468A-30
27	154	52.7	471	4	US-08-994-689C-1

28 151 51.7 264 3 US-09-009-156-6 Sequence 6, Appli
29 151 51.7 264 3 US-09-372-154-6 Sequence 6, Appli
30 151 51.7 267 3 US-08-448-489-18 Sequence 18, Appli
31 151 51.7 267 3 US-09-391-104-27 Sequence 27, Appli
32 151 51.7 271 3 US-08-896-062-2 Sequence 2, Appli
33 150 51.4 135 4 US-09-513-999C-4163 Sequence 4163, Ap
34 147 50.3 471 4 US-08-994-689C-21 Sequence 21, Appli
35 146.5 50.2 920 3 US-09-391-104-7 Sequence 7, Appli
36 144 49.3 462 3 US-08-068-392-3 Sequence 3, Appli
37 144 49.3 462 3 US-08-396-988-3 Sequence 3, Appli
38 144 49.3 631 3 US-08-448-489-17 Sequence 17, Appli
39 144 49.3 660 3 US-08-704-711A-18 Sequence 18, Appli
40 144 49.3 660 3 US-09-521-220-18 Sequence 18, Appli
41 144 49.3 660 3 US-09-391-104-19 Sequence 19, Appli
42 144 49.3 660 4 US-09-517-254-89 Sequence 89, Appli
43 136.5 46.7 604 3 US-09-391-104-30 Sequence 30, Appli
44 136.5 46.7 607 3 US-09-000-041A-2 Sequence 2, Appli
45 136.5 46.7 607 3 US-09-211-704A-10 Sequence 10, Appli

ALIGNMENTS

RESULT 1
US-08-704-711A-16
; Sequence 16, Application US/08704711A
; Patent No. 6114159
; GENERAL INFORMATION:
; APPLICANT: WILLS, Horst
; APPLICANT: HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,711A
; FILING DATE: 20-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/DE95/00357
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 469 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-704-711A-16

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QY 1 MOEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 54
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Db 67 MOEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 120
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RESULT 2
US-08-448-489-12
; Sequence 12, Application US/08448489
; Patent No. 6184022
; GENERAL INFORMATION:
; APPLICANT: SEIKI, Motoharu
; APPLICANT: SAITO, Hiroshi
; APPLICANT: SHINAGAWA, Akira
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
; FILE REFERENCE: 55-290P
; CURRENT APPLICATION NUMBER: US/08/448,489
; CURRENT FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 12
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Known Member of
; OTHER INFORMATION: Matrix Metalloproteinase Family
US-08-448-489-12

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Best Local Similarity 100.0%; Pred. No. 3.8e-31;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 67 MOEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 120
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RESULT 3
US-09-521-220-16
; Sequence 16, Application US/09521220
; Patent No. 6399348
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; APPLICANT: HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/521,220
; APPLICATION NUMBER: US/09/521,220
; FILING DATE: 08-Mar-2000
; CLASSIFICATION: <Unknown>
; 21-OCT-1994
; 17-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/704,711
; FILING DATE: <Unknown>
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APPLICATION NUMBER: DE 4438838.1
FILING DATE: 21-OCT-1994
APPLICATION NUMBER: DE 4409663.1
FILING DATE: 17-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 26083/124
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 469 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-521-220-16

Query Match      100.0%; Score 292; DB 3; Length 469;
Best Local Similarity 100.0%; Pred. No. 3.8e-31;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 54
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Db 67 MOEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 120
|||||

RESULT 4
US-09-391-104-23
; Sequence 23, Application US/09391104
; Patent No. 6399371
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Falduto, Michael T.
; APPLICANT: Magnuson, Scott R.
; APPLICANT: Morgan, Douglas W.
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEINASE GENE,
; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
; FILE REFERENCE: 6073.US.P1
; CURRENT APPLICATION NUMBER: US/09/391,104
; CURRENT FILING DATE: 1999-09-07
; PRIOR APPLICATION NUMBER: US 08/814,394
; PRIOR FILING DATE: 1997-03-11
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-391-104-23

Query Match      100.0%; Score 292; DB 3; Length 469;
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Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 67 MOEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 120
|||||

RESULT 5
US-09-178-002-2
; Sequence 2, Application US/09178002
; Patent No. H001973
; GENERAL INFORMATION:
; APPLICANT: Hu, Shou-Ih
; TITLE OF INVENTION: Human Neutrophil Collagenase Splice Variant
; FILE REFERENCE: CGC 2048
; CURRENT APPLICATION NUMBER: US/09/178,002
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; CURRENT FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-178-002-2

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RESULT 7
US-09-521-220-17
; Sequence 17, Application US/09521220
; Patent No. 6399348
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/521,220
; FILING DATE: 08-Mar-2000
; CLASSIFICATION: <Unknown>
; 21-OCT-1994
; 17-MAR-1994

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 06/704,711
; FILING DATE: <Unknown>
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 466 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-521-220-17

Query Match          73.3%; Score 214; DB 3; Length 466;
Best Local Similarity 70.4%; Pred. No. 1.3e-20;
Matches 38; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

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Db 66 MQRFFGLNVTGKPNNEETLDMKKPRCGVDPDGGFMLTPGNPKWERTNLTIRN 119

RESULT 8
US-09-178-002-4
; Sequence 4, Application US/09178002
; Patent No. H001973
; GENERAL INFORMATION:
; APPLICANT: Hu, Shou-Ih
; TITLE OF INVENTION: Human Neutrophil Collagenase Splice Variant
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; FILE REFERENCE: CGC 2048
; CURRENT APPLICATION NUMBER: US/09/178,002
; CURRENT FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-178-002-4

Query Match          73.3%; Score 214; DB 1; Length 467;
Best Local Similarity 70.4%; Pred. No. 1.3e-20;
Matches 38; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 MOEFFGLKVTGKPDAAETLKVMKQPCGVPDVAQFVLTGEGNPRWEQTHLYRIEN 54
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Db 66 MQRFFGLNVTGKPNETLDMKKKPCGVPDGGFMLTGCNPKWERTNLTIRN 119

RESULT 9
US-09-391-104-24
; Sequence 24, Application US/09391104
; Patent No. 639371
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Falduto, Michael T.
; APPLICANT: Magnuson, Scott R.
; APPLICANT: Morgan, Douglas W.
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,
; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
; TITLE OF INVENTION: OF USING SAME
; FILE REFERENCE: 6073.US.P1
; CURRENT APPLICATION NUMBER: US/09/391,104
; CURRENT FILING DATE: 1999-09-07
; PRIOR APPLICATION NUMBER: US 08/814,394
; PRIOR FILING DATE: 1997-03-11
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-391-104-24

Query Match          73.3%; Score 214; DB 3; Length 467;
Best Local Similarity 70.4%; Pred. No. 1.3e-20;
Matches 38; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

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Db 66 MQRFFGLNVTGKPNETLDMKKKPCGVPDGGFMLTGCNPKWERTNLTIRN 119

RESULT 10
US-08-448-489-13
; Sequence 13, Application US/08448489
; Patent No. 6184022
; GENERAL INFORMATION:
; APPLICANT: SEIKI, Motoharu
; APPLICANT: SATO, Hiroshi
; APPLICANT: SHINAGAWA, Akira
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
; FILE REFERENCE: 55-290P
; CURRENT APPLICATION NUMBER: US/08/448,489
; CURRENT FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 13
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:

; OTHER INFORMATION: X = UNKNOWN
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Known Member of
; OTHER INFORMATION: Matrix Metalloproteinase Family
US-08-448-489-13

Query Match          73.3%; Score 214; DB 3; Length 468;
Best Local Similarity 70.4%; Pred. No. 1.3e-20;
Matches 38; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

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Db 66 MQRFFGLNVTGKPNETLDMKKKPCGVPDGGFMLTGCNPKWERTNLTIRN 119

RESULT 11
US-08-704-711A-21
; Sequence 21, Application US/08704711A
; Patent No. 6114159
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; APPLICANT: HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,711A
; FILING DATE: 20-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: WO PCT/DE95/00357
; APPLICATION NUMBER:
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-704-711A-21

Query Match          64.7%; Score 189; DB 3; Length 476;
Best Local Similarity 63.0%; Pred. No. 3.2e-17;
Matches 34; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

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RESULT 12
US-08-448-489-14
; Sequence 14, Application US/08448489
; Patent No. 6184022
; GENERAL INFORMATION:
; APPLICANT: SEIKI, Motocharu
; APPLICANT: SATO, Hiroshi
; APPLICANT: SHINAGAWA, Akira
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
; FILE REFERENCE: 55-290P
; CURRENT APPLICATION NUMBER: US/08/448,489
; CURRENT FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 14
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Known Member of
; OTHER INFORMATION: Matrix Metalloproteinase Family
US-08-448-489-14

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Best Local Similarity 63.0%; Pred. No. 3.2e-17;
Matches 34; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

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RESULT 13
US-09-521-220-21
; Sequence 21, Application US/09521220
; Patent No. 6393348
; GENERAL INFORMATION:
; APPLICANT: HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/521,220
; FILING DATE: 08-Mar-2000
; CLASSIFICATION: <Unknown>
; 21-OCT-1994
; 17-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/704,711
; FILING DATE: <Unknown>
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124
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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-521-220-21

Query Match      64.7%; Score 189; DB 3; Length 476;
Best Local Similarity 63.0%; Pred. No. 3.2e-17;
Matches 34; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

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RESULT 14
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; Sequence 22, Application US/09391104
; Patent No. 6399371
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Faiduto, Michael T.
; APPLICANT: Magnuson, Scott R.
; APPLICANT: Morgan, Douglas W.
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE.
; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
; TITLE OF INVENTION: OF USING SAME
; FILE REFERENCE: 6073.US.P1
; CURRENT APPLICATION NUMBER: US/09/391,104
; CURRENT FILING DATE: 1999-09-07
; PRIOR APPLICATION NUMBER: US 08/814,394
; PRIOR FILING DATE: 1997-03-11
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-391-104-22

Query Match      64.7%; Score 189; DB 3; Length 476;
Best Local Similarity 63.0%; Pred. No. 3.2e-17;
Matches 34; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

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RESULT 15
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; Sequence 20, Application US/08704711A
; Patent No. 6114159
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; APPLICANT: HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
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us-10-032-376a-9.ra

Mon Nov 15 13:54:01 2004

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COMPUTER: IBM PC compatible
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SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/704,711A
FILING DATE: 20-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/DE95/00357
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4438838.1
FILING DATE: 21-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4409663.1
FILING DATE: 17-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 26083/124
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 477 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-704-711A-20

Query Match 64.7%; Score 189; DB 3; Length 477;
Best Local Similarity 63.0%; Pred. No. 3.2e-17;
Matches 34; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

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Search completed: October 13, 2004, 15:17:05
Job time : 26.6154 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 13, 2004, 15:14:50 ; Search time 76.8462 Seconds
(without alignments)
226.750 Million cell updates/sec

Title: US-10-032-376A-9

Perfect score: 292

Sequence: 1 MQEFGFKVTGKPDATLKV.....VLTEGNPRWEQTHLYRIEN 54

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Gapop 10.0 , Gapext 0.5

Searched: 1356558 seqs, 322682953 residues

Total number of hits satisfying chosen parameters: 1356558

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	292	100.0	54	US-10-153-185-9	Sequence 9, Appli
3	292	100.0	54	US-10-219-561-9	Sequence 9, Appli
4	292	100.0	54	US-10-032-376A-9	Sequence 9, Appli
5	292	100.0	54	US-10-335-207-9	Sequence 9, Appli
6	292	100.0	454	US-10-115-479-32	Sequence 32, Appl
7	292	100.0	454	US-10-115-479-34	Sequence 34, Appl
8	292	100.0	454	US-10-115-479-36	Sequence 36, Appl
9	292	100.0	454	US-10-115-479-38	Sequence 38, Appl
10	292	100.0	469	US-09-391-104-23	Sequence 23, Appl
11	292	100.0	469	US-09-801-196-19	Sequence 19, Appl
12	292	100.0	469	US-09-853-386-100	Sequence 100, App
13	292	100.0	469	US-10-301-822-119	Sequence 119, Appl
14	292	100.0	469	US-10-021-660-76	Sequence 76, Appl

15	292	100.0	469	14	US-10-308-279-34	Sequence 34, Appl
16	292	100.0	469	14	US-10-131-985-23	Sequence 23, Appl
17	292	100.0	469	14	US-10-295-027-12	Sequence 12, Appl
18	292	100.0	469	14	US-10-295-027-14	Sequence 14, Appl
19	292	100.0	469	14	US-10-295-027-1167	Sequence 1167, Ap
20	292	100.0	469	14	US-10-295-027-1168	Sequence 1168, Ap
21	292	100.0	469	15	US-10-115-479-30	Sequence 30, Appl
22	292	100.0	469	15	US-10-115-479-40	Sequence 40, Appl
23	292	100.0	469	15	US-10-211-462-22	Sequence 22, Appl
24	292	100.0	469	15	US-10-188-832-6	Sequence 6, Appli
25	292	100.0	469	16	US-10-734-564-109	Sequence 109, App
26	292	100.0	470	15	US-10-447-315-1	Sequence 1, Appli
27	292	100.0	495	14	US-10-106-698-6283	Sequence 6283, Ap
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29	233	79.8	43	14	US-10-153-185-17	Sequence 17, Appl
30	233	79.8	43	14	US-10-219-561-17	Sequence 17, Appl
31	233	79.8	43	16	US-10-032-376A-17	Sequence 17, Appl
32	233	79.8	43	16	US-10-335-207-17	Sequence 17, Appl
33	214	73.3	55	14	US-10-219-329-10	Sequence 10, Appl
34	214	73.3	55	14	US-10-153-185-10	Sequence 10, Appl
35	214	73.3	55	14	US-10-219-561-10	Sequence 10, Appl
36	214	73.3	55	16	US-10-032-376A-10	Sequence 10, Appl
37	214	73.3	467	9	US-09-391-104-24	Sequence 24, Appl
38	214	73.3	467	9	US-09-801-196-20	Sequence 20, Appl
39	214	73.3	467	10	US-09-759-130B-176	Sequence 176, App
40	214	73.3	467	14	US-10-131-985-31	Sequence 31, Appl
41	214	73.3	467	14	US-10-741-790-176	Sequence 176, App
42	200.5	68.7	267	14	US-10-133-797-73	Sequence 73, Appl
43	191	65.4	173	15	US-10-115-479-48	Sequence 48, Appl
44	190.5	65.2	325	15	US-10-115-479-78	Sequence 78, Appl

ALIGNMENTS

RESULT 1
US-10-219-329-9
; Sequence 9, Application US/10219329
; Publication No. US2003009675A1
; GENERAL INFORMATION:
; APPLICANT: Quirk, Stephen
; APPLICANT: Weart, Ilona f.
; TITLE OF INVENTION: Anti-Cancer and Wound Healing Compounds
; FILE REFERENCE: 1443.035WO1
; CURRENT APPLICATION NUMBER: US/10/219,329
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-219-329-9

Query Match 100.0%; Score 292; DB 14; Length 54;
Best Local Similarity 100.0%; Pred No. 3.8e-30;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MQEFGFKVTGKPDATLKVMPKQRCGVDPVAFVLTGPNRWEQTHLYRIEN 54

RESULT 2
US-10-153-185-9
; Sequence 9, Application US/10153185
; Publication No. US20030148959A1
; GENERAL INFORMATION:

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; APPLICANT: Quirk, Stephen
; APPLICANT: Malik, Sohal
; TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds
; FILE REFERENCE: 1443.034US1
; CURRENT APPLICATION NUMBER: US/10/153,185
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-185-9

Query Match      100.0%; Score 292; DB 14; Length 54;
Best Local Similarity 100.0%; Pred. No. 3.8e-30;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-10-219-561-9
; Sequence 9, Application US/10219561
; Publication No. US20030166567A1
; GENERAL INFORMATION:
; APPLICANT: Quirk, Stephen
; APPLICANT: Malik, Sohal
; APPLICANT: Villanueva, Julie M.
; TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds
; FILE REFERENCE: 1443.008US2
; CURRENT APPLICATION NUMBER: US/10/219,561
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 10/153,185
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-219-561-9

Query Match      100.0%; Score 292; DB 14; Length 54;
Best Local Similarity 100.0%; Pred. No. 3.8e-30;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
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; Sequence 9, Application US/10032376A
; Publication No. US20040127420A1
; GENERAL INFORMATION:
; APPLICANT: Quirk, Steven
; TITLE OF INVENTION: Metalloproteinase Inhibitors for Wound Healing
; FILE REFERENCE: 1443.008US1
; CURRENT APPLICATION NUMBER: US/10/032,376A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/312,726

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; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 20
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; SEQ ID NO 9
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-376A-9

Query Match      100.0%; Score 292; DB 16; Length 54;
Best Local Similarity 100.0%; Pred. No. 3.8e-30;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 54
Db 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 54

RESULT 5
US-10-335-207-9
; Sequence 9, Application US/10335207
; Publication No. US20040127421A1
; GENERAL INFORMATION:
; APPLICANT: Malik, Sohal
; APPLICANT: Quirk, Stephen
; TITLE OF INVENTION: Method to Increase Fibronectin
; FILE REFERENCE: 1443.047US1
; CURRENT APPLICATION NUMBER: US/10/335,207
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-335-207-9

Query Match      100.0%; Score 292; DB 16; Length 54;
Best Local Similarity 100.0%; Pred. No. 3.8e-30;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 54
Db 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 54

RESULT 6
US-10-115-479-32
; Sequence 32, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glendda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.

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APPLICANT: Malyanker, Uriel M.
APPLICANT: Shimkets, Richard A.
APPLICANT: Taupier, Raymond J.
APPLICANT: Edinger, Shlomit R.
APPLICANT: Mazur, Ann
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REFERENCE: 21402-322 B (Cura 622 PT)
CURRENT APPLICATION NUMBER: US/10/115,479
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: 60/281,136
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/281,863
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/281,906
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/282,934
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: 60/283,657
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/283,678
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/283,687
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/283,710
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/284,234
PRIOR FILING DATE: 2001-04-17
PRIOR APPLICATION NUMBER: 60/285,325
PRIOR FILING DATE: 2001-04-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 198
SEQ ID NO 32
LENGTH: 454
TYPE: PRT
ORGANISM: Homo sapiens
US-10-115-479-32

Query Match 100.0%; Score 292; DB 15; Length 454;
Best Local Similarity 100.0%; Pred. No. 4.3e-29;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MQEFFGLKVTGKPDATLKVMPKPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54
DB 50 MQEFFGLKVTGKPDATLKVMPKPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 103

RESULT 7
US-10-115-479-34
Sequence 34, Application US/10115479
Publication No. US20040006205A1
GENERAL INFORMATION:
APPLICANT: Li, Li
APPLICANT: Gerlach, Valerie L.
APPLICANT: Liu, Xiaohong
APPLICANT: Miller, Charles E.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Zerhusen, Bryan D.
APPLICANT: Pena, Carol E.A.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Zhong, Haihong
APPLICANT: Smithson, Glenda
APPLICANT: Casman, Stacie J.
APPLICANT: Boldog, Ferenc L.;
APPLICANT: Voss, Edward
APPLICANT: Vernet, Corine
APPLICANT: MacDougall, John A.
APPLICANT: Rastelli, Luca
APPLICANT: Anderson, David W.
APPLICANT: Zhong, Mei
APPLICANT: Mezes, Peter S.
APPLICANT: Furtak, Katarzyna
APPLICANT: Patturajan, Meera
APPLICANT: Burgess, Catherine E.

APPLICANT: Malyanker, Uriel M.
APPLICANT: Shimkets, Richard A.
APPLICANT: Taupier, Raymond J.
APPLICANT: Edinger, Shlomit R.
APPLICANT: Mazur, Ann
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REFERENCE: 21402-322 B (Cura 622 PT)
CURRENT APPLICATION NUMBER: US/10/115,479
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: 60/281,136
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/281,863
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/281,906
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/282,934
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: 60/283,657
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/283,678
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/283,687
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/283,710
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/284,234
PRIOR FILING DATE: 2001-04-17
PRIOR APPLICATION NUMBER: 60/285,325
PRIOR FILING DATE: 2001-04-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 198
SEQ ID NO 34
LENGTH: 454
TYPE: PRT
ORGANISM: Homo sapiens
US-10-115-479-34

Query Match 100.0%; Score 292; DB 15; Length 454;
Best Local Similarity 100.0%; Pred. No. 4.3e-29;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MQEFFGLKVTGKPDATLKVMPKPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54
DB 50 MQEFFGLKVTGKPDATLKVMPKPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 103

RESULT 8
US-10-115-479-36
Sequence 36, Application US/10115479
Publication No. US20040006205A1
GENERAL INFORMATION:
APPLICANT: Li, Li
APPLICANT: Gerlach, Valerie L.
APPLICANT: Liu, Xiaohong
APPLICANT: Miller, Charles E.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Zerhusen, Bryan D.
APPLICANT: Pena, Carol E.A.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Zhong, Haihong
APPLICANT: Smithson, Glenda
APPLICANT: Casman, Stacie J.
APPLICANT: Boldog, Ferenc L.;
APPLICANT: Voss, Edward
APPLICANT: Vernet, Corine
APPLICANT: MacDougall, John A.
APPLICANT: Rastelli, Luca
APPLICANT: Anderson, David W.
APPLICANT: Zhong, Mei
APPLICANT: Mezes, Peter S.
APPLICANT: Furtak, Katarzyna
APPLICANT: Patturajan, Meera
APPLICANT: Burgess, Catherine E.

```
; APPLICANT: Malyanker, Uriel M.
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 36
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-115-479-36

Query Match 100.0%; Score 292; DB 15; Length 454;
Best Local Similarity 100.0%; Pred. No. 4.3e-29;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQEFGKLVTKGPDATLTKVMKQPCGVPDVAQFVLTEGPRWEQTHLYRIEN 54
Db 50 MQEFGKLVTKGPDATLTKVMKQPCGVPDVAQFVLTEGPRWEQTHLYRIEN 103

RESULT 9
US-10-115-479-38
; Sequence 38, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zernhusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glenda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
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; APPLICANT: Malyanker, Uriel M.
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 38
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-115-479-38

Query Match 100.0%; Score 292; DB 15; Length 454;
Best Local Similarity 100.0%; Pred. No. 4.3e-29;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQEFGKLVTKGPDATLTKVMKQPCGVPDVAQFVLTEGPRWEQTHLYRIEN 54
Db 50 MQEFGKLVTKGPDATLTKVMKQPCGVPDVAQFVLTEGPRWEQTHLYRIEN 103

RESULT 10
US-09-391-104-23
; Sequence 23, Application US/09391104
; Publication No. US20020031817A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Falduto, Michael T.
; APPLICANT: Magnuson, Scott R.
; APPLICANT: Morgan, Douglas W.
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE.
; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
; FILE REFERENCE: 6073.US.P1
; CURRENT APPLICATION NUMBER: US/09/391,104
; CURRENT FILING DATE: 1999-09-07
; PRIOR APPLICATION NUMBER: US 08/814,394
; PRIOR FILING DATE: 1997-03-11
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-391-104-23

Query Match 100.0%; Score 292; DB 9; Length 469;
Best Local Similarity 100.0%; Pred. No. 4.5e-29;
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RESULT 13
US-10-301-822-119

QY 1 MQEFGGLKVTGKPDATLKWVKQRCGVPDVAQFVLTEGNPRWEQTHLTYRIEN 54

Db 67 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLTTRYIEN 120

RESULT 15
 US-10-308-279-34
 ; Sequence 34, Application US/10308279
 ; Publication No. US20030170742A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bristol-Myers Squibb Company
 ; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE DEVELOPMENT
 ; FILE REFERENCE: D0190 NP
 ; CURRENT APPLICATION NUMBER: US/10/308,279
 ; PRIOR FILING DATE: 2002-12-03
 ; PRIOR APPLICATION NUMBER: 60/337,429
 ; PRIOR FILING DATE: 2001-12-03
 ; NUMBER OF SEQ ID NOS: 91
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 34
 ; LENGTH: 469
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 US-10-308-279-34

Query Match 100.0%; Score 292; DB 14; Length 469;
 Best Local Similarity 100.0%; Pred. No. 4.5e-29;
 Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLTTRYIEN 54
 Db 67 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLTTRYIEN 120

Search completed: October 13, 2004, 15:35:40
 Job time : 77.8462 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 13, 2004, 15:01:19 ; Search time 20.4231 Seconds
(without alignments)
254.404 Million cell updates/sec

Title: US-10-032-376A-9
Perfect score: 292
Sequence: 1 MQEFFGLKVTGRPDASTLKV.....VLTEGNPRWEQTHLYRIEN 54

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR,79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	292	100.0	469	1 KCHUI	interstitial colla
2	283	96.9	468	1 KCRBI	interstitial colla
3	270	92.5	459	1 KCPGI	interstitial colla
4	234	80.1	459	1 KCB01	interstitial colla
5	231.5	79.3	384	2 I51267	collagenase (EC 3.1.1.1)
6	214	73.3	467	1 KCHUN	neutrophil collage
7	189	64.7	476	1 KCHUS2	stromelysin 2 (EC 3.4.21.2)
8	189	64.7	477	1 KCHUS1	stromelysin 1 (EC 3.4.21.2)
9	186	63.7	478	1 KCRBS1	stromelysin 1 (EC 3.4.21.2)
10	173	59.2	476	1 JC6505	stromelysin 1 (EC 3.4.21.2)
11	173	59.2	477	1 KCMSS1	stromelysin 1 (EC 3.4.21.2)
12	172	58.9	475	1 KCRTH1	stromelysin 1 (EC 3.4.21.2)
13	172	58.9	483	2 JC5743	matrix metallopro
14	168	57.5	472	2 S29240	interstitial colla
15	167	57.2	476	1 KCRTS2	stromelysin 2 (EC 3.4.21.2)
16	163	55.8	471	2 A53711	collagenase 3 (EC 3.4.21.2)
17	162	55.5	466	2 A23685	interstitial colla
18	159	54.5	470	2 A49499	metalloelastase
19	158	54.1	663	1 S46492	gelatinase A (EC 3.4.21.2)
20	155	53.1	287	2 A57490	gelatinase A (EC 3.4.21.2)
21	151	51.7	267	1 KCHUM	gelatinase A (EC 3.4.21.2)
22	146	50.0	662	2 S70365	gelatinase A (EC 3.4.21.2)
23	144	49.3	462	2 A42401	macrophage elastas
24	144	49.3	660	1 A28153	gelatinase A (EC 3.4.21.2)
25	144	49.3	662	2 A42496	gelatinase A (EC 3.4.21.2)
26	144	49.3	662	2 S34780	gelatinase A (EC 3.4.21.2)
27	135	46.2	708	2 S62507	gelatinase B (EC 3.4.21.2)
28	134.5	46.1	582	2 I38028	matrix metallopro
29	133	45.5	708	2 JC4364	gelatinase B (EC 3.4.21.2)

30	132	45.2	707	1 A34458	gelatinase B (EC 3.4.21.2)
31	130	44.5	707	1 A53796	gelatinase B (EC 3.4.21.2)
32	126.5	43.3	582	2 I84471	matrix metallopro
33	126.5	43.3	669	2 I38029	matrix metallopro
34	126	43.2	712	1 I46031	gelatinase B (EC 3.4.21.2)
35	124	42.5	82	2 PWC052	pro-matrix metallo
36	120.5	41.3	730	1 I52580	gelatinase B (EC 3.4.21.2)
37	120.5	41.3	730	2 JCI456	gelatinase B (EC 3.4.21.2)
38	118.5	40.6	582	2 I48673	matrix metallopro
39	111	38.0	364	2 E71433	probable metallopr
40	108	37.0	341	2 T51957	metalloproteinase
41	108	37.0	342	2 G84885	probable metallopr
42	106.5	36.5	305	2 T08836	probable metallopr
43	103.5	35.4	579	2 T37248	probable matrix me
44	103.5	35.4	598	2 T32166	hypothetical prote
45	100	34.2	521	2 T37252	probable matrix me

ALIGNMENTS

RESULT 1

KCHUI

interstitial collagenase (EC 3.4.24.7) precursor [validated] - human

N:Alternate names: fibroblast collagenase; matrix metalloproteinase 1 (MMP1); tissue co

C:Species: Homo sapiens (man)

C>Date: 13-Aug-1986 #sequence revision 30-Sep-1992 #text change 09-Jul-2004

C:Accession: A37308; S22766; I57620; A00996; D29157; A44518; S06132; B60964; S10595; S5

R:Templeton, N.S.; Brown, P.D.; Levy, A.T.; Margulies, I.M.K.; Liotta, L.A.; Stettler-St

Cancer Res. 50, 5431-5437, 1990

A:Title: Cloning and characterization of human synovial cell collagenase and selection of a single

A:Reference number: A37308; MUID:90352587; PMID:2167156

A:Accession: A37308

A:Molecule type: mRNA

A:Residues: 1-469 <TEM>

A:Cross-references: UNIPROT:P03956; GB:X54925; NID:G30125; PIDN:CAA38691.1; PID:G30126

R:Brinckerhoff, C.E.; Ruby, P.L.; Austin, S.D.; Fini, M.E.; White, H.D.

J. Clin. Invest. 79, 542-546, 1987

A:Title: Molecular cloning of human synovial cell collagenase and selection of a single

A:Reference number: S22766; MUID:87103799; PMID:3027129

A:Accession: S22766

A:Molecule type: DNA

A:Residues: 1-63,65-70 <BRI>

A:Cross-references: EMBL:M15996; NID:G180666; PIDN:AAA35700.1; PID:G180667

R:Angel, P.; Baumann, I.; Stein, B.; Dellus, H.; Rahmsdorf, H.J.; Herrlich, P.

Mol. Cell. Biol. 7, 2256-2266, 1987

A:Title: 12-O-tetradecanoyl-phorbol-13-acetate induction of the human collagenase gene

A:Reference number: I57620; MUID:87257941; PMID:3037355

A:Accession: I57620

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-35 <RES>

A:Cross-references: GB:M16567; NID:G180668; PIDN:AAA52033.1; PID:G180669

R:Goldberg, G.I.; Wilhelm, S.M.; Kronberger, A.; Bauer, E.A.; Grant, G.A.; Eisen, A.Z.

J. Biol. Chem. 261, 6600-6605, 1986

A:Title: Human fibroblast collagenase. Complete primary structure and homology to an on

A:Reference number: A00996; MUID:86196089; PMID:3009463

A:Accession: A00996

A:Molecule type: mRNA

A:Residues: 1-114, 'R', 116-409, 'S', 411-469 <COL>

A:Cross-references: GB:M13509; NID:G180664; PIDN:AAA35699.1; PID:G180665

R:Whitham, S.E.; Murphy, G.; Angel, P.; Rahmsdorf, H.J.; Smith, B.J.; Lyons, A.; Harris

Biochem. J. 240, 913-916, 1986

A:Title: Comparison of human stromelysin and collagenase by cloning and sequence analys

A:Reference number: A90336; MUID:87156645; PMID:3030290

A:Accession: D29157

A:Molecule type: mRNA

A:Residues: 1-199, 'H', 201-207, 'T', 209-469 <WHI>

A:Cross-references: EMBL:X05231; NID:G38266; PIDN:CAA38858.1; PID:G38267

A:Note: parts of this sequence, including the amino end of the proenzyme and of the mat

R:Birkedal-Hansen, B.; Moore, W.G.I.; Taylor, R.E.; Bown, A.S.; Birkedal-Hansen, H.

Biochemistry 27, 6751-6758, 1988

Best Local Similarity 100.0%; Pred. No.2.8e-28;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOEFFGLKVTGKPDATLTKWKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54
DB 67 MOEFFGLKVTGKPDATLTKWKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 120

RESULT 2

KCRBI
Interstitial collagenase (EC 3.4.24.7) precursor - rabbit
N/Alternate names: fibroblast collagenase; matrix metalloproteinase 1 (MMP1); tissue col
lagenase
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text_change 09-Jul-2004
C/Accession: A27500; D27500; I46694
R/Finl, M.E.; Plucinska, I.M.; Mayer, A.S.; Gross, R.H.; Brinckerhoff, C.E.
Biochemistry 26, 6156-6165, 1987
A/Title: A gene for rabbit synovial cell collagenase: member of a family of metalloprote
inases
A/Reference number: A27500; MUID:88077876; PMID:2825772
A/Accession: A27500
A/Molecule type: mRNA
A/Residues: 1-468 <FIN>
A/Cross-references: UNIPROT:P13943; GB:M19240
A/Accession: B27500
A/Molecule type: DNA
A/Residues: 1-391;399-468 <FI2>
A/Cross-references: GB:M17820
A/Note: the location of the intron between exons 7 and 8 is approximate
R/Finl, M.E.; Austin, S.D.; Holt, P.T.; Ruby, P.L.; Gross, R.H.; White, H.D.; Brinckerho
ff, C.E.; Relat. Res. 6, 239-248, 1986
A/Title: Homology between exon-containing portions of rabbit genomic clones for synovial
cell peptidase
A/Reference number: I46694; MUID:87029174; PMID:3021384
A/Accession: I46694
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 449-468 <FI3>
A/Cross-references: GB:M25663; MUID:G531211; PIDN:AAA31203.1; PID:G531212
C/Comment: This enzyme cleaves collagens of types I, II, and III at a Gly-Ile site in th
e activation peptide
C/Comment: Procollagenase can be activated without removal of the activation peptide. SE
ction peptide by other proteinases.
C/Comment: Procollagenase is found in glycosylated and unglycosylated forms, both of whi
ch are active.
C/Genetics: 34/3, 116/2, 166/1, 208/1, 260/1, 299/2, 344/1, 398/1, 433/1
A/Introns: 34/3, 116/2, 166/1, 208/1, 260/1, 299/2, 344/1, 398/1, 433/1
C/Function:
A/Description: hydrolyzes collagens, in particular types I, II, III, and X, serpins, and
C/Suprafamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotei
nase
C/Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo
proteinase
F/1-18/Domain: signal sequence #status predicted <SIG>
F/19-468/Product: procollagenase #status predicted <PRO>
F/19-98/Domain: activation peptide #status predicted <ACT>
F/59-260/Domain: matrix metalloproteinase homology <MMP>
F/89-96/Region: autoinhibitory
F/99-468/Product: interstitial collagenase #status predicted <MAT>
F/971-465/Domain: hemopexin repeat homology <PXN>
F/91, 217, 221, 227/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status
predicted
F/119, 142/Binding site: carbohydrate (Asn) (covalent) #status predicted
F/217, 221, 227/Binding site: zinc, catalytic (His) (active) #status predicted
F/218/Active site: Glu #status predicted
F/277-465/Disulfide bonds: #status predicted

Query Match 96.9%; Score 283; DB 1; Length 468;
Best Local Similarity 96.3%; Pred. No. 3.6e-27;
Matches 52; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MOEFFGLKVTGKPDATLTKWKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54
DB 66 MOEFFGLKVTGKPDATLTKWKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 119

RESULT 3

KCFGI
Interstitial collagenase (EC 3.4.24.7) precursor [validated]. pig
N/Alternate names: fibroblast collagenase; matrix metalloproteinase 1 (MMP1); tissue col
lagenase

C;Species: Sus scrofa domestica (domestic pig)
 C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
 C;Accession: S15986; S153597
 C;Comment: This enzyme cleaves collagens of types I, II, and III at a Gly-Ile site in the Matrix II, 161-167, 1991
 A;Title: Porcine collagenase from synovial fibroblasts: cDNA sequence and modulation of A;Reference number: S15986; MUID:91333421; PMID:1651440
 A;Status: not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-469 <RIC>
 A;Cross-references: UNIPROT:P21692
 A;Note: part of the sequence, including the amino end of the proenzyme, was confirmed by R;Clarke, N.J.; O'Hare, M.C.; Cawston, T.E.; Harper, G.P.
 Nucleic Acids Res. 18, 6703, 1990
 A;Title: Nucleotide sequence of a cDNA for porcine type I collagenase, obtained by PCR. A;Reference number: S15597; MUID:91067477; PMID:2174547
 A;Accession: S15597
 A;Molecule type: mRNA
 A;Residues: 25-469 <CLA>
 A;Cross-references: EMBL:X54724; NID:g2016; PIDN:CAA38526.1; PID:g930269
 Submitted to the Brookhaven Protein Data Bank, April 1995
 R;Li, J.; Brick, P.; Blow, D.M.
 A;Reference number: A65568; PDB:1FBL
 A;Content: annotation; X-ray crystallography, 2.5 angstroms, residues 100-466
 C;Comment: Procollagenase can be activated without removal of the activation peptide. S tion peptide by other proteinases.
 C;Comment: Procollagenase is found in glycosylated and unglycosylated forms, both of which C;Function:
 A;Description: hydrolyzes collagens, in particular types I, II, III, and X, serpins, and A;Note: also hydrolyzes type X collagen, serpins, and alpha-macroglobulins
 C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotease C;Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallopro F;1-19/Domain: signal sequence #status predicted <SIG>
 F;20-469/Product: procollagenase #status predicted <PRO>
 F;20-99/Domain: activation peptide #status experimental <ACT>
 F;60-261/Domain: matrix metalloproteinase homology <MMP>
 F;100-469/Product: interstitial collagenase #status predicted <MAT>
 F;272-466/Domain: hemopexin repeat homology <PXN>
 F;92,218,222,228/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status F;120,143/Binding site: carboxylate (Asn) (covalent) #status predicted
 F;218,222,228/Binding site: zinc, catalytic (His) (active) #status experimental
 F;219/Active site: Glu #status predicted
 F;278-466/Disulfide bonds: #status experimental

Query Match 92.5%; Score 270; DB 1; Length 469;
 Best Local Similarity 90.7%; Pred. No. 1.5e-25;
 Matches 49; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MQEFGKLVTKGKPAETLVKMKQPCGVPDVAQFVLTEGPNRWEQTHLYRIEN 54
 DB 67 MQQFFGLKVTGKPAETLVKMKQPCGVPDVAEFVLTGPNRWENTHLYRIEN 120

RESULT 4
 KCBOI
 Interstitial collagenase (EC 3.4.24.7) precursor - bovine
 N;Alternate names: fibroblast collagenase; matrix metalloproteinase 1 (MMP1); tissue col C;Species: Bos primigenius taurus (cattle)
 C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
 C;Accession: S14654; S20336; S14655
 R;Tamura, M.; Shimokawa, H.; Sasaki, S.
 submitted to the EMBL Data Library, March 1991
 A;Reference number: S14654
 A;Accession: S14654
 A;Molecule type: mRNA
 A;Residues: 1-469 <TAM>
 A;Cross-references: UNIPROT:P28053; EMBL:X58256; NID:g259; PIDN:CAA41210.1; PID:g260 R;Sudbeck, B.D.; Jeffrey, J.J.; Welgus, H.G.; Mecham, R.P.; McCourt, D.; Parks, W.C. Arch. Biochem. Biophys. 293, 370-376, 1992
 A;Title: Purification and characterization of bovine interstitial collagenase and tissue A;Reference number: S20336; MUID:92161820; PMID:1311165
 A;Accession: S20336

A;Molecule type: protein
 A;Residues: 19-21, 'FP', 24-29, 'L', 31-34, 'LL', 37-39, 'F', 86-105, 'NPR', 109-112, 'D', 114-125
 C;Comment: This enzyme cleaves collagens of types I, II, and III at a Gly-Ile site in t C;Comment: Procollagenase can be activated without removal of the activation peptide. S tion peptide by other proteinases.
 C;Comment: Procollagenase is found in glycosylated and unglycosylated forms, both of wh C;Function:
 A;Description: hydrolyzes collagens, in particular types I, II, III, and X, serpins, an A;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotease C;Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo F;1-18/Domain: signal sequence #status predicted <SIG>
 F;19-469/Product: procollagenase #status predicted <PRO>
 F;19-99/Domain: activation peptide #status predicted <ACT>
 F;60-261/Domain: matrix metalloproteinase homology <MMP>
 F;90-97/Region: autoinhibitory
 F;100-469/Product: interstitial collagenase #status predicted <MAT>
 F;272-466/Domain: hemopexin repeat homology <PXN>
 F;92,218,222,228/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status F;120,143/Binding site: carboxylate (Asn) (covalent) #status predicted
 F;218,222,228/Binding site: zinc, catalytic (His) (active) #status predicted
 F;219/Active site: Glu #status predicted
 F;278-466/Disulfide bonds: #status predicted

Query Match 80.1%; Score 234; DB 1; Length 469;
 Best Local Similarity 81.5%; Pred. No. 4.2e-21;
 Matches 44; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 MQEFGKLVTKGKPAETLVKMKQPCGVPDVAQFVLTEGPNRWEQTHLYRIEN 54
 DB 67 MQEFGKLVTKGKPAETLVKMKQPCGVPDVAEPVLTGKSCWENTLTYRIEN 120

RESULT 5
 I51267
 collagenase (EC 3.4.24.-) - bullfrog
 C;Species: Rana catesbeiana (bullfrog)
 C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
 C;Accession: I51267
 R;Corruga, K.; Yomori, S.; Yoshizato, K.
 Int. J. Dev. Biol. 38, 345-350, 1994
 A;Title: Regionally and hormonally regulated expression of genes of collagen and collag A;Reference number: I51267; MUID:95071832; PMID:7981043
 A;Accession: I51267
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-384 <OOP>
 A;Cross-references: UNIPROT:Q11133; GB:S75623; NID:g913070; PIDN:AAB32661.1; PID:g91307 C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotease C;Keywords: hydrolase; metalloproteinase; zinc; zymogen
 F;53-231/Domain: matrix metalloproteinase homology <MMP>
 F;236-381/Domain: hemopexin repeat homology <PXN>
 F;81,189,193,199/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status F;189,193,199/Binding site: zinc, catalytic (His) (active) #status predicted
 F;190/Active site: Glu #status predicted

Query Match 79.3%; Score 231.5; DB 2; Length 384;
 Best Local Similarity 79.6%; Pred. No. 6.9e-21;
 Matches 43; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

QY 1 MQEFGKLVTKGKPAETLVKMKQPCGVPDVAQFVLTEGPNRWEQTHLYRIEN 54
 DB 57 LKQFFGLKVTGKPAETLVKMKQTCGVPDVGXYLTPGNRWENTHLYRIEN 109

RESULT 6
 KCHUN
 neutrophil collagenase (EC 3.4.24.34) precursor [validated] - human
 N;Alternate names: matrix metalloproteinase 8
 C;Species: Homo sapiens (man)
 C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
 A;Title: Purification and characterization of bovine interstitial collagenase and tissue R;Hasty, K.A.; Pourmotabbed, T.F.; Goldberg, G.I.; Thompson, J.P.; Spinella, D.G.; Stev J. Biol. Chem. 265, 11421-11424, 1990

R;Title: Human neutrophil collagenase. A distinct gene product with homology to other matrix metalloproteinases.
 A;Reference number: A37073; MUID:90307647; PMID:2164002
 A;Accession: A37073
 A;Molecule type: mRNA
 A;Residues: 1-467 <HAS>
 A;Cross-references: UNIPROT:P22894; GB:J05556; NID:G180617; PIDN:AAA88021.1; PID:G180618
 R;Devarajan, P.; Mookhtiar, K.; Van Wart, H.; Berliner, N.
 Blood 77, 2731-2738, 1991
 A;Title: Structure and expression of the cDNA encoding human neutrophil collagenase.
 A;Reference number: A61175; MUID:91255696; PMID:1646048
 A;Accession: A61175
 A;Status: not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-31, 'I', 33-86, 'E', 88-467 <DEV>
 A;Accession: B61175
 A;Molecule type: protein
 A;Residues: 263-264, 'X', 266-270, 'X', 272-273, 'X', 275, 'X', 277 <DE2>
 R;Malliyil, S.K.; Mookhtiar, K.A.; Gao, Y.; Brew, K.; Dioszegi, M.; Birkedal-Hansen, H.; V.
 Biochemistry 29, 10628-10634, 1990
 A;Title: Characterization and activation of procollagenase from human polymorphonuclear
 A;Reference number: S09680; MUID:90249372; PMID:2159879
 A;Accession: S09680
 A;Molecule type: protein
 A;Residues: 21-31, 'I', 33-39, 'I', 41-47, 'V', 49-53, 'I', 55-72, 'G', 74-86, 'E', 88-111, 'X', 113-119
 A;Note: 67-Lys was also found
 R;Knaeuper, V.; Kraemer, S.; Reinke, H.; Tschesche, H.
 Biol. Chem. Hoppe-Seyler 371, 733, 1990
 A;Title: Corrigendum. Partial amino-acid sequence of human PMN leukocyte procollagenase.
 A;Reference number: S11026; MUID:91000455; PMID:2169766
 A;Note: Original publication was Biol. Chem. Hoppe-Seyler 371 (Suppl.), 295-304, 1990
 A;Accession: S11026
 A;Molecule type: protein
 A;Residues: 21-31, 'I', 33-53, 'I', 55-72, 'G', 74-111, 'X', 113-140; 183-203, 'X', 205-209; 248-261
 A;Note: 87-Glu was also found
 R;Blaeser, J.; Knaeuper, V.; Osthus, A.; Reinke, H.; Tschesche, H.
 Eur. J. Biochem. 202, 1223-1230, 1991
 A;Title: Mercurial activation of human polymorphonuclear leucocyte procollagenase.
 A;Reference number: S19576; MUID:92111500; PMID:1662606
 A;Accession: S19576
 A;Molecule type: protein
 A;Residues: 69-103 <BL>
 R;Blaeser, J.; Triebel, S.; Reinke, H.; Tschesche, H.
 FEBS Lett. 313, 59-61, 1992
 A;Title: Formation of a covalent Hg-Cys-bond during mercurial activation of PMNL procollagenase.
 A;Reference number: S27225; MUID:93050220; PMID:1330697
 A;Accession: S27225
 A;Molecule type: protein
 A;Residues: 68-103 <BL>
 R;Knaeuper, V.; Osthus, A.; DeClerck, Y.A.; Langley, K.E.; Blaeser, J.; Tschesche, H.
 Biochem. J. 291, 847-854, 1993
 A;Title: Fragmentation of human polymorphonuclear-leucocyte collagenase.
 A;Reference number: S32527; MUID:93256897; PMID:8489511
 A;Accession: S32527
 A;Molecule type: protein
 A;Residues: 100-112; 263-276 <KN3>
 R;Knaeuper, V.; Murphy, G.; Tschesche, H.
 Eur. J. Biochem. 235, 187-191, 1996
 A;Title: Activation of human neutrophil procollagenase by stromelysin 2.
 A;Reference number: S62608; MUID:96202934; PMID:8631328
 A;Accession: S62608
 A;Molecule type: protein
 A;Residues: 21-39, 'I', 41-47, 'V', 49-122 <KN4>
 R;Stams, T.; Spurlino, J.C.; Smith, D.L.; Rubin, B.
 Submitted to the Brookhaven Protein Data Bank, January 1994
 A;Reference number: A67078; PDB:1MNC
 A;Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 'G', 106-149, 'G', 1

R;Stams, T.; Spurlino, J.C.; Smith, D.L.; Wahl, R.C.; Ho, T.F.; Qoronfleh, M.W.; Banks, Nat. Struct. Biol. 1, 119-123, 1994
 A;Title: Structure of human neutrophil collagenase reveals large S1' specificity pocket.
 A;Reference number: A58274; MUID:95384762; PMID:7656015
 A;Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 'G', 106-149, 'G', 1
 C;Comment: This protein is more highly glycosylated than interstitial collagenase and is C;Genetics:
 A;Gene: GDB:MMP8; CLG1
 A;Cross-references: GDB:128173; OMIM:120355
 A;Map position: 11q22.2-11q22.3
 C;Function:
 A;Description: hydrolyzes collagen types I, II, and III at Gly-Ile sites in collagenous
 A;Note: cleaves type I collagen most rapidly
 C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloproteinase
 C;Keywords: calcium; extracellular matrix; glycoprotein; hydrolase; metalloproteinase; n
 F;1-20/Domain: signal sequence #status predicted <SIG>
 F;21-467/Product: procollagenase #status predicted <PRO>
 F;21-100/Domain: activation peptide #status experimental <ACT>
 F;59-263/Domain: matrix metalloproteinase homology <MMP>
 F;89-96/Region: autoinhibitory
 F;101-467/Product: neutrophil collagenase #status predicted <MAT>
 F;273-464/Domain: hemopexin repeat homology <PXN>
 F;54-73, 112, 119, 204, 246/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;73-74/Cleavage site: Asp-Val (autolytic) #status experimental
 F;84-85/Cleavage site: Asp-Met (autolytic) #status experimental
 F;91-217, 221-227/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
 F;99-100/Cleavage site: Phe-Met (autolytic) #status experimental
 F;167, 169, 182, 195/Binding site: zinc, noncatalytic (His, Asp, His, His) #status experime
 F;174, 175, 177, 179, 197, 200/Binding site: calcium (Asp, Gly, Asn, Ile, Asp, Glu) #status e
 F;217, 221, 227/Binding site: zinc, catalytic (His) (active) #status experimental
 F;218/Active site: Glu #status predicted
 F;262-263/Cleavage site: Gly-Leu (autolytic) #status experimental
 F;279-464/Disulfide bonds: #status predicted
 Query Match 73.3%; Score 214; DB 1; Length 467;
 Best Local Similarity 70.4%; Pred. No. 1.2e-18;
 Matches 38; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
 QY 1 MQSFGLKVTGKPDASTLKMVKPCGVPDVAQFVLTEGPNRWEOPHLTYRIEN 54
 Db 66 MQRFGLNVTGKPNETLDMVKPCGVPDVGSGFMTLPNGKERTNLTIRRN 119
 RESULT 7
 KCHUS2
 stromelysin 2 (EC 3.4.24.22) precursor [validated] - human
 N;Alternate names: matrix metalloproteinase 10 (MMP10); transin-2
 C;Species: Homo sapiens (man)
 C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
 C;Accession: A28816; A47496
 R;Muller, D.; Quantin, B.; Gesnel, M.C.; Millon-Collard, R.; Abecassis, J.; Breathnach, Biochem. J. 253, 187-192, 1988
 A;Title: The collagenase gene family in humans consists of at least four members.
 A;Reference number: A90339; MUID:86339885; PMID:2844164
 A;Accession: A28816
 A;Molecule type: mRNA
 A;Residues: 1-476 <NUL>
 A;Cross-references: UNIPROT:P09238; EMBL:X07820; NID:G36628; PIDN:CAA30679.1; PID:G36629
 A;Note: mRNA for this protein was detected in several human tumors
 R;Windsor, L.J.; Grenett, H.; Birkedal-Hansen, B.; Bodden, M.K.; Engler, J.A.; Birkedal-J. Biol. Chem. 268, 17341-17347, 1993
 A;Title: Cell type-specific regulation of SL-1 and SL-2 genes. Induction of the SL-2 gen
 A;Reference number: A47496; MUID:93352520; PMID:8349617
 A;Accession: A47496
 A;Molecule type: protein
 A;Residues: 17-33 <WIN>
 C;Comment: This enzyme degrades various extracellular matrix proteins, including fibron
 C;Genetics:
 A;Gene: GDB:MMP10; STMY2
 A;Cross-references: GDB:120392; OMIM:185260
 A;Map position: 11q22.3-11q23
 C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotein
 C;Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo

Biochemistry 37, 4699-4702, 1998
A;Title: Generation of an angiotensin-like fragment from plasminogen by stromelysin-1 (A;Reference number: A59812; PMID:9548733; PMID:9548733
A;Contents: annotation
R;Becker, J.W.
submitted to the Brookhaven Protein Data Bank, February 1997
A;Reference number: A69466; PDB:1HFS
A;Contents: annotation; X-ray crystallography, 1.70 angstroms, residues 105-160
R;Becker, J.W.; Marcy, A.I.; Rokosz, L.L.; Axel, M.G.; Burbaum, J.J.; Fitzgerald, P.M.D.
Protein Sci. 4, 1966-1976, 1995
A;Title: Stromelysin-1: three-dimensional structure of the inhibited catalytic domain and
A;Reference number: A59814; PMID:96117647; PMID:8535233
A;Contents: annotation; X-ray crystallography, 1.70 angstroms
R;Marcy, A.I.; Elberger, L.L.; Harrison, R.; Chan, H.K.; Hutchinson, N.I.; Hagmann, W.K.; Es
Biochemistry 30, 6476-6483, 1991
A;Title: Human fibroblast stromelysin catalytic domain: expression, purification, and c
A;Reference number: A39569; PMID:91274298; PMID:1647201
A;Contents: annotation
R;Becker, J.W.
submitted to the Brookhaven Protein Data Bank, August 1995
A;Reference number: A66637; PDB:1SLM
A;Contents: annotation; X-ray crystallography, 1.90 angstroms, residues 33-47;57-267
R;Gooley, P.R.; O'connell, J.F.
submitted to the Brookhaven Protein Data Bank, March 1995
A;Reference number: A67284; PDB:2SRT
A;Contents: annotation; conformation by (1)H-NMR, residues 100-272
R;Gooley, P.R.; Johnson, B.A.; Marcy, A.I.; Cuca, G.C.; Salowe, S.P.; Hagmann, W.K.; Es
Biochemistry 32, 13998-14008, 1993
A;Title: Secondary structure and zinc ligation of human recombinant short-form stromely
A;Reference number: A59815; PMID:94059987; PMID:8241164
A;Contents: annotation; conformation by (1)H-NMR
C;Comment: Stromelysin 1 activates its proenzyme after cleavage(s) within the activation
C;Comment: Stromelysin 1 is found in glycosylated and unglycosylated forms, both of wh
C;Genes: MMP3; STMY; STMY1
A;Cross-references: GDB:120727; OMIM:185250
A;Map position: 11q23-11q23
C;Function:
A;Description: endopeptidase preferentially hydrolyzing peptide bonds on the carboxyl s
A;Note: degrades various extracellular matrix proteins, including fibronectin, plasmin
plasminogen to yield a fragment with angiostatin activity
C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprote
C;Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-477/Product: prostromelysin 1 #status experimental <PRO>
F;18-99/Domain: activation peptide #status experimental <ACT>
F;60-264/Domain: matrix metalloproteinase homology <MMP>
F;100-477/Product: stromelysin 1 #status experimental <MAT>
F;284-477/Domain: hemopexin repeat homology <PXN>
F;92,218,222,228/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status
F;120/Binding site: carbonyl (Asn) (covalent) #status predicted
F;218,222,228/Binding site: zinc, catalytic (His) (active) #status experimental
F;219/Active site: Glu #status predicted
F;230-477/Disulfide bonds: #status predicted

Query Match 64.7%; Score 189; DB 1; Length 477;
Best Local Similarity 63.0%; Pred. No. 1.6e-15;
Matches 34; Conservative 9; Mismatches 11; Indels 0; Gaps 0;
QY 1 MQEFFGLKVTKGDKDAETLKVMKPRCGVDPVAFVLTEGNPRMQTHLTYYRIEN 54
DB 67 MQKFLGLEVTGKLDSDTLEWKRRCGVDPVGHRTFPGIPKWRKTHLYRIVN 120

RESULT 9
KCRBS1
stromelysin 1 (EC 3.4.24.17) precursor - rabbit
N;Alternate names: collagenase activating protein; matrix metalloproteinase 3 (MMP3); p
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
C;Accession: A37306; A29157
R;Finzi, M.E.; Karmilowicz, M.J.; Ruby, P.L.; Beeman, A.M.; Borges, K.A.; Brinckerhoff,
Arthritis Rheum. 30, 1254-1264, 1987

RESULT 12

KCRTH

stromelysin 1 (EC 3.4.24.17) precursor - rat
N:Alternate names: collagenase activating protein; matrix metalloproteinase 3 (MMP3); pro-
C:Species: Rattus norvegicus (Norway rat)
C:Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 09-Jul-2004
R:Accession: A00997; PS0150; S22767
R:Matrisian, L.M.; Glaichenhaus, N.; Gesnel, M.C.; Breathnach, R.
EMBO J. 4, 1435-1440, 1985
A:Title: Epidermal growth factor and oncogenes induce transcription of the same cellular
A:Reference number: A00997; MUID:85284930; PMID:3875482
A:Accession: A00997
A:Molecule type: mRNA
A:Residues: 1-475 <MAT>
A:Cross-references: UNIPROT:P03957; GB:X02601; NID:957460; PIDN:CAA26448.1; PID:G57461
R:Umenishi, F.; Yasumitsu, H.; Ahsida, Y.; Yamauti, J.; Umeda, M.; Miyazaki, K.
J. Biochem. 108, 537-543, 1990
A:Title: Purification and properties of extracellular matrix-degrading metallo-proteinase
A:Reference number: PS0150; MUID:91154156; PMID:1963430
A:Accession: PS0150
A:Molecule type: protein
A:Residues: 19-20,'X',22-28;110-112,'X',114-115,'X',117,'X',119;309-325 <UME>
R:Breathnach, R.; Matrisian, L.M.; Gesnel, M.C.; Staub, A.; Leroy, P.
Nucleic Acids Res. 15, 1139-1151, 1987
A:Title: Sequences coding for part of oncogene-induced transin are highly conserved in a
A:Reference number: A26403; MUID:87146421; PMID:3547333
A:Contents: annotation; introns
A:Note: Intron positions were determined by comparison of the previously reported cDNA s
R:Sanchez-Lopez, R.; Nicholson, R.; Gesnel, M.C.; Matrisian, L.M.; Breathnach, R.
J. Biol. Chem. 263, 11892-11899, 1988
A:Title: Structure-function relationships in the collagenase family member transin.
A:Reference number: S22767; MUID:8829869; PMID:2841336
A:Contents: annotation; active site; activation
A:Note: molecules with mutations in the autoinhibitory region showed a much increased te
A:Note: mutations of His-216, Glu-217, and His-226 inactivate the enzyme
R:Park, A.J.; Matrisian, L.M.; Kells, A.F.; Pearson, R.; Yuan, Z.; Navre, M.
J. Biol. Chem. 266, 1584-1590, 1991
A:Title: Mutational analysis of the transin (rat stromelysin) autoinhibitor region demon
A:Reference number: A43028; MUID:91107652; PMID:1988438
A:Contents: annotation; autoinhibitory region
A:Note: Arg-89 and Cys-92 are essential for maintaining latency
C:Comment: This enzyme degrades various extracellular matrix proteins, including fibron
C:Comment: Stromelysin 1 hydrolyzes peptide bonds in plasminogen to yield a fragment wi
C:Comment: Stromelysin 1 activates its proenzyme after cleavage(s) within the activation
C:Comment: Prostromelysin is found in glycosylated and unglycosylated forms, both of whi
C:Genetics:
A:Introns: 33/3; 115/2; 165/1; 207/1; 262/1; 310/2; 355/1; 408/2; 443/1
A:Function:
A:Description: endopeptidase preferentially hydrolyzing peptide bonds on the carboxyl si
C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metallopro
C:Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-475/Product: prostromelysin 1 #status predicted <PRO>
F:18-97/Domain: activation peptide #status predicted <ACT>
F:58-262/Domain: matrix metalloproteinase homology <MMP>
F:88-95/Region: autoinhibitory
F:98-475/Product: stromelysin 1 #status predicted <MAT>
F:282-475/Domain: hemopexin repeat homology <PXN>
F:90,216,220,226/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status
F:118/Binding site: carboxylate (Asn) (covalent) #status predicted
F:216,220,226/Binding site: zinc, catalytic (His) (active) #status predicted
F:217/Active site: Glu #status experimental
F:288-475/Disulfide bonds: #status predicted

Query Match 58.9%; Score 172; DB 1; Length 475;
Best Local Similarity 53.7%; Pred. No. 2e-13;
Matches 29; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

Qy 1 MQEFGFKVTGKPDATLTKVWKQPCGVDVAQFVLTEGNPRWEQTHLYRIEN 54

Db 65 MQKFLGLKVTGKLDNTMLMHRKPCGVDVGFTFGSPKPKKNHISYRIVN 118

RESULT 13

JCS743

matrix metalloproteinase (EC 3.4.24.-) precursor - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 09-Dec-1997 #sequence_revision 23-Jan-1998 #text_change 09-Jul-2004
R:Accession: JCS743
R:Bartlett, J.D.; Simmer, J.P.; Xue, J.; Margolis, H.C.; Moreno, E.C.
Gene 183, 123-128, 1996
A:Title: Molecular cloning and mRNA tissue distribution of a novel matrix metalloprotei
A:Reference number: JCS743; MUID:97149288; PMID:8996096
A:Accession: JCS743
A:Molecule type: mRNA
A:Residues: 1-483 <BAR>
A:Cross-references: UNIPROT:P79287; GB:U54825; NID:G1800212; PIDN:BA841396.1; PID:G1800
C:Experimental source: enamel organ
C:Comment: This enzyme plays a role in enamel biomineralization and development.
C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprote
C:Keywords: hydrolase; metalloproteinase; zinc
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-483/Product: matrix metalloproteinase #status predicted <MAT>
F:68-271/Domain: matrix metalloproteinase homology <MMP>
F:290-483/Domain: hemopexin repeat homology <PXN>
F:100,226,230,236/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status
F:226,230,236/Binding site: zinc, catalytic (His) #status predicted
F:227/Active site: Glu #status predicted
Query Match 58.9%; Score 172; DB 2; Length 483;
Best Local Similarity 59.6%; Pred. No. 2e-13;
Matches 31; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

Qy 1 MQEFGFKVTGKPDATLTKVWKQPCGVDVAQFVLTEGNPRWEQTHLYRIEN 52

Db 75 LQAFGLGLRVTKGLDRTMDVIKRCGCPDVAQFVLTEGNPRWEQTHLYRIEN 126

RESULT 14

S29243

interstitial collagenase (EC 3.4.24.7) precursor - mouse
N:Alternate names: matrix metalloproteinase 1 (MMP1)
C:Species: Mus musculus (house mouse)
C:Date: 22-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
R:Accession: S29243
R:Henriët, P.; Rousseau, G.G.; Beckhout, Y.
FEBS Lett. 310, 175-178, 1992
A:Title: Cloning and sequencing of mouse collagenase cDNA. Divergence of mouse and rat
A:Reference number: S29243; MUID:93011910; PMID:11383028
A:Accession: S29243
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-472 <HEN>
C:Cross-references: UNIPROT:P33435; EMBL:X66473; NID:G53603; PIDN:CAA47102.1; PID:G5360
C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprote
C:Keywords: hydrolase; metalloproteinase; zinc; zymogen
F:65-266/Domain: matrix metalloproteinase homology <MMP>
F:279-472/Domain: hemopexin repeat homology <PXN>
F:97,223,227,233/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status
F:223,227,233/Binding site: zinc, catalytic (His) (active) #status predicted
F:224/Active site: Glu #status predicted

Query Match 57.5%; Score 168; DB 2; Length 472;
Best Local Similarity 57.4%; Pred. No. 6.2e-13;
Matches 31; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

Qy 1 MQEFGFKVTGKPDATLTKVWKQPCGVDVAQFVLTEGNPRWEQTHLYRIEN 54

Db 72 MQSFFGLGVTKGLDPTDLMRXRCGCPDVAQFVLTEGNPRWEQTHLYRIEN 125

RESULT 15

KCRYS2

stromelysin 2 (EC 3.4.24.22) precursor - rat

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 13, 2004, 15:00:44 ; Search time 110.769 Seconds
(without alignments)
280.495 Million cell updates/sec

Title: US-10-032-376A-9

Perfect score: 292

Sequence: 1 MQEFFGLKVTGKPDATLKV.....VLTEGNPRWEQHLTYRIEN 54

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 02:*

1: uniprot_prot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	292	100.0	469	1 MM01_HUMAN	P03956 homo sapien
2	292	100.0	469	2 AAP3520	AAP3520 homo sapi
3	283	96.9	468	1 MM01_RABIT	P13943 oryctolagus
4	279	95.5	469	1 MM01_HORSE	Q9X825 equus caball
5	270	92.5	469	1 MM01_PIG	P21692 sus scrofa
6	234	80.1	469	1 MM01_BOVIN	P28053 bos taurus
7	231.5	79.3	384	1 MM01_RANCA	Q11133 rana catesb
8	214	73.3	467	1 MM08_HUMAN	P22894 homo sapien
9	204	69.9	205	2 Q810Z2	Q810Z2 mus musculu
10	204	69.9	463	2 Q9EPL6	Q9EPL6 mus musculu
11	204	69.9	464	2 Q9EPL5	Q9EPL5 mus musculu
12	196	67.1	466	1 MM08_RAT	O88766 rattus norv
13	189	64.7	476	1 MM10_HUMAN	P09238 homo sapien
14	189	64.7	476	2 AAP36110	AAP36110 homo sapi
15	189	64.7	477	1 MM03_HUMAN	P08254 homo sapien
16	189	64.7	477	2 AAH63676	AAH63676 homo sapi
17	189	64.7	477	2 AAH69716	AAH69716 homo sapi
18	189	64.7	478	2 Q6Y4Q5	Q6Y4Q5 canis fami
19	189	64.7	478	2 AAQ63580	AAQ63580 canis fam
20	186	63.7	145	2 Q9N283	Q9N283 bos taurus
21	186	63.7	393	2 Q8MI18	Q8MI18 felis silve
22	186	63.7	478	1 MM03_RABIT	P28863 oryctolagus
23	184	63.0	252	2 Q6FWQ3	Q6FWQ3 xenopus lae
24	184	63.0	252	2 AAT00547	AAT00547 xenopus l
25	184	63.0	259	2 Q7ZT19	Q7ZT19 xenopus lae
26	183	62.7	472	2 Q93342	Q93342 gallus gall
27	183	62.7	477	1 MM03_HORSE	Q28397 equus caball
28	181	62.0	466	2 Q7SYX1	Q7SYX1 xenopus lae
29	180	61.6	269	2 Q7SZT5	Q7SZT5 xenopus lae
30	179	61.3	458	2 Q6DCN8	Q6DCN8 xenopus lae
31	178	61.0	258	2 Q7SZS8	Q7SZS8 xenopus lae

32	178	61.0	259	2 Q6DF35	Q6DF35 xenopus tro
33	178	61.0	481	1 MM20_BOVIN	O18767 bos taurus
34	176	60.3	465	2 Q8C209	Q8C209 mus musculu
35	176	60.3	465	2 Q8C230	Q8C230 mus musculu
36	176	60.3	465	2 AAH42742	AAH42742 mus muscu
37	176	60.3	465	2 BAC40805	BAC40805 mus muscu
38	176	60.3	471	1 MM13_RABIT	O52806 oryctolagus
39	174	59.6	167	2 Q7ZWD0	Q7ZWD0 brachydanio
40	174	59.6	482	1 MM20_MOUSE	P57748 mus musculu
41	173	59.2	476	1 MM10_MOUSE	O55123 mus musculu
42	173	59.2	477	1 MM03_MOUSE	P28862 mus musculu
43	173	59.2	479	2 Q922W6	Q922W6 mus musculu
44	172	58.9	475	1 MM03_RAT	P03957 rattus norv
45	172	58.9	483	1 MM20_HUMAN	O50882 homo sapien

ALIGNMENTS

RESULT 1
MM01_HUMAN STANDARD; PRT; 469 AA.
AC P03956; P08156;
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Interstitial collagenase precursor (EC 3.4.24.7) (Matrix metalloproteinase-1) (MMP-1) (Fibroblast collagenase).
GN Name=MMP1; Synonyms=CLG;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RX SEQUENCE FROM N.A.
RA MEDLINE=90352587; PubMed=2167156;
RA Templeton N.S., Brown P.D., Levy A.T., Margulies I.M.K., Liotta L.A., Stetler-Stevenson W.G.;
RT "Cloning and characterization of human tumor cell interstitial collagenase."
RL Cancer Res. 50:5431-5437(1990).
RN [2]
RX SEQUENCE FROM N.A.
RA MEDLINE=87156645; PubMed=3030290;
RA Whitham S.E., Murphy G., Angel P., Rahmsdorf H.J., Smith B., Lyons A., Harris T.J.R., Reynolds J.J., Herrlich P., Docherty A.J.P.;
RT "Comparison of human stromelysin and collagenase by cloning and sequence analysis."
RL Biochem. J. 240:913-916(1986).
RN [3]
RX SEQUENCE FROM N.A.
RA MEDLINE=86196089; PubMed=3009463;
RA Goldberg G.I., Wilhelm S.M., Kronberger A., Bauer E.A., Grant G.A., Eisen A.Z.;
RT "Human fibroblast collagenase. Complete primary structure and homology to an oncogene transformation-induced rat protein."
RL J. Biol. Chem. 261:6600-6605(1986).
RN [4]
RX SEQUENCE FROM N.A.
RA Lin D., Duncan M., Allen E., Araujo R., Aparicio A., Chai A., Chung E., Davis K., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lashkari D., Lew H., Namath A., Oefner P., Roberts D., Heller R., Davis R.W.;
RT Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
RN [5]
RX SEQUENCE FROM N.A.
RA Tissue=Ovary;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.T., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [16]
RN SEQUENCE OF 1-35 FROM N.A.
RP MEDLINE=87257941; PubMed=3037355;
RA Angel P., Baumann I., Stein B., Delius H., Rahmsdorf H.J.,
RA Herrlich P.,
RT "12-O-tetradecanoyl-phorbol-13-acetate induction of the human
RT collagenase gene is mediated by an inducible enhancer element located
RT in the 5'-flanking region.";
RL Mol. Cell. Biol. 7:2256-2266 (1987).
RN [7]
RN SEQUENCE OF 1-70 FROM N.A.
RP TISSUE=Synovial cell.
RX MEDLINE=87109799; PubMed=3027129;
RA Brinckerhoff C.E., Ruby P.L., Ausin S.D., Fini M.E., White H.D.,
RT "Molecular cloning of human synovial cell collagenase and selection of
RT a single gene from genomic DNA.";
RL J. Clin. Invest. 79:542-546 (1987).
RN [8]
RN SEQUENCE OF 100-112 AND 270-287.
RP TISSUE=Fibroblast;
RX MEDLINE=90104231; PubMed=2557822;
RA Clark I.M., Cawston T.E.,
RT "Fragments of human fibroblast collagenase. Purification and
RT characterization.";
RL Biochem. J. 263:201-206 (1989).
RN [9]
RN SIMILARITY TO THERMOLYSIN TYPE PROTEASES.
RP MEDLINE=87194799; PubMed=3032950;
RA McKerrow J.H.,
RT "Human fibroblast collagenase contains an amino acid sequence
RT homologous to the zinc-binding site of Serratia protease.";
RL J. Biol. Chem. 262:5943-5943 (1987).
RN [10]
RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 100-269.
RX MEDLINE=95394760; PubMed=7656013;
RA Borkakoti N., Winkler F.K., Williams D.H., D'Arcy A., Broadhurst M.J.,
RA Brown P.A., Johnson W.H., Murray E.J.,
RT "Structure of the catalytic domain of human fibroblast collagenase
RT complexed with an inhibitor.";
RL Nat. Struct. Biol. 1:106-110 (1994).
RN [11]
RN X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 102-269.
RX MEDLINE=94304829; PubMed=8031754;
RA Lovejoy B., Hassell A.M., Luther M.A., Weigl D., Jordan S.R.,
RT "Crystal structures of recombinant 19-kDa human fibroblast collagenase
RT complexed to itself.";
RL Biochemistry 33:8207-8217 (1994).
RN [12]
RN X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 102-269.
RX MEDLINE=94105765; PubMed=8278810;
RA Lovejoy B., Cleasby A., Hassell A.M., Longley K., Luther M.A.,
RA Weigl D., McGeehan G., McElroy A.B., Drewry D., Lambert M.H.,
RA Jordan S.R.,
RT "Structure of the catalytic domain of fibroblast collagenase complexed
RT with an inhibitor.";
RL Science 263:375-377 (1994).
RN [13]
RN X-RAY CRYSTALLOGRAPHY (1.56 ANGSTROMS) OF 101-269.

RX MEDLINE=94377426; PubMed=8090713;
RA Spurlino J.C., Smallwood A.M., Carlton D.D., Banks T.M., Vavra K.J.,
RA Johnson J.S., Cook E.R., Falvo J., Wahl R.C., Pulvino T.A., Et A.L.,
RT "1.56-A structure of mature truncated human fibroblast collagenase.";
RL Proteins 19:98-109 (1994).
RN [14]
RN STRUCTURE BY NMR OF 101-269.
RX MEDLINE=98145213; PubMed=9484219;
RA Moy F.J., Chanda P.K., Cosmi S., Pisano M.R., Urbano C., Wilhelm J.,
RA Powers R.,
RT "High-resolution solution structure of the inhibitor-free catalytic
RT fragment of human fibroblast collagenase determined by
RT multidimensional NMR.";
RL Biochemistry 37:1495-1504 (1998).
CC -I- FUNCTION: Cleaves collagens of types I, II, and III at one site in
CC the helical domain. Also cleaves collagens of types VII and X.
CC -I- CATALYTIC ACTIVITY: Cleaves preferentially one bond in native
CC collagen. Cleavage of the triple helix of collagen at about three-
CC quarters of the length of the molecule from the N-terminus, at
CC 775-Gly-|-Ile-776 in the alpha-1(I) chain. Cleaves synthetic
CC substrates and alpha-macroglobulins at bonds where p1' is a
CC hydrophobic residue.
CC -I- COPACTOR: Binds 2 zinc ions and 4 calcium ions per subunit.
CC -I- ENZYME REGULATION: Can be activated without removal of the
CC activation peptide.
CC -I- DOMAIN: There are two distinct domains in this protein; the
CC catalytic N-terminal, and the C-terminal which is involved in
CC substrate specificity and in binding TIMP (tissue inhibitor of
CC metalloproteinases).
CC -I- PTM: Undergoes autolytic cleavage to two major forms (22 kDa and
CC 27 kDa). A minor form (25 kDa) is the glycosylated form of the 22
CC kDa form. The 27 kDa form has no activity while the 22/25 kDa form
CC can act as activator for collagenase.
CC -I- SIMILARITY: Belongs to peptidase family M10A.
CC -I- SIMILARITY: Contains 1 hemopexin-like domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
EMBL; X05231; CAA28858.1; -;
DR EMBL; M13509; AAA35699.1; -;
DR EMBL; M16567; AAA52033.1; -;
DR EMBL; U78045; AAB36941.1; -;
DR EMBL; BC013875; AAH13875.1; -;
DR EMBL; M15996; AAA35700.1; -;
DR EMBL; X54925; CAA35693.1; -;
DR PIN; A37308; KCHUI.
DR PDB; 1AYK; NMR; @=101-269.
DR PDB; 1CGF; X-ray; @=102-269.
DR PDB; 1CGF; X-ray; A/B=102-263.
DR PDB; 1CGL; X-ray; A/B=101-269.
DR PDB; 1HFC; X-ray; @=101-269.
DR PDB; 2AYK; NMR; @=101-269.
DR PDB; 2TCL; X-ray; @=101-269.
DR PDB; 3AYK; NMR; A=101-269.
DR PDB; 4AYK; NMR; A=101-269.
DR MEROPS; M10.001; -;
DR GlycoSuiteDB; P03956; -;
DR Genew; HGNC:7155; MWP1.
DR MIM; 120353; -;
DR GO; GO:0008433; F:collagenase activity; TAS.
DR GO; GO:0008270; F:zinc ion binding; TAS.
DR GO; GO:0006508; P:proteolysis and peptidolysis; TAS.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR006026; Peptidase M.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_2a_BS.
DR InterPro; IPR009070; PGSD_like.

```

DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF00413; Peptidase_M10; 1.

Query Match      100.0%; Score 292; DB 1; Length 469;
Best Local Similarity 100.0%; Pred. No. 8.2e-29;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQEFFGLKVTGKPDATLKVMPKQRCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54
    |||||
Db 67 MQEFFGLKVTGKPDATLKVMPKQRCGVPDVAQFVLTEGNPRWEQTHLYRIEN 120

RESULT 2
AAP35520 PRELIMINARY; PRT; 469 AA.
AC AAP35520;
DT 02-MAR-2004 (T-EMBLrel. 27, Created)
DT 02-MAR-2004 (T-EMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (T-EMBLrel. 27, Last annotation update)
DE Matrix metalloproteinase 1 (Interstitial collagenase).
OS Homo sapiens (Human).
OC Sukariyora; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kalline N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA Koundinya M., Raphael J., Moreira D., Kelley T., Labaer J., Lin Y.,
RA Phelan M., Farmer A.;
RT "Cloning of human full-length cDNAs in BD Creator(TM) System Donor
RT vector."
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BT006874; AAP35520.1; -
KW Collagen.
SQ SEQUENCE 469 AA; 54007 MW; 4B1361DCF454B20 CRC64;

Query Match      100.0%; Score 292; DB 2; Length 469;
Best Local Similarity 100.0%; Pred. No. 8.2e-29;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQEFFGLKVTGKPDATLKVMPKQRCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54
    |||||
Db 67 MQEFFGLKVTGKPDATLKVMPKQRCGVPDVAQFVLTEGNPRWEQTHLYRIEN 120

RESULT 3
MM01_RABIT STANDARD; PRT; 468 AA.
ID MM01_RABIT
AC F13943;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interstitial collagenase precursor (EC 3.4.24.7) (Matrix
DE metalloproteinase-1) (MMP-1).
GN Name=MMP1;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Synovial cell;
RX MEDLINE=88077876; PubMed=2825772;
RA Fini M.E., Plucinska I.M., Mayer A.S., Gross R.H., Brinckerhoff C.E.;
RT "A gene for rabbit synovial cell collagenase: member of a family of
RT metalloproteinases that degrade the connective tissue matrix."
RL Biochemistry 25:6156-6165(1987).
RN [2]
RP SEQUENCE OF 449-468 FROM N.A.
RC STRAIN=New Zealand white;
RX MEDLINE=87029174; PubMed=3021384;
RA Fini M.E., Austin S.D., Holt P.T., Ruby P.L., Gross R.H., White H.D.,
RA Brinckerhoff C.E.;

```

"Homology between exon-containing portions of rabbit genomic clones for synovial cell collagenase and human foreskin and synovial cell mRNAs.";

Coll. Relat. Res. 6:239-248(1986).

-!- FUNCTION: Cleaves collagens of types I, II, and III at one site in the helical domain. Also cleaves collagens of types VII and X.

-!- CATALYTIC ACTIVITY: Cleaves preferentially one bond in native collagen. Cleavage of the triple helix of collagen at about three-quarters of the length of the molecule from the N-terminus, at 775-Gly-Ile-776 in the alpha-1(I) chain. Cleaves synthetic substrates and alpha-macroglobulins at bonds where P1' is a hydrophobic residue.

-!- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit (By similarity).

-!- ENZYME REGULATION: Can be activated without removal of the activation peptide.

-!- SIMILARITY: Belongs to peptidase family M10A.

-!- SIMILARITY: Contains 1 hemopexin-like domain.

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EMBL; M17823; AAB88016.1; -

EMBL; M17820; AAB88016.1; JOINED.

EMBL; M17821; AAB88016.1; JOINED.

EMBL; M17822; AAB88016.1; JOINED.

EMBL; M19240; AAB88016.1; JOINED.

EMBL; M25663; AAB31203.1; -

PIR; A27500; KCRBI.

HSBP; P03956; 1CGL.

MEROPS; M10.001; -

InterPro; IPR000585; Hemopexin.

InterPro; IPR006026; Peptidase M.

InterPro; IPR001818; Pept_M10A_M12B.

InterPro; IPR006025; Pept_M_Zn_BS.

InterPro; IPR009070; PGHD_like.

Pfam; PF00045; Hemopexin; 4.

Pfam; PF00413; Peptidase_M10; 1.

Pfam; PF03933; Peptidase_M10_N; 1.

PRINTS; PR00138; MATRINX.

SMART; SM00120; HX; 4.

SMART; SM00235; ZnMC; 1.

PROSITE; PS00546; CYSTEINE SWITCH; 1.

PROSITE; PS00024; HEMOPEXIN; 1.

PROSITE; PS00142; ZINC_PROTEASE; 1.

Calcium-binding; Collagen degradation; Extracellular matrix; Glycoprotein; Hydrolase; Metal-binding; Metalloprotease; Signal; Zinc; Zymogen.

SIGNAL

1	18	Activation peptide.
19	98	Interstitial collagenase.
99	468	Hemopexin-like.
274	468	Cysteine switch (Potential).
91	91	Calcium 1 (By similarity).
123	123	Calcium 2 (By similarity).
157	157	Zinc 1 (By similarity).
167	167	Zinc 1 (By similarity).
169	169	Calcium 3 (By similarity).
174	174	Calcium 3 (via carbonyl oxygen) (By similarity).
175	175	Calcium 3 (via carbonyl oxygen) (By similarity).
177	177	Calcium 3 (via carbonyl oxygen) (By similarity).
179	179	Calcium 3 (via carbonyl oxygen) (By similarity).
182	182	Zinc 1 (By similarity).
189	189	Calcium 2 (via carbonyl oxygen) (By similarity).
191	191	Calcium 2 (via carbonyl oxygen) (By similarity).


```

FT METAL      193 193 Calcium 2 (By similarity)
FT METAL      195 195 Zinc 1 (By similarity)
FT METAL      197 197 Calcium 3 (By similarity)
FT METAL      198 198 Calcium 1 (By similarity)
FT METAL      200 200 Calcium 3 (By similarity)
FT METAL      217 217 Zinc 2 (catalytic) (By similarity).
FT ACT_SITE   218 218 By similarity.
FT METAL      221 221 Zinc 2 (catalytic) (By similarity).
FT METAL      227 227 Zinc 2 (catalytic) (By similarity).
FT METAL      284 284 Calcium 4 (via carbonyl oxygen) (By
FT                                     similarity).
FT METAL      328 328 Calcium 4 (via carbonyl oxygen) (By
FT                                     similarity).
FT METAL      377 377 Calcium 4 (via carbonyl oxygen) (By
FT                                     similarity).
FT METAL      426 426 Calcium 4 (via carbonyl oxygen) (By
FT                                     similarity).
FT CARBOHYD    119 119 N-linked (GlcNAc...) (Probable).
FT DISULFID    277 455 By similarity.
FT SEQUENCE   468 AA; 53739 MW; DA90538919952B8C CR664;

Query Match          Score 283; DB 1; Length 468;
Best Local Similarity 96.3%; Pred. No. 1.2e-27;
Matches 52; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MOEFFGLKVTGKPDAETLKMVKOPRCGVDPVAQVLTETGNPWEQHLYRIEN 54
|||||:|||||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 66 MOEFFGLKVTGKPDAETLKMVKOPRCGVDPVAQVLTETGNPWEQHLYRIEN 119

RESULT 4
MMO1_HORSE
ID_MMOL_HORSE STANDARD; PRT; 469 AA.
AC Q9XSZ5;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interstitial collagenase'precursor (EC 3.4.24.7) (Matrix
DE metalloproteinase-1) (MMP-1).
DE Names=MMP1; GN
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796; [1]
RN [1]
RP SEQUENCE FROM N.A.
RA Richardson D.W.;
RT "Cloning and expression of equine matrix metalloproteinase 1
RT (interstitial collagenase).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -! FUNCTION: Cleaves collagens of types I, II, and III at one site in
CC the helical domain. Also cleaves collagens of types VII and X.
CC -! CATALYTIC ACTIVITY: Cleaves preferentially one bond in native
CC collagen. Cleavage of the triple helix of collagen at about three-
CC quarters of the length of the molecule from the N-terminus, at
CC 775-Gly-Ile-776 in the alpha-1(I) chain. Cleaves synthetic
CC substrates and alpha-macroglobulins at bonds where P1' is a
CC hydrophobic residue.
CC -! COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit (By
CC similarity).
CC -! ENZYME REGULATION: Can be activated without removal of the
CC activation peptide.
CC -! SIMILARITY: Belongs to peptidase family M10A.
CC -! SIMILARITY: Contains 1 hemopexin-like domain.
CC -----CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
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ID AC P21692; STANDARD; PRT; 469 AA.
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Interstitial collagenase precursor (EC 3.4.24.7) (Matrix
 metalloproteinase-1) (MMP-1).
 GN Name=MMP1;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 CX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=9133421; PubMed=1651440;
 RA Richards C.D., Rafferty J.A., Reynolds J.J., Saklatvala J.;
 RT "Porcine collagenase from synovial fibroblasts: cDNA sequence and
 modulation of expression of RNA in vitro by various cytokines.";
 RL Matrix 11:161-167(1991).
 RN [2]
 RP SEQUENCE OF 25-469 FROM N.A.
 RX TISSUE=Synovial cell;
 RC MEDLINE=9104747; PubMed=2174547;
 RA Clarke N.J., O'Hare M.C., Cawston T.E., Harper G.P.;
 RT "Nucleotide sequence of a cDNA for porcine type I collagenase,
 obtained by PCR.";
 RL Nucleic Acids Res. 18:6703-6703(1990).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 100-469.
 RX MEDLINE=96173003; PubMed=8590015;
 RA Li J., Brick P., O'Hare M.C., Skarzynski T., Lloyd L.F., Curry V.A.,
 Clark I.M., Bigg H.F., Hazleman B.L., Cawston T.E., Blow D.M.;
 RT "Structure of full-length porcine synovial collagenase reveals a C-
 terminal domain containing a calcium-linked, four-bladed beta-
 propeller.";
 RL Structure 3:541-543(1995).
 RN [4]
 RP SEQUENCE OF 100-104 AND 248-282, AND AUTOPROTEOLYTIC CLEAVAGE SITE.
 RX MEDLINE=95142615; PubMed=7840605;
 RA Clark I.M., Mitchell R.E., Powell L.K., Bigg H.F., Cawston T.E.,
 O'Hare M.C.;
 RT "Recombinant porcine collagenase: purification and autolysis.";
 RL Arch. Biochem. Biophys. 316:123-127(1995).
 CC -!- FUNCTION: Cleaves collagens of types I, II, and III at one site in
 the helical domain. Also cleaves collagens of types VII and X.
 CC -!- CATALYTIC ACTIVITY: Cleaves preferentially one bond in native
 collagen. Cleavage of the triple helix of collagen at about three-
 quarters of the length of the molecule from the N-terminus, at
 775-Gly-|-Ile-776 in the alpha-1(I) chain. Cleaves synthetic
 substrates and alpha-macroglobulins at bonds where P1' is a
 hydrophobic residue.
 CC -!- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit.
 CC -!- ENZYME REGULATION: Can be activated without removal of the
 activation peptide.
 CC -!- PTM: Undergoes autolytic cleavage to produce a N-terminal fragment
 having reduced collagenolytic activity.
 CC -!- SIMILARITY: Belongs to peptidase family M10A.
 CC -!- SIMILARITY: Contains 1 hemopexin-like domain.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 CC EMBL; X54724; CAA38526.1; -;
 CC PIR; S15986; KCPGI.
 CC PDB; 1PBL; X-ray; @=100-469.
 CC MEROPS; M10.001; -;
 CC InterPro; IPR000585; Hemopexin.
 CC InterPro; IPR006026; Peptidase_M.

DR InterPro; IPR001818; Pept_M10A_M12B.
 DR InterPro; IPR006025; Pept_M_Zn_BS.
 DR InterPro; IPR009070; PCBD-like.
 DR Pfam; PF00045; Hemopexin; 4.
 DR Pfam; PF00413; Peptidase_M10; 1.
 DR Pfam; PF03933; Peptidase_M10_N; 1.
 DR PRINTS; PRO0138; MATRXIN.
 DR SMART; SM00120; HX; 4.
 DR SMART; SM00235; ZnMG; 1.
 DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
 DR PROSITE; PS00024; HEMOPEXIN; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 KW 3D-structure: Autocatalytic cleavage; Calcium-binding;
 KW Collagen degradation; Direct protein sequencing; Extracellular matrix;
 KW Glycoprotein; Hydrolase; Metal-binding; Metalloprotease; Signal; Zinc;
 KW Zymogen.
 FT SIGNAL 1 19
 FT PROPEP 20 99 Activation peptide.
 FT CHAIN 100 469 Interstitial collagenase.
 FT CHAIN 100 258 18 kDa interstitial collagenase.
 FT DOMAIN 275 469 Hemopexin-like.
 FT SITE 92 92 Cysteine switch (Potential).
 FT SITE 258 259 Cleavage (autolytic).
 FT METAL 124 124 Calcium 1.
 FT METAL 158 158 Calcium 2.
 FT METAL 168 168 Zinc 1.
 FT METAL 170 170 Zinc 1.
 FT METAL 175 175 Calcium 3.
 FT METAL 176 176 Calcium 3 (via carbonyl oxygen).
 FT METAL 178 178 Calcium 3 (via carbonyl oxygen).
 FT METAL 180 180 Calcium 3 (via carbonyl oxygen).
 FT METAL 183 183 Zinc 1.
 FT METAL 190 190 Calcium 2 (via carbonyl oxygen).
 FT METAL 192 192 Calcium 2 (via carbonyl oxygen).
 FT METAL 194 194 Calcium 2.
 FT METAL 196 196 Zinc 1.
 FT METAL 198 198 Calcium 3.
 FT METAL 199 199 Calcium 1.
 FT METAL 201 201 Calcium 3.
 FT METAL 218 218 Zinc 2 (catalytic).
 FT ACT_SITE 219 219 Zinc 2 (catalytic).
 FT METAL 222 222 Zinc 2 (catalytic).
 FT METAL 228 228 Calcium 4 (via carbonyl oxygen).
 FT METAL 285 285 Calcium 4 (via carbonyl oxygen).
 FT METAL 329 329 Calcium 4 (via carbonyl oxygen).
 FT METAL 378 378 Calcium 4 (via carbonyl oxygen).
 FT METAL 427 427 Calcium 4 (via carbonyl oxygen).
 FT DISULFID 278 466
 FT CARBOHYD 120 120
 FT STRAND 101 102 N-linked (GlcNAc...) (Potential).
 FT TURN 104 105
 FT STRAND 113 118
 FT TURN 123 124
 FT TURN 127 142
 FT TURN 143 144
 FT STRAND 148 152
 FT STRAND 159 164
 FT STRAND 182 184
 FT TURN 190 193
 FT STRAND 195 198
 FT TURN 199 200
 FT STRAND 204 204
 FT STRAND 211 211
 FT HELIX 212 223
 FT TURN 224 225
 FT STRAND 226 227
 FT TURN 232 233
 FT TURN 235 236
 FT HELIX 250 260
 FT TURN 277 281
 FT TURN 280 281
 FT STRAND 285 290
 FT TURN 291 292

FT STRAND 293 298
FT TURN 299 300
FT STRAND 301 305
FT STRAND 313 316
FT STRAND 317 320
FT STRAND 330 334
FT TURN 335 338
FT STRAND 339 344
FT TURN 345 346
FT STRAND 347 352
FT TURN 353 354
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FT STRAND 362 363
FT STRAND 364 368
FT HELIX 372 373
FT STRAND 379 383
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FT STRAND 406 407
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FT STRAND 415 418
FT TURN 420 421
FT STRAND 428 432
FT TURN 433 434
FT STRAND 435 440
FT TURN 441 442
FT STRAND 443 448
FT TURN 449 452
FT STRAND 453 459
FT TURN 460 461
FT STRAND 462 464
FT HELIX 465 465
SQ SEQUENCE 469 AA; 53666 NM; 7952D72B2753F682 CRC64;

Query Match 92.5%; Score 270; DB 1; Length 469;
Best Local Similarity 90.7%; Pred. No. 5.5e-26;
Matches 49; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MQBFGLKVTGPDARTLNMKQPCGVDVAQFVLTEGNPWEOTHLTYRIEN 54
||:|||||||||||||||||||||||||||||||||||||||||
DB 67 MQQFGLKVTGPDARTLNMKQPCGVDVAQFVLTEGNPWEOTHLTYRIEN 120

RESULT 6
MM01_BOVIN STANDARD; PRT; 469 AA.
AC P28053;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interstitial collagenase precursor (EC 3.4.24.7) (Matrix metalloproteinase-1) (MMP-1) (fibroblast collagenase).
GN Name=MMP1; Synonyms=CLG;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
SEQUENCE FROM N.A.
RP TISSUE=Periosteum fibroblast;
RX MEDLINE=95201294; PubMed=7894061;
RA Tamura M., Shimokawa H., Sasaki S.;
RT "Primary structure of bovine interstitial collagenase deduced from cDNA sequence."
RL DNA Seq. 5:63-66(1994).
RN [2]
RP SEQUENCE OF 19-39 AND 85-125.
RX PubMed=1311165;

RA Sudbeck B.D., Jeffrey J.J., Welgus H.G., Mecham R.P., McCourt D., Parks W.C.;
RT "Purification and characterization of bovine interstitial collagenase and tissue inhibitor of metalloproteinases.";
RL Arch. Biochem. Biophys. 293:370-376(1992).
CC -|- FUNCTION: Cleaves collagens of types I, II, and III at one site in the helical domain. Also cleaves collagen of types VII and X.
CC -|- CATALYTIC ACTIVITY: Cleaves preferentially one bond in native collagen. Cleavage of the triple helix of collagen at about three-quarters of the length of the molecule from the N-terminus, at 775-Gly-|-Ile-776 in the alpha-1(I) chain. Cleaves synthetic substrates and alpha-macroglobulins at bonds where P1' is a hydrophobic residue.
CC -|- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit (By similarity).
CC -|- ENZYME REGULATION: Can be activated without removal of the activation peptide.
CC -|- SIMILARITY: Belongs to peptidase family M10A.
CC -|- SIMILARITY: Contains 1 hemopexin-like domain.
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CC -----
CC EMBL: X58256; CAA41210.1; -;
CC PIR: S14554; KCB01.
CC HSP: P03956; IHFC.
CC MEROPS: M10.001; -;
CC InterPro: IPR000585; Hemopexin.
CC InterPro: IPR006026; Peptidase M.
CC InterPro: IPR001818; Pept M10A M12B.
CC InterPro: IPR006025; Pept M Zn BS.
CC InterPro: IPR009070; PGSD-like.
CC Pfam: PF00045; Hemopexin_4.
CC Pfam: PF00413; Peptidase_M10; 1.
CC Pfam: PF03933; Peptidase_M10_N; 1.
CC PRINTS: PR00138; MATRIXIN.
CC SMART: SM00120; HX; 4.
CC SMART: SM00235; ZnMc; 1.
CC PROSITE: PS00546; CYSTEINE_SWITCH; 1.
CC PROSITE: PS00024; HEMOPEXIN; 1.
CC PROSITE: PS00142; ZINC_PROTEASE; 1.
CC Calcium-binding; Collagen degradation; Direct protein sequencing; Extracellular matrix; Glycoprotein; Hydrolase; Metal-binding; Metalloprotease; Signal; Zinc; Zymogen.
FT SIGNAL 1 18
FT PROPEP 19 99 Activation peptide.
FT CHAIN 100 469 Interstitial collagenase.
FT DOMAIN 275 469 Hemopexin-like.
FT SITE 92 92 Cysteine switch. (potential).
FT METAL 124 124 Calcium 1 (By similarity).
FT METAL 158 158 Calcium 2 (By similarity).
FT METAL 168 168 Zinc 1 (By similarity).
FT METAL 170 170 Zinc 1 (By similarity).
FT METAL 175 175 Calcium 3 (By similarity).
FT METAL 176 176 Calcium 3 (via carbonyl oxygen) (By similarity).
FT METAL 178 178 Calcium 3 (via carbonyl oxygen) (By similarity).
FT METAL 180 180 Calcium 3 (via carbonyl oxygen) (By similarity).
FT METAL 183 183 Zinc 1 (By similarity).
FT METAL 190 190 Calcium 2 (via carbonyl oxygen) (By similarity).
FT METAL 192 192 Calcium 2 (via carbonyl oxygen) (By similarity).
FT METAL 194 194 Calcium 2 (By similarity).
FT METAL 196 196 Zinc 1 (By similarity).
FT METAL 198 198 Calcium 3 (By similarity).


```
DR Genew: HGNC.7175; MWP8.
DR MIM: 120355;
DR GO: GO:0005615; C:extracellular space; TAS.
DR GO: GO:0008130; F:neutrophil collagenase activity; TAS.
DR GO: GO:0008270; F:zinc ion binding; TAS.
DR GO: GO:0006508; P:proteolysis and peptidolysis; TAS.
DR GO: GO:0005585; Hemopexin.
DR InterPro: IPR001818; Pept_M10A_M12B.
DR InterPro: IPR006025; Pept_M_Zn_BS.
DR InterPro: IPR009070; PGSD_like.
DR Pfam: PF00045; Hemopexin; 4.
DR Pfam: PF00413; Peptidase_M10; 1.
DR Pfam: PF03933; Peptidase_M10_N; 1.
DR PRINTS: PR00138; MATRIXIN.
DR PROSITE: PS00546; CYSTEINE_SWITCH; 1.
DR PROSITE: PS00142; ZINC_PROTEASE; 1.
DR 3D-structure; Calcium-binding; Collagen degradation;
KW Direct protein sequencing; Extracellular matrix; Glycoprotein;
KW Hydrolase; Metal-binding; Metalloprotease; Signal; Zinc; Zymogen.
FT SIGNAL 1 20
FT PROPEP 21 100 Activation peptide.
FT CHAIN 101 467 Neutrophil collagenase.
FT DOMAIN 276 467 Hemopexin-like.
FT SITE 91 91 Cysteine switch.
FT METAL 157 157 Calcium 1.
FT METAL 167 167 Zinc 1.
FT METAL 169 169 Zinc 1.
FT METAL 174 174 Calcium 2.
FT METAL 175 175 Calcium 2.
FT METAL 177 177 Calcium 2 (via carbonyl oxygen).
FT METAL 179 179 Calcium 2 (via carbonyl oxygen).
FT METAL 182 182 Calcium 2 (via carbonyl oxygen).
FT METAL 189 189 Zinc 1.
FT METAL 191 191 Calcium 1 (via carbonyl oxygen).
FT METAL 193 193 Calcium 1.
FT METAL 195 195 Calcium 1.
FT METAL 197 197 Zinc 1.
FT METAL 200 200 Calcium 2.
FT METAL 217 217 Zinc 2 (catalytic).
FT ACT_SITE 218 218 Zinc 2 (catalytic).
FT METAL 221 221 Zinc 2 (catalytic).
FT METAL 227 227 Calcium 3 (via carbonyl oxygen) (By
FT METAL 286 286 similarity).
FT METAL 378 378 Calcium 3 (via carbonyl oxygen) (By
FT METAL 425 425 similarity).
FT CARBOHYD 54 54 N-linked (GlcNAc...) (Probable).
FT CARBOHYD 73 73 N-linked (GlcNAc...) (Probable).
FT CARBOHYD 112 112 N-linked (GlcNAc...) (Probable).
FT CARBOHYD 204 204 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 246 246 N-linked (GlcNAc...) (Potential).
FT DISULFID 279 464 Probable.

Query Match 73.3%; Score 214; DB 1; Length 467;
Best Local Similarity 70.4%; Pred. No. 8.9e-19;
Matches 38; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 MQEFLGLKVTGKPAETLKVMPKQPCGVDPVDAQFVLTEGNPRWEOTHLTYRIEN 54
DB 66 MQEFLGLNVTGKPNETLDMKPKPCGVDPDSGGFMTLPNGPKWETNLTIRRN 119

RESULT 9
Q81022 ID PRELIMINARY; PRT; 205 AA.
AC Q81022;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Collagenase-like B (Fragment).

Query Match 73.3%; Score 214; DB 1; Length 467;
Best Local Similarity 70.4%; Pred. No. 8.9e-19;
Matches 38; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 MQEFLGLKVTGKPAETLKVMPKQPCGVDPVDAQFVLTEGNPRWEOTHLTYRIEN 54
DB 66 MQEFLGLNVTGKPNETLDMKPKPCGVDPDSGGFMTLPNGPKWETNLTIRRN 119

RESULT 9
Q81022 ID PRELIMINARY; PRT; 205 AA.
AC Q81022;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Collagenase-like B (Fragment).

Query Match 69.9%; Score 204; DB 2; Length 205;
Best Local Similarity 66.7%; Pred. No. 7.2e-18;
Matches 36; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

QY 1 MQEFLGLKVTGKPAETLKVMPKQPCGVDPVDAQFVLTEGNPRWEOTHLTYRIEN 54
DB 64 MQEFLGLKVTGNSDPETLRAMKPCGVDPVAPVATHNPRWTKHTLTYILN 117

RESULT 10
Q9EPL6 ID PRELIMINARY; PRT; 463 AA.
AC Q9EPL6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative matrix metalloproteinase.
GN Name=Mmp1b; Synonyms=McolB;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21167837; PubMed=1113146;
RA Balbin M., Fuyo A., Knauper V., Lopez J.M., Alvarez J., Sanchez L.M.,
RA Quesada V., Bordallo J., Murphy G., Lopez-Otin C.;
RT "Identification and enzymatic characterization of two diverging murine
RT counterparts of human interstitial collagenase (MMP-1) expressed at
RT sites of embryo implantation."
RL J. Biol. Chem. 276:10253-10262(2001).
DR EMBL; AJ278461; CAC18879.1; -.
DR HSSP; P08254; 1HV7.
DR MEROPS; M10.034; -.
DR MGD; MGI:1933847; Mmp1b.
DR GO: GO:0008233; F:peptidase activity; IDA.
DR InterPro: IPR00585; Hemopexin.
DR InterPro: IPR006026; Peptidase_M.
DR InterPro: IPR001843; Pept_M10A_M10C.
DR InterPro: IPR001818; Pept_M10A_M12B.
DR InterPro: IPR006025; Pept_M_Zn_BS.
DR Pfam: PF02051; Fragilysin; 1.
DR Pfam: PF00045; Hemopexin; 4.
DR Pfam: PF00413; Peptidase_M10; 1.
DR Pfam: PF03933; Peptidase_M10_N; 1.
DR PRINTS; PR00138; MATRIXIN.
```


CC and V; weakly collagens III, IV, and V. Activates procollagenase.
CC -I- CATALYTIC ACTIVITY: Similar to stromelysin 1, but action on
CC collagen types III, IV and V is weak.
CC -I- COFACTOR: Binds 2 zinc ions per subunit, calcium (By similarity).
CC -I- SIMILARITY: Belongs to peptidase family M10A.
CC -I- SIMILARITY: Contains 1 hemopexin-like domain.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X07820; CAA30679.1; -.
CC EMBL; BC002591; AAB02591.1; -.
CC FIR; A28816; KCHUS2.
CC HSSP; P08254; IG05.
CC MEROPS; M10.006; -.
CC Genew; HGNC:7156; MMP10.
CC MIM; 185260; -.
CC GO; GO:0005578; C:extracellular matrix; TAS.
CC GO; GO:0005615; F:extracellular space; TAS.
CC GO; GO:0004222; F:metalloendopeptidase activity; TAS.
CC GO; GO:0008270; F:zinc ion binding; TAS.
CC GO; GO:0006508; P:proteolysis and peptidolysis; TAS.
CC InterPro; IPR000585; Hemopexin.
CC InterPro; IPR006026; Peptidase M.
CC InterPro; IPR001818; Pept_M10A_M12B.
CC InterPro; IPR006025; Pept_M_Zn_BS.
CC InterPro; IPR009070; PGSD like.
CC Pfam; PF00413; Peptidase M10; 1.
CC Pfam; PF03933; Peptidase M10_N; 1.
CC PRINTS; PR00138; MATRIXIN.
CC SMART; SM00120; HX; 4.
CC SWART; SM00235; ZnMc; 1.
CC PROSITE; PS00546; CYSTEINE SWITCH; 1.
CC PROSITE; PS00024; HEMOPEXIN; 1.
CC PROSITE; PS00142; ZINC PROTEASE; 1.
CC Calcium; Collagen degradation; Extracellular matrix; Hydrolase;
KW Metalloprotease; Signal; Zinc; Zymogen.
FT SIGNAL 1 17 Probable.
FT PROPEP 18 98 Activation peptide.
FT CHAIN 99 476 Stromelysin-2.
FT DOMAIN 286 476 Hemopexin-like.
FT SITE 91 91 Cysteine switch (By similarity).
FT METAL 217 217 Zinc (catalytic) (By similarity).
FT ACT_SITE 218 218 By similarity.
FT METAL 221 221 Zinc (catalytic) (By similarity).
FT METAL 227 227 Zinc (catalytic) (By similarity).
FT DISULFID 289 476 By similarity.
SQ SEQUENCE 476 AA; 54151 MW; 516DCDDFEF92A0D6 CRC64;

Query Match 64.7%; Score 189; DB 1; Length 476;
Best Local Similarity 63.0%; Pred.No. 1.5e-15;
Matches 34; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

Qy 1 MQBFFGLKVTGKPDATLTKVMKPRGCVDPDVAQVLTGPNRWEQTHLYRIEN 54
Db 66 MQKFLGLEVTGKLDTDLEVMKPRGCVDPDVGHFSSFFGMPKWKTHLYRIYN 119

RESULT 14
ID AAP36110 PRELIMINARY; PRT; 476 AA.
AC AAP36110;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Matrix metalloproteinase 10 (stromelysin 2).
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kainline N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
RA Phelan M., Farmer A.;
RT "Cloning of human full-length cDNAs in BD Creator(TM) System Donor
vector";
RL Submitted (May-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BT007442; AAP36110.1; -; 516DCDDFEF92A0D6 CRC64;
SQ SEQUENCE 476 AA; 54151 MW; 516DCDDFEF92A0D6 CRC64;

Query Match 64.7%; Score 189; DB 2; Length 476;
Best Local Similarity 63.0%; Pred.No. 1.5e-15;
Matches 34; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

Qy 1 MQBFFGLKVTGKPDATLTKVMKPRGCVDPDVAQVLTGPNRWEQTHLYRIEN 54
Db 66 MQKFLGLEVTGKLDTDLEVMKPRGCVDPDVGHFSSFFGMPKWKTHLYRIYN 119

RESULT 15
MM03_HUMAN
ID MM03_HUMAN STANDARD; PRT; 477 AA.
AC P08254;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Stromelysin-1 precursor (EC 3.4.24.17) (Matrix metalloproteinase-3)
DE (MMP-3) (Transin-1) (SL-1).
GN Name=MMP3; Synonyms=STMY1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606; [1]
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 18-24.
RX MEDLINE=88198243; PubMed=3360803;
RA Saus J., Quinones S., Otani Y., Nagase H., Harris E.D. Jr.,
RA Kurkinen M.;
RT "The complete primary structure of human matrix metalloproteinase-3.
RT Identity with stromelysin.";
RL J. Biol. Chem. 263:6742-6745 (1988).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Fibroblast;
RX MEDLINE=87156645; PubMed=3030290;
RA Whitham S.E., Murphy G., Angel P., Rahmsdorf H.J., Smith B., Lyons A.,
RA Harris T.J.R., Reynolds J.J., Herrlich P., Docherty A.J.P.;
RT "Comparison of human stromelysin and collagenase by cloning and
RT sequence analysis.";
RL Biochem. J. 240:913-916 (1986).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=88016164; PubMed=3477804;
RA Wilhelm S.M., Collier I.E., Kronberger A., Eisen A.Z., Marmer B.L.,
RA Grant G.A., Bauer E.A., Goldberg G.I.;
RT "Human skin fibroblast stromelysin: structure, glycosylation,
RT substrate specificity, and differential expression in normal and
RT tumorigenic cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:6725-6729 (1987).
RN [4]
RP SEQUENCE FROM N.A.
RA Lin D., Duncan M., Allen E., Araujo R., Aparicio A., Chai A.,
RA Chung E., Davis K., Federspiel N., Hyman R., Kalman S., Komp C.,
RA Kurdi O., Lashkari D., Lew H., Namath A., Oefner P., Roberts D.,
RA Heller R., Davis R.W.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A., AND VARIANT GLU-45.
RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Posl C.L., Yi Q.,

RA Nickerson D.A.;
RT "SeattleSNP. NHLBI HL6682 program for genomic applications, UW-FHCRC, Seattle, WA (URL: <http://pga.gs.washington.edu/>).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
[6]
RN
RX ZMOGEN ACTIVATION
RA MEDLINE=90344802; PubMed=2383557;
RA Nagase H., Enghild J.J., Suzuki K., Salvesen G.;
RT "Stepwise activation mechanisms of the precursor of matrix metalloproteinase 3 (stromelysin) by proteinases and (4-aminophenyl)mercuric acetate.";
RL Biochemistry 29:5783-5789(1990).
[7]
RN
RX STRUCTURE BY NMR OF CATALYTIC DOMAIN.
RA MEDLINE=95384761; PubMed=765604;
RA Gooley P.R., O'Connell J.F., Marcy A.I., Cuca G.C., Salowe S.P., Bush B.L., Hermes J.D., Esser C.K., Hagmann W.K., Springer J.P., Johnson B.A.;
RA "The NMR structure of the inhibited catalytic domain of human stromelysin-1";
RL Nat. Struct. Biol. 1:111-118(1994).
[8]
RN
RX STRUCTURE BY NMR OF 100-267.
RA MEDLINE=99043696; PubMed=9827994;
RA Stockman B.J., Waldon D.J., Gates J.A., Scallill T.A., Klooterman D.A., Myszak S.A., Jacobsen E.J., Belonga K.L., Mitchell M.A., Mao B., Petke J.D., Goodman L., Powers E.A., Ledbetter S.R., Kaytes P.S., Vogel G., Marshall V.P., Petzold G.L., Foorman R.A.;
RA "Solution structures of stromelysin complexed to thiazidazole inhibitors";
RL Protein Sci. 7:2281-2286(1998).
[9]
RN
RX X-RAY CRYSTALLOGRAPHY. (1.9 ANGSTROMS) OF 18-272.
RA Beckler J.W., Marcy A.I., Rokosz L.L., Axel M.G., Burbaum J.J., Fitzgerald P.M.D., Cameron P.M., Esser C.K., Hagmann W.K., Hermes J.D., Springer J.P.;
RA "Stromelysin-1: three-dimensional structure of the inhibited catalytic domain and of the C-truncated proenzyme.";
RL Protein Sci. 4:1966-1976(1995).
[10]
RN
RX X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 100-266.
RA MEDLINE=96311273; PubMed=8740360;
RA Dhanraj V., Ye Q.-Z., Johnson L.L., Hupe D.J., Otwine D.F., Dhanraj V., Rubin J.R., Pavlovsky A., Humblet C., Blundell T.L.;
RT "X-ray structure of a hydroxamate inhibitor complex of stromelysin catalytic domain and its comparison with members of the zinc metalloproteinase superfamily.";
RL Structure 4:375-386(1996).
[11]
RN
RX X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 105-264.
RA Esser C.K., Bugianesi R.L., Caldwell C.G., Chapman K.T., Durette P.L., Girotta N.N., Kopka I.E., Lanza T.J., Levorse D.A., Maccoss M., Owens K.A., Ponnipom M.M., Simione J.P., Harrison R.K., Niedwiecki L., Becker J.W., Marcy A.I., Axel M.G., Christen A.J., McDonnell J., Moore V.L., Olszewski J.M., Saphos C., Visco D.M., Shen F., Colletti A., Krieter P.A., Hagmann W.K.;
RT "Inhibition of stromelysin-1 (MMP-3) by PI'-biphenylylethyl carboxylalkyl dipeptides";
RL J. Med. Chem. 40:1026-1040(1997).
[12]
RN
RX X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 100-267 IN COMPLEX WITH TIMP1.
RA MEDLINE=97433330; PubMed=9288970;
RA Gomis-Rueh F.-X., Maskos K., Betz M., Bergner A., Huber R., Suzuki K., Yoshida N., Nagase H., Brew K., Bourenkov G.P., Bartunik H., Bode W.;
RT "Mechanism of inhibition of the human matrix metalloproteinase stromelysin-1 by TIMP-1";
RL Nature 389:77-81(1997).
[13]
RN
RX X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 100-264.
RA MEDLINE=99008562; PubMed=9792098;
RA Finzel B.C., Baldwin E.T., Bryant G.L. Jr., Hess G.F., Wilks J.W., Trepod C.M., Mott J.E., Marshall V.P., Petzold G.L., Poorman R.A., O'Sullivan T.J., Schostarez H.J., Mitchell M.A.;
RT "Structural characterizations of nonpeptidic thiazidazole inhibitors of matrix metalloproteinases reveal the basis for stromelysin selectivity.";
RL Protein Sci. 7:2118-2126(1998).
[14]
RN
RX X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 100-272.
RA MEDLINE=20013067; PubMed=10543949;
RA Chen L., Rydel T.J., Gu F., Dunaway C.M., Pikul S., Dunham K.M., Barnett B.J.;
RT "Crystal structure of the stromelysin catalytic domain at 2.0-A resolution: inhibitor-induced conformational changes.";
RL J. Mol. Biol. 293:545-557(1999).
[15]
RN
RX X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 100-267.
RA MEDLINE=99349695; PubMed=10422833;
RA Pavlovsky A.G., Williams M.G., Ye Q.-Z., Ortwine D.F., Johnson L.L., Purchase C.F. II, White A.D., Dhanraj V., Roth B.D., Johnson L.L., Hupe D., Humblet C., Blundell T.L.;
RT "X-ray structure of human stromelysin catalytic domain complexed with nonpeptide inhibitors: implications for inhibitor selectivity.";
RL Protein Sci. 8:1455-1462(1999).
[16]
RN
RX STRUCTURE BY NMR OF 100-272.
RA MEDLINE=98434377; PubMed=9760240;
RA Li Y.C., Zhang X., Melton R., Ganu V., Gonnella N.C.;
RT "Solution structure of the catalytic domain of human stromelysin-1 complexed to a potent, nonpeptidic inhibitor";
RL Biochemistry 37:14048-14056(1998).
CC
CC -!- FUNCTION: Can degrade fibronectin, laminin, gelatins of type I, III, IV, and V; collagens III, IV, X, and IX, and cartilage proteoglycans. Activates procollagenase.
CC
CC -!- CATALYTIC ACTIVITY: Preferential cleavage where P1', P2' and P3' are hydrophobic residues.
CC
CC -!- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit.
CC
CC -!- SIMILARITY: Belongs to peptidase family M10A.
CC
CC -!- SIMILARITY: Contains 1 hemoxepin-like domain.
CC
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DR EMBL; X05232; CAA28859.1; -
DR EMBL; J03209; AAA36321.1; -
DR EMBL; U78045; AAB36942.1; -
DR EMBL; AF405705; AAK95247.1; -
DR PIR; A28156; KCHUS1.
DR PDB; 1B3D; X-ray; A/B=100-272.
DR PDB; 1B8Y; X-ray; A/B=100-266.
DR PDB; 1B1W; X-ray; A/B=100-272.
DR PDB; 1BM6; NMR; @=100-272.
DR PDB; 1BQO; X-ray; A/B=100-272.
DR PDB; 1C3I; X-ray; A/B=100-272.
DR PDB; 1C8T; X-ray; A/B=103-269.
DR PDB; 1CAQ; X-ray; A=100-287.
DR PDB; 1CIZ; X-ray; A=100-267.
DR PDB; 1CQR; X-ray; A/B=100-272.
DR PDB; 1D5J; X-ray; A/B=100-272.
DR PDB; 1D7X; X-ray; A/B=100-272.
DR PDB; 1D8F; X-ray; A/B=100-272.
DR PDB; 1D8M; X-ray; A/B=100-272.
DR PDB; 1G05; X-ray; A/B=100-272.
DR PDB; 1G49; X-ray; A/B=100-272.
DR PDB; 1G4K; X-ray; A/B/C=100-267.
DR PDB; 1HFS; X-ray; @=105-264.

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DR  PDB; 1HY7; X-ray; A/B=100-272.
DR  PDB; 1MIW; Model; A=100-268.
DR  PDB; 1OO9; NMR; A=100-267.
DR  PDB; 1QIA; X-ray; A/B/C/D=106-267.
DR  PDB; 1QIC; X-ray; A/B/C/D=106-266.
DR  PDB; 1SLM; X-ray; @=18-272.

Query Match      64.7%; Score 189; DB 1; Length 477;
Best Local Similarity 63.0%; Pred. No. 1.5e-15;
Matches 34; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

QY      1 MQEFPGLKVTGKPDATLKMKQPCRCGVPDVAQFVLTEGNPRWEOHTLTYYRIEN 54
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      67 MQKFLGLEVTGKLDSDTLEVMRKPCGVPDVGHFRTFPGIPKWKTKTLTYRIVN 120

Search completed: October 13, 2004, 15:14:41
Job time : 111.769 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 13, 2004, 14:57:16 ; Search time 104.359 Seconds
(without alignments)
189.060 Million cells updates/sec

Title: US-10-032-376A-10

Perfect score: 307

Sequence: 1 MQRFFGLNVTGKPNETLDX.....LTPGNKWKERTNLTIRNY 55

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_23sep04:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003as:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	307	100.0	55	6	ABP97132 Human mat
2	307	100.0	55	6	ABG76318 Human mat
3	307	100.0	55	8	ADQ17093 Human mat
4	307	100.0	444	4	AAG65357 Human MMP
5	307	100.0	467	4	AAB84610 Amino aci
6	307	100.0	467	4	AAL10416 Human mat
7	307	100.0	467	4	AAG65358 Human neu
8	307	100.0	467	6	ABO32581 Secreted
9	307	100.0	467	8	ADQ10212 Human pol
10	226	73.6	454	8	ADL93947 Human G-c
11	221	72.0	454	7	ADL16002 G-coupled
12	221	72.0	454	7	ADL16004 G-coupled
13	221	72.0	454	7	ADL16008 G-coupled
14	221	72.0	454	7	ADL16006 G-coupled
15	221	72.0	454	8	ADL93945 Human G-c
16	221	72.0	454	8	ADL93943 Human G-c
17	221	72.0	455	8	ADL93941 Human G-c
18	221	72.0	469	4	AAB84606 Amino aci
19	221	72.0	469	4	AAL10415 Human mat
20	221	72.0	469	6	ABU03466 Angiogene
21	221	72.0	469	6	ABR58843 Human can
22	221	72.0	469	6	ABR58842 Human can
23	221	72.0	469	6	ABR48148 Human bla
24	221	72.0	469	6	ABU56596 Lung canc
25	221	72.0	469	6	ABU56597 Lung canc

26	221	72.0	469	6	ABU07454	Abu07454 Protein d
27	221	72.0	469	6	ABP54454	Abp54454 Matrix me
28	221	72.0	469	7	ADB79176	Abd79176 Matrix me
29	221	72.0	469	7	AD34550	Ade34550 Human ski
30	221	72.0	469	7	AD316000	Ade16000 G-coupled
31	221	72.0	469	7	AD316010	Ade16010 G-coupled
32	221	72.0	469	7	AD319849	Adn39849 Cancer/an
33	221	72.0	469	7	AD318694	Adn38694 Cancer/an
34	221	72.0	469	7	AD318696	Adn38696 Cancer/an
35	221	72.0	469	7	AD319850	Adn39850 Cancer/an
36	221	72.0	469	7	AD319538	Adn35538 Human BEC
37	221	72.0	469	8	ADL93949	Adl93949 Human G-c
38	221	72.0	469	8	ADL93939	Adl93939 Human G-c
39	221	72.0	470	8	ADN07695	Adn07695 Human mat
40	221	72.0	490	8	ADE07892	Ade07892 Novel pro
41	221	72.0	496	4	AAG75509	Aag75509 Human col
42	215	70.0	457	1	AAP36228	Aap36228 Sequence
43	215	70.0	469	1	AAP70611	Aap70611 Sequence
44	215	70.0	469	8	ADQ18359	Adq18359 Human sof
45	214	69.7	54	6	ABP97131	Abp97131 Human mat

ALIGNMENTS

RESULT 1

ABP97132
ID ABP97132 standard; peptide; 55 AA.

XX AC ABP97132;

XX AC (first entry)

DT 24-JUN-2003 (first entry)

DE Human matrix metalloproteinase 8 cleavage region peptide SEQ ID NO:10.

XX Human; matrix metalloproteinase; MMP; anticancer; wound healing;
KW matrix metalloproteinase inhibitor; antitumor; angiogenic; cardiant;
KW vascular endothelial growth factor inhibitor; VEGF inhibitor; cytostatic;
KW vulnary; cerebroprotective; antidiabetic; ophthalmological; tumor;
KW dermatological; metastatic; non-metastatic; vascularised; heart disease;
KW non-vascularised; surgical incision; chronic wound; stroke; angiogenesis;
KW macular degeneration; diabetic retinopathy; cleavage region.

XX Homo sapiens.

OS WO2003018748-A2.

XX PD 06-MAR-2003.

XX PF 15-AUG-2002; 2002WO-US026319.

XX PR 16-AUG-2001; 2001US-0312726P.

XX PR 21-DEC-2001; 2001US-00032376.

XX PR 21-MAY-2002; 2002US-00153185.

XX PA (KIMB) KIMBERLY-CLARK WORLDWIDE INC.

XX PI Quirk S, Weart IF;

XX DR WPI; 2003-381408/36.

XX PT Anti-angiogenic composition comprising peptide inhibitor of matrix metalloproteinase, useful for decreasing the expression of vascular endothelial growth factor and treating cancers and tissue injuries.

XX PS Claim 17; Page 16; 103pp; English.

XX CC The present invention describes an anti-angiogenic composition (I) for inhibiting expression of vascular endothelial growth factor (VEGF). (I) comprises an effective amount of a peptide inhibitor of matrix metalloproteinase (MMP), where the peptide can inhibit the expression of VEGF. (I) has cytostatic, vulnary, cardiant, cerebroprotective, antidiabetic, ophthalmological and dermatological activities. (I) can be

CC used for inhibiting expression of VEGF, and so can be used for inhibiting
 CC growth of tumours and diminishing tumours size. The tumour can be
 CC metastatic, non-metastatic, vascularised, non-vascularised, hard or soft.
 CC (I) is also useful for treating injuries including wounds, surgical
 CC incisions, chronic wounds, heart diseases and stroke. (I) is also useful
 CC for treating disorders characterised by excessive angiogenesis e.g.
 CC macular degeneration and diabetic retinopathy. The present sequence
 CC represents a human MMP cleavage region peptide, which is used in the
 CC exemplification of the present invention
 XX
 XX Sequence 55 AA;

Query Match 100.0%; Score 307; DB 6; Length 55;
 Best Local Similarity 100.0%; Pred. No. 3.4e-34;
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORFFGLNVTGPNNEETLDMKKPCGVPDGGFMLTPGNPKWERTNLTIRNY 55
 DB 1 MORFFGLNVTGPNNEETLDMKKPCGVPDGGFMLTPGNPKWERTNLTIRNY 55

RESULT 2
 ABG76318
 ID ABG76318 standard; protein; 55 AA.
 XX
 AC ABG76318;
 XX
 DT 10-MAY-2003 (first entry)
 XX
 DE Human matrix metalloproteinase (MMP) peptide inhibitor #10.
 XX
 KW Human; peptide inhibitor; matrix metalloproteinase-8; MMP-8;
 KW cleavage region; proenzyme form; cellular proliferation; fibroblast;
 KW keratinocyte; healthy skin development; wound healing; scarring;
 KW skin tone; wrinkle; anti-aging; vulnerary.
 XX
 OS Homo sapiens.

XX WO2003016520-A1.

XX 27-FEB-2003.

XX 15-AUG-2002; 2002WO-US026198.

XX 16-AUG-2001; 2001US-0312726P.

XX 21-DEC-2001; 2001US-00023376.

XX 21-MAY-2002; 2002US-00153195.

XX (KIMB) KIMBERLY-CLARK WORLDWIDE INC.

XX Quirk S, Malik S, Villanueva JM;

XX WPI; 2003-289380/28.

XX Novel peptide inhibitor of proteinase activity of matrix
 PT metalloproteinases, e.g. matrix metalloproteinase-2, useful for
 PT stimulating cellular proliferation of fibroblasts or keratinocytes.

XX Claim 1; Page 16; 120pp; English.

XX The present invention relates to peptide inhibitors of metalloproteinases
 CC (MMPs), particularly metalloproteinase-2 (MMP-2). The inhibitors have
 CC peptide sequences related to the cleavage regions of the proenzyme forms
 CC of the MMPs. The peptide inhibitors are useful for stimulating cellular
 CC proliferation of fibroblasts or keratinocytes, promoting healthy skin
 CC development, treating wounds, preventing scarring, improving skin tone,
 CC reducing wrinkling and for simulating the development of smooth, healthy
 CC skin. The peptide inhibitors are useful as anti-aging and wound healing
 CC compounds. ABG76309-ABG76321 represent peptide inhibitors of MMPs

XX Sequence 55 AA;

Query Match 100.0%; Score 307; DB 6; Length 55;

Best Local Similarity 100.0%; Pred. No. 3.4e-34;
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORFFGLNVTGPNNEETLDMKKPCGVPDGGFMLTPGNPKWERTNLTIRNY 55
 DB 1 MORFFGLNVTGPNNEETLDMKKPCGVPDGGFMLTPGNPKWERTNLTIRNY 55

RESULT 3

ADQ17093

ID ADQ17093 standard; peptide; 55 AA.

XX

AC ADQ17093;

XX 23-SEP-2004 (first entry)

XX

DE Human matrix metalloproteinase-8 (MMP8) cleavage region peptide.

XX Fibronectin; healthy skin; wrinkle; wound; vulnerary; dermatological;

KW human; matrix metalloproteinase; MMP.

XX Homo sapiens.

XX US2004127421-A1.

XX 01-JUL-2004.

XX 30-DEC-2002; 2002US-00335207.

XX 30-DEC-2002; 2002US-00335207.

XX (MALI/) MALIK S.

XX (QUIR/) QUIRK S.

XX Malik S, Quirk S;

XX WPI; 2004-506456/48.

XX Composition used for preventing and treating wrinkles and treating wounds

PT comprises peptide having sequence related to matrix metalloproteinase

PT proenzyme.

XX Example 1; SEQ ID NO 10; 60pp; English.

XX The present invention provides peptides and compositions containing such
 CC peptides that are useful as agents to maintain healthy skin and to
 CC promote the condition of the skin. The invention is useful for increasing
 CC the amount of fibronectin in tissue. The invention is also useful for
 CC encouraging the maintenance and development of healthy skin, preventing
 CC and treating wrinkles and for treating wounds. The invention acts as
 CC vulnerary and dermatological agents. The present sequence is human matrix
 CC metalloproteinase (MMP) cleavage region peptide. This sequence is used in
 CC the exemplification of the invention.

XX Sequence 55 AA;

Query Match 100.0%; Score 307; DB 8; Length 55;

Best Local Similarity 100.0%; Pred. No. 3.4e-34;

Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORFFGLNVTGPNNEETLDMKKPCGVPDGGFMLTPGNPKWERTNLTIRNY 55

DB 1 MORFFGLNVTGPNNEETLDMKKPCGVPDGGFMLTPGNPKWERTNLTIRNY 55

RESULT 4

AAG55357

ID AAG55357 standard; protein; 444 AA.

XX

XX AAG55357;

XX 30-NOV-2001 (first entry)

XX

DE Human MMP-8alt polypeptide.
XX MMP-8alt; MMP-8; matrix metalloproteinase; neutrophil collagenase;
XX anti-arthritis; cytostatic; anti-Parkinsonian; neuroprotective;
KW neotropic; cancer; apoptosis; Parkinson's disease; Alzheimer's disease;
KW Huntington's disease; human; splice variant.
XX
OS Homo sapiens.
XX
XX US-973-H.
PN
XX
XX 03-JUL-2001.
PD
XX 22-OCT-1998; 98US-00178002.
PF
XX 22-OCT-1998; 98US-00178002.
PR
XX (NOVS) NOVARTIS AG.
PA
XX Hu S;
PI
XX WPI; 2001-431511/46.
DR N-PSDB; AAH47515.
XX
XX New MMP-8alt polynucleotides and polypeptides useful as research reagents
PT and materials for discovering treatments and diagnostics to human
PT disease, or as targets for identifying inhibitors of MMP-8alt expression.
PT
XX
PS Claim 11; Col 25-30; 25pp; English.
XX
XX The invention relates to human MMP-8alt polypeptide and polynucleotides.
CC MMP-8alt is a splice variant of the MMP-8 (matrix metalloproteinase)
CC cDNA. The MMP-8alt polypeptide can be expressed by standard recombinant
CC methodology. The polynucleotides and polypeptides may be used as research
CC reagents and materials for the discovery of treatments and diagnostics to
CC human disease, and as targets for identifying modulators. Inhibitors of
CC MMP-8alt polynucleotide or polypeptide expression may be used to treat
CC and/or prevent arthritis, cancer and cancer metastasis, and diseases
CC caused by cellular apoptosis including Parkinson's disease, Alzheimer's
CC disease and Huntington's disease. The present sequence represents the
CC human MMP-8alt polypeptide
XX
XX Sequence 444 AA;
SQ
Query Match 100.0%; Score 307; DB 4; Length 444;
Best Local Similarity 100.0%; Pred. No. 4.4e-33;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MORFFGLNVTGKNEETLDMKKPRCGVDSGGFMTFCGNPKWERTNLTIRNY 55
DB 43 MORFFGLNVTGKNEETLDMKKPRCGVDSGGFMTFCGNPKWERTNLTIRNY 97
RESULT 5
AAB84610
ID AAB84610 standard; protein; 467 AA.
XX
XX AAB84610;
AC
XX 05-SEP-2001 (first entry)
DT
XX Amino acid sequence of matrix metalloproteinase-8.
DE
XX Growth factor; protein inhibitor; protease; damaged tissue;
KW platelet-derived growth factor; PDGF; fibroblast growth factor; FGF;
KW connective tissue derived growth factor; CTGF; chrysalin; VEGF;
KW keratinocyte-derived growth factor; KGF; epidermal growth factor; EGF;
KW transforming growth factor-beta; TGF-beta; matrix metalloproteinase; MMP;
KW granulocyte macrophage colony stimulating factor; GM-CSF; uPA;
KW vascular endothelial growth factor; urokinase plasminogen activator;
KW dermal ulcer; wound.
XX
XX Homo sapiens.
OS

XX WO200149309-A2.
PN
XX 12-JUL-2001.
PD
XX 21-DEC-2000; 2000WO-IB001935.
XX
XX 29-DEC-1999; 99GB-00030768.
PR
XX (PF12) PFIZER LTD.
PA (PF12) PFIZER INC.
PA
XX Davies MJ, Huggins JP, McIntosh FS, Occleston NL;
PI WPI; 2001-418351/44.
XX N-PSDB; AAH28225.
DR
XX Composition for the treatment of damaged tissue i.e. chronic wounds and
PT dermal ulcers comprises an inhibitor agent i.e. a protease and a growth
PT factor.
PT
XX
PS Disclosure; Page 555; 572pp; English.
XX
XX The specification describes a pharmaceutical composition, comprising a
CC growth factor, an inhibitor agent, i.e. a protease. The inhibitor agent
CC inhibits the action of at least one specific adverse protein, i.e. a
CC protease, that is upregulated in a damaged tissue such as a wound
CC environment. Growth factors which are included in the composition of the
CC invention are platelet-derived growth factor (PDGF), fibroblast growth
CC factor (FGF), connective tissue derived growth factor (CTGF),
CC keratinocyte-derived growth factor (KGF), transforming growth factor-beta
CC (TGF-beta), granulocyte macrophage colony stimulating factor (GM-CSF),
CC epidermal growth factor (EGF), vascular endothelial growth factor (VEGF),
CC and chrysalin. Inhibitors which are included in the composition of the
CC invention include inhibitors of urokinase-type plasminogen activator
CC (uPA) and matrix metalloproteinase (MMP). The composition is useful for
CC the treatment of chronic damaged tissue, i.e. wounds and dermal ulcers.
CC The present sequence represents a human MMP-8, and is used to produce the
CC composition of the invention
XX
XX Sequence 467 AA;
SQ
Query Match 100.0%; Score 307; DB 4; Length 467;
Best Local Similarity 100.0%; Pred. No. 4.7e-33;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MORFFGLNVTGKNEETLDMKKPRCGVDSGGFMTFCGNPKWERTNLTIRNY 55
DB 66 MORFFGLNVTGKNEETLDMKKPRCGVDSGGFMTFCGNPKWERTNLTIRNY 120
RESULT 6
AAE10416
ID AAE10416 standard; protein; 467 AA.
XX
XX AAE10416;
AC
XX 10-DEC-2001 (first entry)
DT
XX Human matrix metalloproteinase-8 (MMP-8) protein.
DE
XX Human; matrix metalloproteinase; MMP-8; hair growth; antisense therapy;
KW endopeptidase; skin cell; breast cancer; hair follicle; chromosome 11q22.
XX
XX Homo sapiens.
OS
XX Key Location/Qualifiers
XX Peptide 1..20 /label= Signal_peptide
XX Protein 21..467 /label= Mature_MMP_8_protein
XX Domain 89..95 /label= Cysteine_switch_domain
XX

CC the following activities: antidiabetic, anorectic, antibacterial,
 CC virucide, fungicide, cytostatic, neurotropic, neuroprotective,
 CC antiparkinsonian, haemostatic, and antilipaeamic. The G-coupled protein
 CC receptor related polypeptides are useful in a method of treating or
 CC preventing in a human, a pathology associated with the G-coupled protein
 CC receptor related polypeptides. The polypeptides are useful in the
 CC manufacture of a medicament for treating a syndrome associated with a
 CC human disease, preferably a NOVX-associated disorder. The novel
 CC polypeptides are useful for treating, preventing or diagnosing diseases,
 CC such as metabolic disorders, diabetes, obesity, infectious diseases,
 CC anorexia, cancer-associated diseases, neurodegenerative disorders,
 CC Alzheimer's disease, Parkinson's disease, immune disorders, hematopoietic
 CC disorders, and various dyslipidaemias, metabolic disturbances associated
 CC with obesity, metabolic X syndrome and wasting disorders associated with
 CC chronic diseases and various cancers. The nucleic acids and polypeptides
 CC may also be used as targets for the identification of small molecules
 CC that modulate or inhibit e.g. neurogenesis, cell differentiation, cell
 CC proliferation, hematopoiesis, wound healing and angiogenesis, in gene
 CC therapy, in generation of antibodies that bind immunospecifically to NOVX
 CC substances for use in therapeutic or diagnostic methods. The nucleic
 CC acids are further used as hybridization probes, in chromosome mapping,
 CC tissue typing, preventive medicine, and pharmacogenomics. This sequence
 CC represents one of the novel G-coupled protein receptor related
 CC polypeptides of the invention.
 XX
 SQ Sequence 454 AA;

Query Match 72.0%; Score 221; DB 7; Length 454;
 Best Local Similarity 70.9%; Pred. No. 2.9e-21;
 Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
 QY 1 MQRFFGLNVTGKFNBEETLDMKKKPCGVPDSCGFMLTFCNPKWERTNLTYYIRNY 55
 DB 50 MQEFFGLKVTGKPDABETLKVMPQRCGVPDVAQFVLTEGNPWEQTHLYIRNY 104

RESULT 13
 ADE16008
 ID ADE16008 standard; protein; 454 AA.
 AC ADE16008;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE G-coupled protein receptor related polypeptide, SEQ ID NO 38.
 XX
 KW G-coupled protein receptor; antidiabetic; anorectic; antibacterial;
 KW virucide; fungicide; cytostatic; neurotropic; neuroprotective;
 KW antiparkinsonian; haemostatic; antilipaeamic; neurogenesis;
 KW cell differentiation; cell proliferation; hematopoiesis; wound healing;
 KW angiogenesis; gene therapy; chromosome mapping; tissue typing;
 KW preventive medicine; pharmacogenomics; human.
 XX
 OS Homo sapiens.
 XX
 PN WO200283841-A2.
 XX
 PD 24-OCT-2002.
 XX
 XX 03-APR-2002; 2002WO-US010713.

XX
 PR 03-APR-2001; 2001US-0281136P.
 PR 05-APR-2001; 2001US-0281863P.
 PR 10-APR-2001; 2001US-0281906P.
 PR 13-APR-2001; 2001US-0282934P.
 PR 13-APR-2001; 2001US-0283657P.
 PR 13-APR-2001; 2001US-0283678P.
 PR 13-APR-2001; 2001US-0283687P.
 PR 17-APR-2001; 2001US-0283710P.
 PR 17-APR-2001; 2001US-0284234P.
 PR 19-APR-2001; 2001US-0285325P.
 PR 20-APR-2001; 2001US-0285609P.
 PR 23-APR-2001; 2001US-0285748P.

PR 23-APR-2001; 2001US-0285890P.
 PR 24-APR-2001; 2001US-0286068P.
 PR 27-APR-2001; 2001US-0287213P.
 PR 03-MAY-2001; 2001US-0288509P.
 PR 30-MAY-2001; 2001US-0294495P.
 PR 31-MAY-2001; 2001US-0294801P.
 PR 31-JUN-2001; 2001US-0309216P.
 PR 25-SEP-2001; 2001US-0324775P.
 PR 28-NOV-2001; 2001US-0333900P.
 PR 02-APR-2002; 2002US-00115479.
 XX (CURA-) CURAGEN CORP.
 PA
 XX Li L, Gerlach V, Liu X, Miller CE, Spytek KA, Zertusen BD;
 PI Pena CEA, Shenoy SG, Zhong H, Smithson G, Casman SJ, Boldog FL;
 PI Voss EZ, Vernet CAM, Macdougall JR, Rastelli L, Anderson DW;
 PI Zhong M, Mezes PD, Furtak K, Patturajan M, Burgess CE, Malyankar UM;
 PI Shimkets RA, Taupier RJ, Edinger SR, Mazur A;
 XX WPI; 2003-067574/06.
 DR N-PSDB; ADE16007.
 DR
 XX New isolated NOVX polypeptides and polynucleotides, useful for
 PT preventing, diagnosing or treating NOVX-associated disorders e.g.
 PT diabetes, obesity, dyslipidaemias, cancer, Parkinson's disease,
 PT Alzheimer's disease, infections.
 XX
 Claim 1; SEQ ID NO 38, 320pp; English.

XX
 CC The invention relates to a novel isolated G-coupled protein receptor
 CC related polypeptides. The novel polypeptide comprise any of the 22 fully
 CC defined sequences of 87-1780 amino acids, given in the specification;
 CC their mature forms; and possible variants. The novel polypeptides have
 CC the following activities: antidiabetic, anorectic, antibacterial,
 CC virucide, fungicide, cytostatic, neurotropic, neuroprotective,
 CC antiparkinsonian, haemostatic, and antilipaeamic. The G-coupled protein
 CC receptor related polypeptides are useful in a method of treating or
 CC preventing in a human, a pathology associated with the G-coupled protein
 CC receptor related polypeptides. The polypeptides are useful in the
 CC manufacture of a medicament for treating a syndrome associated with a
 CC human disease, preferably a NOVX-associated disorder. The novel
 CC polypeptides are useful for treating, preventing or diagnosing diseases,
 CC such as metabolic disorders, diabetes, obesity, infectious diseases,
 CC anorexia, cancer-associated diseases, neurodegenerative disorders,
 CC Alzheimer's disease, Parkinson's disease, immune disorders, hematopoietic
 CC disorders, and various dyslipidaemias, metabolic disturbances associated
 CC with obesity, metabolic X syndrome and wasting disorders associated with
 CC chronic diseases and various cancers. The nucleic acids and polypeptides
 CC may also be used as targets for the identification of small molecules
 CC that modulate or inhibit e.g. neurogenesis, cell differentiation, cell
 CC proliferation, hematopoiesis, wound healing and angiogenesis, in gene
 CC therapy, in generation of antibodies that bind immunospecifically to NOVX
 CC substances for use in therapeutic or diagnostic methods. The nucleic
 CC acids are further used as hybridization probes, in chromosome mapping,
 CC tissue typing, preventive medicine, and pharmacogenomics. This sequence
 CC represents one of the novel G-coupled protein receptor related
 CC polypeptides of the invention.
 XX
 SQ Sequence 454 AA;

Query Match 72.0%; Score 221; DB 7; Length 454;
 Best Local Similarity 70.9%; Pred. No. 2.9e-21;
 Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
 QY 1 MQRFFGLNVTGKFNBEETLDMKKKPCGVPDSCGFMLTFCNPKWERTNLTYYIRNY 55
 DB 50 MQEFFGLKVTGKPDABETLKVMPQRCGVPDVAQFVLTEGNPWEQTHLYIRNY 104

RESULT 14
 ADE16006
 ID ADE16006 standard; protein; 454 AA.
 XX

AC ADE16006;
 XX 29-JAN-2004 (first entry)
 DE G-coupled protein receptor related polypeptide, SEQ ID NO 36.
 XX
 KW G-coupled protein receptor; antidiabetic; anorectic; antibacterial;
 KW viricide; fungicide; cytostatic; nootropic; neuroprotective;
 KW antiparkinsonian; haemostatic; antilipemic; neurogenesis;
 KW cell differentiation; cell proliferation; hematopoiesis; wound healing;
 KW angiogenesis; gene therapy; chromosome mapping; tissue typing;
 KW preventive medicine; pharmacogenomics; human.
 XX
 OS Homo sapiens.
 XX
 PN WO200283841-A2.
 XX
 PD 24-OCT-2002.
 XX
 PF 03-APR-2002; 2002WO-US010713.
 XX
 PR 03-APR-2001; 2001US-0281136P.
 PR 05-APR-2001; 2001US-0281863P.
 PR 05-APR-2001; 2001US-0281906P.
 PR 10-APR-2001; 2001US-0282934P.
 PR 13-APR-2001; 2001US-0283657P.
 PR 13-APR-2001; 2001US-0283678P.
 PR 13-APR-2001; 2001US-0283687P.
 PR 13-APR-2001; 2001US-0283710P.
 PR 17-APR-2001; 2001US-0284234P.
 PR 19-APR-2001; 2001US-0285325P.
 PR 20-APR-2001; 2001US-0285509P.
 PR 23-APR-2001; 2001US-0285748P.
 PR 23-APR-2001; 2001US-0285890P.
 PR 24-APR-2001; 2001US-0286068P.
 PR 27-APR-2001; 2001US-0287213P.
 PR 30-MAY-2001; 2001US-0288509P.
 PR 30-MAY-2001; 2001US-0294495P.
 PR 31-MAY-2001; 2001US-0294801P.
 PR 31-JUL-2001; 2001US-0309216P.
 PR 25-SEP-2001; 2001US-0324775P.
 PR 28-NOV-2001; 2001US-0333900P.
 PR 02-APR-2002; 2002US-00115479.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Li L, Gerlach V, Liu X, Miller CE, Spytek KA, Zethusen BD;
 PI Pena CE, Shenoy SG, Zhong H, Smithson G, Casman SJ, Boldog FL;
 PI Voss EZ, Vernet CAM, Macdougall JR, Rastelli L, Anderson DW;
 PI Zhong M, Mezes PD, Furtak K, Patturajan M, Burgess CE, Malyankar UM;
 PI Shimkets RA, Taupier RJ, Edinger SR, Nazur A;
 XX
 DR WPI; 2003-067574/06.
 DR N-PSDB; ADE16005.
 XX
 XX New isolated NOVX polypeptides and polynucleotides, useful for
 PT preventing, diagnosing or treating NOVX-associated disorders e.g.
 PT diabetes, obesity, dyslipidemias, cancer, Parkinson's disease,
 PT Alzheimer's disease, infections.
 XX
 PS Claim 1; SEQ ID NO 36; 320bp; English.
 XX
 CC The invention relates to a novel isolated G-coupled protein receptor
 CC related polypeptides. The novel polypeptide comprises any of the 22 fully
 CC defined sequences of 87-1780 amino acids, given in the specification;
 CC their mature forms; and possible variants. The novel polypeptides have
 CC the following activities: antidiabetic, anorectic, antibacterial,
 CC viricide, fungicide, cytostatic, nootropic, neuroprotective,
 CC antiparkinsonian, haemostatic, and antilipemic. The G-coupled protein
 CC receptor related polypeptides are useful in a method of treating or
 CC preventing in a human, a pathology associated with the G-coupled protein
 CC receptor related polypeptides. The polypeptides are useful in the
 CC manufacture of a medicament for treating a syndrome associated with a

CC human disease, preferably a NOVX-associated disorder. The novel
 CC polypeptides are useful for treating, preventing or diagnosing diseases,
 CC such as metabolic disorders, diabetes, obesity, infectious diseases,
 CC anorexia cancer-associated diseases, neurodegenerative disorders,
 CC Alzheimer's disease, Parkinson's disease, immune disorders, hematopoietic
 CC disorders, and various dyslipidemias, metabolic disturbances associated
 CC with obesity, metabolic X syndrome and wasting disorders associated with
 CC chronic diseases and various cancers. The nucleic acids and polypeptides
 CC may also be used as targets for the identification of small molecules
 CC that modulate or inhibit e.g. neurogenesis, cell differentiation, cell
 CC proliferation, hematopoiesis, wound healing and angiogenesis, in gene
 CC therapy, in generation of antibodies that bind immunospecifically to NOVX
 CC substances for use in therapeutic or diagnostic methods. The nucleic
 CC acids are further used as hybridization probes, in chromosome mapping,
 CC tissue typing, preventive medicine, and pharmacogenomics. This sequence
 CC represents one of the novel G-coupled protein receptor related
 CC polypeptides of the invention.
 XX
 XX Sequence 454 AA;
 XX
 Query Match 72.0%; Score 221; DB 7; Length 454;
 Best Local Similarity 70.9%; Pred. No. 2.9e-21;
 Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
 OY 1 MQRFFGLNVTGKNEETLDMKKPCGVPDGGFMLTPGNPKWERTNLTYRINY 55
 DB 50 MQEFFFGLKVTGKPDATLTKVKKQPCGVPDVAQFVLTEGNPRWEQTHLTIRIENY 104
 RESULT 15
 ADL93945
 ID ADL93945 standard; protein; 454 AA.
 XX AC ADL93945;
 XX 20-MAY-2004 (first entry)
 DT
 DE Human G-coupled protein receptor-related protein #18.
 XX
 KW human; transgenic; Gene Therapy; Protein Therapy; cardiomyopathy;
 KW atherosclerosis; hypertension; congenital heart defect; aortic stenosis;
 KW atrial septal defect; atrioventricular canal defect; ductus arteriosus;
 KW pulmonary stenosis; subaortic stenosis; ventricular septal defect;
 KW valve disease; tuberculous sclerosis; scleroderma; obesity; transplantation;
 KW adrenoleukodystrophy; congenital adrenal hyperplasia; prostate cancer;
 KW neoplasm; adenocarcinoma; lymphoma; uterus cancer; fertility;
 KW haemophilia; hypercoagulation; idiopathic thrombocytopenic purpura;
 KW immunodeficiency; graft versus host disease; AIDS; bronchial asthma;
 KW Crohn's disease; G-coupled protein receptor; metabolic disorder;
 KW neurodegenerative disorder; receptor.
 OS Homo sapiens.
 XX
 XX US2004006205-A1.
 XX
 PD 08-JAN-2004.
 XX
 PF 02-APR-2002; 2002US-00115479.
 XX
 PR 03-APR-2001; 2001US-0281136P.
 PR 05-APR-2001; 2001US-0281863P.
 PR 05-APR-2001; 2001US-0281906P.
 PR 10-APR-2001; 2001US-0282934P.
 PR 13-APR-2001; 2001US-0283657P.
 PR 13-APR-2001; 2001US-0283678P.
 PR 13-APR-2001; 2001US-0283687P.
 PR 13-APR-2001; 2001US-0283710P.
 PR 17-APR-2001; 2001US-0284234P.
 PR 19-APR-2001; 2001US-0285325P.
 PR 20-APR-2001; 2001US-0285509P.
 PR 23-APR-2001; 2001US-0285748P.
 PR 23-APR-2001; 2001US-0285890P.
 PR 24-APR-2001; 2001US-0286068P.

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OM protein - protein search, using sw model

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(without alignments)
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Perfect score: 307
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 56318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	307	100.0	444	1	US-09-178-002-2
2	307	100.0	456	3	US-08-704-711A-17
3	307	100.0	466	3	US-09-521-220-17
4	307	100.0	467	1	US-09-178-002-4
5	307	100.0	467	3	US-09-391-104-24
6	307	100.0	468	3	US-08-448-489-13
7	221	72.0	469	3	US-08-704-711A-16
8	221	72.0	469	3	US-08-448-489-12
9	221	72.0	469	3	US-09-521-220-16
10	221	72.0	469	3	US-09-391-104-23
11	196	63.8	477	3	US-08-704-711A-20
12	196	63.8	477	3	US-08-448-489-15
13	196	63.8	477	3	US-08-281-313-1
14	196	63.8	477	3	US-09-521-220-20
15	196	63.8	477	3	US-09-391-104-21
16	195	63.5	476	3	US-08-704-711A-21
17	195	63.5	476	3	US-08-448-489-14
18	195	63.5	476	3	US-09-521-220-21
19	195	63.5	476	3	US-09-391-104-22
20	188	61.2	471	3	US-09-391-104-25
21	179	58.3	471	4	US-08-994-689C-1
22	172	56.0	471	4	US-08-394-689C-21
23	164	53.4	513	4	US-10-140-002-192
24	164	53.4	513	4	US-09-862-631-4
25	160	52.1	264	3	US-09-009-156-6
26	160	52.1	264	3	US-09-372-154-6
27	160	52.1	267	3	US-08-448-489-18

Sequence 27, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 26, Appli
Sequence 30, Appli
Sequence 4163, Ap
Sequence 7, Appli
Sequence 17, Appli
Sequence 18, Appli
Sequence 15, Appli
Sequence 19, Appli
Sequence 89, Appli
Sequence 30, Appli
Sequence 2, Appli
Sequence 10, Appli
Sequence 2, Appli
Sequence 4639, Ap

ALIGNMENTS

RESULT 1
US-09-178-002-2
; Sequence 2, Application US/09178002
; Patent No. H001973
; GENERAL INFORMATION:
; APPLICANT: Hu, Shou-Ih
; TITLE OF INVENTION: Human Neutrophil Collagenase Splice Variant
; FILE REFERENCE: CGC 2048
; CURRENT APPLICATION NUMBER: US/09/178,002
; CURRENT FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-178-002-2

Query Match 100.0%; Score 307; DB 1; Length 444;
Best Local Similarity 100.0%; Pred. No. 5.2e-32;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MCRFFGLNVTGKPNKEETLDMKKPRCGVDPGSGGFMLTGPNKWERNTLTIRNY 55
Db 43 MCRFFGLNVTGKPNKEETLDMKKPRCGVDPGSGGFMLTGPNKWERNTLTIRNY 97

RESULT 2
US-08-704-711A-17
; Sequence 17, Application US/08704711A
; Patent No. 6114159
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; APPLICANT: HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/704,711A
; FILING DATE: 20-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/DE95/00357
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 466 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-704-711A-17

Query Match 100.0%; Score 307; DB 3; Length 466;
Best Local Similarity 100.0%; Pred. No. 5.5e-32;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQRFFGLNVTGKNEETLDMKKPCGVPDGGFMLTPGNPKWERTNLTIRNY 55
Db 66 MQRFFGLNVTGKNEETLDMKKPCGVPDGGFMLTPGNPKWERTNLTIRNY 120

RESULT 3
US-09-521-220-17
; Sequence 17, Application US/09521220
; Patent No. 6399348
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/521,220
; FILING DATE: 08-Mar-2000
; CLASSIFICATION: <Unknown>
; 21-OCT-1994
; 17-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/704,711
; FILING DATE: <Unknown>
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 466 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-521-220-17

Query Match 100.0%; Score 307; DB 3; Length 466;
Best Local Similarity 100.0%; Pred. No. 5.5e-32;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQRFFGLNVTGKNEETLDMKKPCGVPDGGFMLTPGNPKWERTNLTIRNY 55
Db 66 MQRFFGLNVTGKNEETLDMKKPCGVPDGGFMLTPGNPKWERTNLTIRNY 120

RESULT 4
US-09-178-002-4
; Sequence 4, Application US/09178002
; Patent No. H001973
; GENERAL INFORMATION:
; APPLICANT: Hu Shou-th
; TITLE OF INVENTION: Human Neutrophil Collagenase Splice Variant
; FILE REFERENCE: CCC 2048
; CURRENT APPLICATION NUMBER: US/09/178,002
; CURRENT FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-178-002-4

Query Match 100.0%; Score 307; DB 1; Length 467;
Best Local Similarity 100.0%; Pred. No. 5.6e-32;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQRFFGLNVTGKNEETLDMKKPCGVPDGGFMLTPGNPKWERTNLTIRNY 55
Db 66 MQRFFGLNVTGKNEETLDMKKPCGVPDGGFMLTPGNPKWERTNLTIRNY 120

RESULT 5
US-09-391-104-24
; Sequence 24, Application US/09391104
; Patent No. 6399371
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Falduto, Michael T.
; APPLICANT: Magnuson, Scott R.
; APPLICANT: Morgan, Douglas W.
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,
; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
; TITLE OF INVENTION: OF USING SAME
; FILE REFERENCE: 6073.US.P1
; CURRENT APPLICATION NUMBER: US/09/391,104
; CURRENT FILING DATE: 1999-09-07
; PRIOR APPLICATION NUMBER: US 08/814,394
; PRIOR FILING DATE: 1997-03-11
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 467
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/DE95/00357
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 469 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-704-711A-16

Query Match 72.0%; Score 221; DB 3; Length 469;
Best Local Similarity 70.9%; Pred. No. 1.le-20;
Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 MQRFFGLNVTGKNEETLDMKKPRCGVPDSGGFMLTPGPKVETNLTVRIY 55
Db 67 MQEFGGLKVTGKPDAAETLVKMKPRCGVPDVAQFVLTEGAPRWEQHTLYRIENY 121

RESULT 8
US-08-448-489-12
; Sequence 12, Application US/08448489
; Patent No. 6184022
; GENERAL INFORMATION:
; APPLICANT: SEIKI, Motoharu
; APPLICANT: SATO, Hiroshi
; APPLICANT: SHINAGAWA, Akira
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
; FILE REFERENCE: 55-290P
; CURRENT APPLICATION NUMBER: US/08/448,489
; CURRENT FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 12
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Known Member of
; OTHER INFORMATION: Matrix Metalloproteinase Family
; US-08-448-489-12

Query Match 72.0%; Score 221; DB 3; Length 469;
Best Local Similarity 70.9%; Pred. No. 1.le-20;
Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 MQRFFGLNVTGKNEETLDMKKPRCGVPDSGGFMLTPGPKVETNLTVRIY 55
Db 67 MQEFGGLKVTGKPDAAETLVKMKPRCGVPDVAQFVLTEGAPRWEQHTLYRIENY 121

RESULT 9
US-09-521-220-16
; Sequence 16, Application US/09521220
; Patent No. 6393348
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; APPLICANT: HINZMANN, Bernd

```

TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/521,220.
FILING DATE: 08-Mar-2000
CLASSIFICATION: <Unknown>
21-OCT-1994
17-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/704,711
FILING DATE: <Unknown>
APPLICATION NUMBER: DE 4438838.1
FILING DATE: 21-OCT-1994
APPLICATION NUMBER: DE 4409663.1
FILING DATE: 17-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 26083/124
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 469 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-521-220-16
Query Match 72.0%; Score 221; DB 3; Length 469;
Best Local Similarity 70.9%; Pred. No. 1.1e-20;
Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
QY 1 MQRFFGLNVTGKNEETLDMKKPRCGVDPDSGGFMLTPGNPKWERTNLTYYRNY 55
Db 67 MQEFGKLVGTGPDATLTKVMKQPRCGVDPVAQFVLTEGNPRWEQTHLYRIENY 121
RESULT 10
US-09-391-104-23
Sequence 23, Application US/093911104
Patent No. 6399371
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Falduto, Michael T.
APPLICANT: Magnuson, Scott R.
APPLICANT: Morgan, Douglas W.
TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,
TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
FILE REFERENCE: 6073.US.21
CURRENT APPLICATION NUMBER: US/09/391,104
CURRENT FILING DATE: 1999-09-07
PRIOR APPLICATION NUMBER: US 08/814,394
PRIOR FILING DATE: 1997-03-11
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 23
LENGTH: 469
TYPE: PRT
ORGANISM: Homo sapiens
US-09-391-104-23
Query Match 72.0%; Score 221; DB 3; Length 469;
Best Local Similarity 70.9%; Pred. No. 1.1e-20;
Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
QY 1 MQRFFGLNVTGKNEETLDMKKPRCGVDPDSGGFMLTPGNPKWERTNLTYYRNY 55
Db 67 MQEFGKLVGTGPDATLTKVMKQPRCGVDPVAQFVLTEGNPRWEQTHLYRIENY 121
RESULT 11
US-08-704-711A-20
Sequence 20, Application US/08704711A
Patent No. 6114159
GENERAL INFORMATION:
APPLICANT: WILL, Horst
APPLICANT: HINZMANN, Bernd
TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/704,711A
FILING DATE: 20-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/DE95/00357
FILING DATE: 17-MAR-1995
PRIOR APPLICATION NUMBER: DE 4438838.1
FILING DATE: 21-OCT-1994
APPLICATION NUMBER: DE 4409663.1
FILING DATE: 17-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 26083/124
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 477 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-704-711A-20
Query Match 63.8%; Score 196; DB 3; Length 477;
Best Local Similarity 63.8%; Pred. No. 2.1e-17;
Matches 35; Conservative 8; Mismatches 12; Indels 0; Gaps 0;
QY 1 MQRFFGLNVTGKNEETLDMKKPRCGVDPDSGGFMLTPGNPKWERTNLTYYRNY 55
Db 67 MQEFGKLVGTGPDATLTKVMKQPRCGVDPVAQFVLTEGNPRWEQTHLYRIENY 121

RESULT 12
US-08-448-489-15
; Sequence 15, Application US/08448489
; Patent No. 6184022
; GENERAL INFORMATION:
; APPLICANT: SEIKI, Motoharu
; APPLICANT: SATO, Hiroshi
; APPLICANT: SHINAGAWA, Akira
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
; FILE REFERENCE: 55-230P
; CURRENT APPLICATION NUMBER: US/08/448,489
; CURRENT FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 15
; LENGTH: 477
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Known Member of
; OTHER INFORMATION: Matrix Metalloproteinase Family
US-08-448-489-15

Query Match 63.8%; Score 196; DB 3; Length 477;
Best Local Similarity 63.6%; Pred. No. 2.1e-17;
Matches 35; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 MQRFFGLNVTGKPNNEETLDMKPRCGVDPDGGFMLTPGNPKWERTNLTIRINY 55
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Db 67 MQKFLGLEVTGKLDSDTLEVMKPRCGVDPDVGHFRTFGIPKWKRLTLYRINY 121

RESULT 13
US-08-281-313-1
; Sequence 9, Application US/09368169
; Patent No. 6284511
; GENERAL INFORMATION:
; APPLICANT: Tetsuya INAKA et al.
; TITLE OF INVENTION: HEAT-STABLE PROLYENDOPEPTIDASE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
; STREET: 2033 K Street, N.W., Suite 800
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/368,169
; FILING DATE: August 5, 1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/750,816
; FILING DATE: January 8, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee Cheng
; REGISTRATION NUMBER: 40,949
; REFERENCES/DOCKET NUMBER: 99-0868/LC (WMC) 49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-721-8200
; TELEFAX: 202-721-8250
; TELEX:

INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acid residues
; TYPE: amino acid

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; ORIGINAL SOURCE:
; ORGANISM: Flavobacterium meningosepticum
; ORGANISM: Met Lys Tyr Asn Lys Leu Ser Val Ala Val Ala Phe Ala Phe Ala Ala V
; ORGANISM: 1
; Sequence 1, Application US/08281313
; Patent No. 6284513
; GENERAL INFORMATION:
; APPLICANT: Ye, Qi-Zhuang
; APPLICANT: Johnson, Linda L.
; APPLICANT: Hupe, Donald J.
; APPLICANT: Bakagi, Vijaykumar
; TITLE OF INVENTION: Process for the Production of
; TITLE OF INVENTION: Stromelysin Catalytic Domain Protein
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Warner-Lambert Company
; STREET: 2800 Plymouth Rd.
; CITY: Ann Arbor
; STATE: MI
; COUNTRY: US
; ZIP: 48105

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/281,313
; FILING DATE:
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/012,705
; FILING DATE: 03-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Tinney, Francis J.
; REGISTRATION NUMBER: 33,069
; REFERENCE/DOCKET NUMBER: 4415-01-FJT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 313 996-7295
; TELEFAX: 313 996-1553

; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 477 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 100..273
; OTHER INFORMATION: /note= "Mature stromelysin
; OTHER INFORMATION: catalytic domain protein"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..17
; OTHER INFORMATION: /note= "Signal peptide"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 18..99
; OTHER INFORMATION: /note= "Propeptide"
US-08-281-313-1

Query Match 63.8%; Score 196; DB 3; Length 477;
Best Local Similarity 63.6%; Pred. No. 2.1e-17;
Matches 35; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 MQRFFGLNVTGKPNNEETLDMKPRCGVDPDGGFMLTPGNPKWERTNLTIRINY 55
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 67 MQKFLGLEVTGKLDSDTLEVMKPRCGVDPDVGHFRTFGIPKWKRLTLYRINY 121

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RESULT 14
US-09-521-220-20
; Sequence 20, Application US/09521220
; Patent No. 6399348
; GENERAL INFORMATION:
; APPLICANT: WILL, Horet
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/521,220
; FILING DATE: 08-Mar-2000
; CLASSIFICATION: <Unknown>
; 21-OCT-1994
; 17-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/704,711
; FILING DATE: <Unknown>
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 477 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
;
US-09-521-220-20
Query Match 63.8%; Score 196; DB 3; Length 477;
Best Local Similarity 63.6%; Pred. No. 2.1e-17;
Matches 35; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

Qy 1 MQRFFGLNVTGKPNBETLDMKKPCGVPDVGFMTPGNPKWERTNLTIRNY 55
Db 67 MQKFLGLEVTGKLDSDTLEVMRKPCGVPDVGHFRTFPGIPKWRKTHLTIRVNY 121

RESULT 15
US-09-391-104-21
; Sequence 21, Application US/09391104
; Patent No. 6399371
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Palduto, Michael T.
; APPLICANT: Magnuson, Scott R.
; APPLICANT: Morgan, Douglas W.
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,
; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS

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; TITLE OF INVENTION: OF USING SAME
; FILE REFERENCE: 6073 US P1
; CURRENT APPLICATION NUMBER: US/09/391,104
; CURRENT FILING DATE: 1999-09-07
; PRIOR APPLICATION NUMBER: US 08/814,394
; PRIOR FILING DATE: 1997-03-11
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 477
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-391-104-21
Query Match 63.8%; Score 196; DB 3; Length 477;
Best Local Similarity 63.6%; Pred. No. 2.1e-17;
Matches 35; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

Qy 1 MQRFFGLNVTGKPNBETLDMKKPCGVPDVGFMTPGNPKWERTNLTIRNY 55
Db 67 MQKFLGLEVTGKLDSDTLEVMRKPCGVPDVGHFRTFPGIPKWRKTHLTIRVNY 121

Search completed: October 13, 2004, 15:17:05
Job time : 26.0897 secs

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OM protein - protein search, using sw model

Run on: October 13, 2004, 15:14:50 ; Search time 78.2692 Seconds
(without alignments)
226.750 Million cell updates/sec

Title: US-10-032-376A-10
Perfect score: 307
Sequence: 1 MQRFGLVNVTGKPNKEETLDM.....LTPGNPKWERTNLTYYRIYNY 55

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1356558 seqs, 322682953 residues

Total number of hits satisfying chosen parameters: 1356558

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	307	100.0	55	US-10-219-329-10	Sequence 10, Appl
2	307	100.0	55	US-10-153-185-10	Sequence 10, Appl
3	307	100.0	55	US-10-219-561-10	Sequence 10, Appl
4	307	100.0	55	US-10-032-376A-10	Sequence 10, Appl
5	307	100.0	55	US-10-335-207-10	Sequence 10, Appl
6	307	100.0	467	US-09-391-104-24	Sequence 24, Appl
7	307	100.0	467	US-09-801-196-20	Sequence 20, Appl
8	307	100.0	467	US-09-759-130B-176	Sequence 176, Appl
9	307	100.0	467	US-10-131-985-31	Sequence 31, Appl
10	307	100.0	467	US-10-741-790-176	Sequence 176, Appl
11	221	72.0	454	US-10-115-479-32	Sequence 32, Appl
12	221	72.0	454	US-10-115-479-34	Sequence 34, Appl
13	221	72.0	454	US-10-115-479-36	Sequence 36, Appl
14	221	72.0	454	US-10-115-479-38	Sequence 38, Appl

15	221	72.0	469	9	US-09-391-104-23	Sequence 23, Appl
16	221	72.0	469	9	US-09-801-196-19	Sequence 19, Appl
17	221	72.0	469	9	US-09-853-386-100	Sequence 100, Appl
18	221	72.0	469	14	US-10-301-822-119	Sequence 119, Appl
19	221	72.0	469	14	US-10-021-660-76	Sequence 76, Appl
20	221	72.0	469	14	US-10-308-279-34	Sequence 34, Appl
21	221	72.0	469	14	US-10-131-985-23	Sequence 23, Appl
22	221	72.0	469	14	US-10-295-027-12	Sequence 12, Appl
23	221	72.0	469	14	US-10-295-027-14	Sequence 14, Appl
24	221	72.0	469	14	US-10-295-027-1167	Sequence 1167, Appl
25	221	72.0	469	14	US-10-295-027-1168	Sequence 1168, Appl
26	221	72.0	469	15	US-10-115-479-30	Sequence 30, Appl
27	221	72.0	469	15	US-10-115-479-40	Sequence 40, Appl
28	221	72.0	469	15	US-10-211-463-22	Sequence 22, Appl
29	221	72.0	469	15	US-10-188-832-6	Sequence 6, Appl
30	221	72.0	469	16	US-10-734-564-109	Sequence 109, Appl
31	221	72.0	470	15	US-10-447-315-1	Sequence 1, Appl
32	221	72.0	496	14	US-10-106-698-6283	Sequence 6283, Appl
33	221	69.7	54	14	US-10-219-329-9	Sequence 9, Appl
34	214	69.7	54	14	US-10-153-185-9	Sequence 9, Appl
35	214	69.7	54	14	US-10-219-561-9	Sequence 9, Appl
36	214	69.7	54	16	US-10-032-376A-9	Sequence 9, Appl
37	214	69.7	54	16	US-10-335-207-9	Sequence 9, Appl
38	198	64.5	173	15	US-10-115-479-48	Sequence 48, Appl
39	196	63.8	267	14	US-10-133-797-73	Sequence 73, Appl
40	196	63.8	477	9	US-09-391-104-21	Sequence 21, Appl
41	196	63.8	477	9	US-09-801-196-24	Sequence 24, Appl
42	196	63.8	477	14	US-10-171-311-137	Sequence 137, Appl
43	196	63.8	477	14	US-10-301-822-127	Sequence 127, Appl
44	196	63.8	477	14	US-10-131-985-27	Sequence 27, Appl
45	196	63.8	477	14	US-10-295-027-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1
US-10-219-329-10
; Sequence 10, Application US/10219329
; Publication No. US20030096757A1
; GENERAL INFORMATION:
; APPLICANT: Quirk, Stephen
; APPLICANT: Weart, Ilona f.
; TITLE OF INVENTION: Anti-Cancer and Wound Healing Compounds
; FILE REFERENCE: 1443.035WO1
; CURRENT APPLICATION NUMBER: US/10/219,329
; CURRENT FILING DATE: 2002-08-15
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-219-329-10

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Best Local Similarity 100.0%; Pred. No. 8.8e-33;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-10-153-185-10
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; Publication No. US20030148959A1
; GENERAL INFORMATION:

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; APPLICANT: Quirk, Stephen
; APPLICANT: Malik, Schail
; TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds
; FILE REFERENCE: 1443.034US1
; CURRENT APPLICATION NUMBER: US/10/153,185
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-185-10

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RESULT 3
US-10-219-561-10
; Sequence 10, Application US/10/219,561
; Publication No. US2003016567A1
; GENERAL INFORMATION:
; APPLICANT: Quirk, Stephen
; APPLICANT: Malik, Schail
; APPLICANT: Villanueva, Julie M.
; TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds
; FILE REFERENCE: 1443.008US2
; CURRENT APPLICATION NUMBER: US/10/219,561
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 10/153,185
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-219-561-10

Query Match      100.0%; Score 307; DB 14; Length 55;
Best Local Similarity 100.0%; Pred. No. 8.8e-33;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
US-10-032-376A-10
; Sequence 10, Application US/10032376A
; Publication No. US20040127420A1
; GENERAL INFORMATION:
; APPLICANT: Quirk, Steven
; TITLE OF INVENTION: Metalloproteinase Inhibitors for Wound Healing
; FILE REFERENCE: 1443.008US1
; CURRENT APPLICATION NUMBER: US/10/032,376A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/312,726
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; PRIOR FILING DATE: 2001-08-16
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; LENGTH: 55
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-376A-10

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Best Local Similarity 100.0%; Pred. No. 8.8e-33;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-10-335-207-10
; Sequence 10, Application US/10335207
; Publication No. US20040127421A1
; GENERAL INFORMATION:
; APPLICANT: Malik, Schail
; APPLICANT: Quirk, Stephen
; TITLE OF INVENTION: Method to Increase Fibronection
; FILE REFERENCE: 1443.047US1
; CURRENT APPLICATION NUMBER: US/10/335,207
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-335-207-10

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Best Local Similarity 100.0%; Pred. No. 8.8e-33;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 6
US-09-391-104-24
; Sequence 24, Application US/09391104
; Publication No. US20020031817A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Falduto, Michael T.
; APPLICANT: Magnuson, Scott R.
; APPLICANT: Morgan, Douglas W.
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEINASE GENE,
; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
; TITLE OF INVENTION: OF USING SAME
; FILE REFERENCE: 6073 US. P1
; CURRENT APPLICATION NUMBER: US/09/391,104
; CURRENT FILING DATE: 1999-09-07
; PRIOR APPLICATION NUMBER: US 08/814,394
; PRIOR FILING DATE: 1997-03-11
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-391-104-24

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Db 66 MQRFFGLNVTGKNEETLDMKKPRCGVDSGGFMLTPGNPKWERTNLTIRNY 120

RESULT 7
US-09-801-196-20
; Sequence 20, Application US/09801196
; Patent No. US20020037827A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Kai
; APPLICANT: Smith, Ryan
; APPLICANT: Fajardo, Mark
; APPLICANT: Moos, Patrick
; TITLE OF INVENTION: A NOVEL MATRIX METALLOPROTEINASE (MMP-25)
; TITLE OF INVENTION: EXPRESSED IN SKIN CELLS
; FILE REFERENCE: 240083.509
; CURRENT APPLICATION NUMBER: US/09/801,196
; CURRENT FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-801-196-20

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Best Local Similarity 100.0%; Pred. No. 1.1e-31;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 8
US-09-759-130B-176
; Sequence 176, Application US/09759130B
; Publication No. US2003002279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirst, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; FILE REFERENCE: MP100-5350NIM
; CURRENT APPLICATION NUMBER: US/09/759,130B
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
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; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 176
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-130B-176

Query Match 100.0%; Score 307; DB 10; Length 467;
Best Local Similarity 100.0%; Pred. No. 1.1e-31;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQRFFGLNVTGKNEETLDMKKPRCGVDSGGFMLTPGNPKWERTNLTIRNY 55
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RESULT 9
US-10-131-985-31
; Sequence 31, Application US/10131985
; Publication No. US2003019940A1
; GENERAL INFORMATION:
; APPLICANT: Dack, Kevin N
; APPLICANT: Davies, Michael J
; APPLICANT: Fish, Paul V
; APPLICANT: Huggins, Jonathan P
; APPLICANT: McIntosh, Fraser S
; APPLICANT: Occleston, Nicholas L
; TITLE OF INVENTION: Composition
; FILE REFERENCE: PCS 10391A
; CURRENT APPLICATION NUMBER: US/10/131,985
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US/09/726,295
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: GB 9930768.8
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 31
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-131-985-31

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Best Local Similarity 100.0%; Pred. No. 1.1e-31;
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RESULT 10
US-10-741-790-176
; Sequence 176, Application US/10741790
; Publication No. US20040121396A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirst, Susan J
; APPLICANT: Mackay, Charles R
```

APPLICANT: Myers, Paul S
APPLICANT: Leiby, Kevin R
APPLICANT: Wrighton, Nicolas
APPLICANT: Goodearl, Andrew
APPLICANT: Holtzman, Douglas A
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
TITLE OF INVENTION: USES
FILE REFERENCE: MPI00-5350NMIM
CURRENT APPLICATION NUMBER: US/10/741,790
CURRENT FILING DATE: 2003-12-19
PRIOR APPLICATION NUMBER: US 09/479,249
PRIOR FILING DATE: 2000-01-07
PRIOR APPLICATION NUMBER: US 09/559,497
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/578,063
PRIOR FILING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: US 09/333,159
PRIOR FILING DATE: 1999-06-14
PRIOR APPLICATION NUMBER: US 09/596,194
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/342,364
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: US 09/608,452
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/393,996
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: US 09/602,871
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 09/420,707
PRIOR FILING DATE: 1999-10-19
NUMBER OF SEQ ID NOS: 460
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 176
LENGTH: 467
TYPE: PRT
ORGANISM: Homo sapiens
US-10-741-790-176

Query Match 100.0%; Score 307; DB 16; Length 467;
Best Local Similarity 100.0%; Pred. No. 1.1e-31;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 66 MQRFFGLVNTGKNEETLDMKKPRCGVDPDSGGFVLTGPNPKWERTNLTYYIRNY 120

RESULT 11
US-10-115-479-32
Sequence 32, Application US/10115479
Publication No. US20040006205A1
GENERAL INFORMATION:
APPLICANT: Li, Li
APPLICANT: Gerlach, Valerie L.
APPLICANT: Liu, Xiaohong
APPLICANT: Miller, Charles E.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Zerhusen, Bryan D.
APPLICANT: Pena, Carol E.A.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Zhong, Haihong
APPLICANT: Smithson, Glendda
APPLICANT: Casman, Stacie J.
APPLICANT: Boldog, Ferenc L.;
APPLICANT: Voss, Edward
APPLICANT: Vernet, Corine
APPLICANT: MacDougall, John A.
APPLICANT: Rastelli, Luca
APPLICANT: Anderson, David W.
APPLICANT: Zhong, Mei
APPLICANT: Mezes, Peter S.
APPLICANT: Furtak, Katarzyna

APPLICANT: Patturajan, Meera
APPLICANT: Burgess, Catherine E.
APPLICANT: Malyanker, Uriel M.
APPLICANT: Shimkets, Richard A.
APPLICANT: Taupier, Raymond J.
APPLICANT: Edinger, Shlomit R.
APPLICANT: Mazur, Ann
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REFERENCE: 21402-322 B (Cura 622 PI)
CURRENT APPLICATION NUMBER: US/10/115,479
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: 60/281,136
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/281,863
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/281,906
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/282,934
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: 60/283,657
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/283,678
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/283,687
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/283,710
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/284,234
PRIOR FILING DATE: 2001-04-17
PRIOR APPLICATION NUMBER: 60/285,325
PRIOR FILING DATE: 2001-04-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 198
SEQ ID NO 32
LENGTH: 454
TYPE: PRT
ORGANISM: Homo sapiens
US-10-115-479-32

Query Match 72.0%; Score 221; DB 15; Length 454;
Best Local Similarity 70.9%; Pred. No. 2.3e-20;
Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
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Db 50 MQEFFFGLVNTGKNEETLDMKKPRCGVDPDSGGFVLTGPNPKWERTNLTYYIRNY 104

RESULT 12
US-10-115-479-34
Sequence 34, Application US/10115479
Publication No. US20040006205A1
GENERAL INFORMATION:
APPLICANT: Li, Li
APPLICANT: Gerlach, Valerie L.
APPLICANT: Liu, Xiaohong
APPLICANT: Miller, Charles E.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Zerhusen, Bryan D.
APPLICANT: Pena, Carol E.A.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Zhong, Haihong
APPLICANT: Smithson, Glendda
APPLICANT: Casman, Stacie J.
APPLICANT: Boldog, Ferenc L.;
APPLICANT: Voss, Edward
APPLICANT: Vernet, Corine
APPLICANT: MacDougall, John A.
APPLICANT: Rastelli, Luca
APPLICANT: Anderson, David W.
APPLICANT: Zhong, Mei
APPLICANT: Mezes, Peter S.
APPLICANT: Furtak, Katarzyna

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/ APPLICANT: Patturajan, Meera
/ APPLICANT: Burgess, Catherine E.
/ APPLICANT: Malyanker, Uriel M.
/ APPLICANT: Shimkets, Richard A.
/ APPLICANT: Taupier, Raymond J.
/ APPLICANT: Edinger, Shlomit R.
/ APPLICANT: Mazur, Ann
/ TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
/ FILE REFERENCE: 21402-322 B (Cura 622 PT)
/ CURRENT APPLICATION NUMBER: US/10/115,479
/ CURRENT FILING DATE: 2002-11-18
/ PRIOR APPLICATION NUMBER: 60/281,136
/ PRIOR FILING DATE: 2001-04-03
/ PRIOR APPLICATION NUMBER: 60/281,863
/ PRIOR FILING DATE: 2001-04-05
/ PRIOR APPLICATION NUMBER: 60/281,906
/ PRIOR FILING DATE: 2001-04-05
/ PRIOR APPLICATION NUMBER: 60/282,934
/ PRIOR FILING DATE: 2001-04-10
/ PRIOR APPLICATION NUMBER: 60/283,657
/ PRIOR FILING DATE: 2001-04-13
/ PRIOR APPLICATION NUMBER: 60/283,678
/ PRIOR FILING DATE: 2001-04-13
/ PRIOR APPLICATION NUMBER: 60/283,687
/ PRIOR FILING DATE: 2001-04-13
/ PRIOR APPLICATION NUMBER: 60/283,710
/ PRIOR FILING DATE: 2001-04-13
/ PRIOR APPLICATION NUMBER: 60/284,234
/ PRIOR FILING DATE: 2001-04-17
/ PRIOR APPLICATION NUMBER: 60/285,325
/ PRIOR FILING DATE: 2001-04-19
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 198
/ SEQ ID NO 34
/ LENGTH: 454
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-115-479-34
```

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Query Match 72.0%; Score 221; DB 15; Length 454;
Best Local Similarity 70.9%; Pred. No. 2.3e-20;
Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
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```
OY 1 MQRFFGLNVTGKNEETLDMKKPRCGVDSGGFMLTPGNPKWERTNLTIRNY 55
Db 50 MQEFGKLVTKGKPDATLTKVMKQPRCGVDPVQFVLTEGNPRWEQTHLTIRNY 104
```

```
RESULT 13
US-10-115-479-36
/ Sequence 36, Application US/10115479
/ Publication No. US20040006205A1
/ GENERAL INFORMATION:
/ APPLICANT: Li, Li
/ APPLICANT: Gerlach, Valerie L.
/ APPLICANT: Liu, Xiaohong
/ APPLICANT: Miller, Charles E.
/ APPLICANT: Spyttek, Kimberly A.
/ APPLICANT: Zerhusen, Bryan D.
/ APPLICANT: Pena, Carol E.A.
/ APPLICANT: Shenoy, Suresh G.
/ APPLICANT: Zhong, Haihong
/ APPLICANT: Smithson, Glenda
/ APPLICANT: Casman, Stacie J.
/ APPLICANT: Boldog, Ferenc L.;
/ APPLICANT: Voss, Edward
/ APPLICANT: Vernet, Corine
/ APPLICANT: MacDougall, John A.
/ APPLICANT: Rastelli, Luca
/ APPLICANT: Anderson, David W.
/ APPLICANT: Zhong, Mei
/ APPLICANT: Mezes, Peter S.
/ APPLICANT: Furtak, Katarzyna
```

```
/ APPLICANT: Patturajan, Meera
/ APPLICANT: Burgess, Catherine E.
/ APPLICANT: Malyanker, Uriel M.
/ APPLICANT: Shimkets, Richard A.
/ APPLICANT: Taupier, Raymond J.
/ APPLICANT: Edinger, Shlomit R.
/ APPLICANT: Mazur, Ann
/ TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
/ FILE REFERENCE: 21402-322 B (Cura 622 PT)
/ CURRENT APPLICATION NUMBER: US/10/115,479
/ CURRENT FILING DATE: 2002-11-18
/ PRIOR APPLICATION NUMBER: 60/281,136
/ PRIOR FILING DATE: 2001-04-03
/ PRIOR APPLICATION NUMBER: 60/281,863
/ PRIOR FILING DATE: 2001-04-05
/ PRIOR APPLICATION NUMBER: 60/281,906
/ PRIOR FILING DATE: 2001-04-05
/ PRIOR APPLICATION NUMBER: 60/282,934
/ PRIOR FILING DATE: 2001-04-10
/ PRIOR APPLICATION NUMBER: 60/283,657
/ PRIOR FILING DATE: 2001-04-13
/ PRIOR APPLICATION NUMBER: 60/283,678
/ PRIOR FILING DATE: 2001-04-13
/ PRIOR APPLICATION NUMBER: 60/283,687
/ PRIOR FILING DATE: 2001-04-13
/ PRIOR APPLICATION NUMBER: 60/283,710
/ PRIOR FILING DATE: 2001-04-13
/ PRIOR APPLICATION NUMBER: 60/284,234
/ PRIOR FILING DATE: 2001-04-17
/ PRIOR APPLICATION NUMBER: 60/285,325
/ PRIOR FILING DATE: 2001-04-19
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 198
/ SEQ ID NO 36
/ LENGTH: 454
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-115-479-36
```

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Query Match 72.0%; Score 221; DB 15; Length 454;
Best Local Similarity 70.9%; Pred. No. 2.3e-20;
Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
```

```
OY 1 MQRFFGLNVTGKNEETLDMKKPRCGVDSGGFMLTPGNPKWERTNLTIRNY 55
Db 50 MQEFGKLVTKGKPDATLTKVMKQPRCGVDPVQFVLTEGNPRWEQTHLTIRNY 104
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RESULT 14
US-10-115-479-38
/ Sequence 38, Application US/10115479
/ Publication No. US20040006205A1
/ GENERAL INFORMATION:
/ APPLICANT: Li, Li
/ APPLICANT: Gerlach, Valerie L.
/ APPLICANT: Liu, Xiaohong
/ APPLICANT: Miller, Charles E.
/ APPLICANT: Spyttek, Kimberly A.
/ APPLICANT: Zerhusen, Bryan D.
/ APPLICANT: Pena, Carol E.A.
/ APPLICANT: Shenoy, Suresh G.
/ APPLICANT: Zhong, Haihong
/ APPLICANT: Smithson, Glenda
/ APPLICANT: Casman, Stacie J.
/ APPLICANT: Boldog, Ferenc L.;
/ APPLICANT: Voss, Edward
/ APPLICANT: Vernet, Corine
/ APPLICANT: MacDougall, John A.
/ APPLICANT: Rastelli, Luca
/ APPLICANT: Anderson, David W.
/ APPLICANT: Zhong, Mei
/ APPLICANT: Mezes, Peter S.
/ APPLICANT: Furtak, Katarzyna
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 13, 2004, 15:01:19 ; Search time 20.8013 Seconds
(without alignments)
254.404 Million cell updates/sec

Title: US-10-032-376A-10
Perfect score: 307
Sequence: 1 MQRFFGLNVTGPKNEETLDM.....LTPGNPKWERTNLTLYRNY 55

Scoring table: BLOSUM62
Gapop'10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: Pir1: *
2: Pir2: *
3: Pir3: *
4: Pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	307	100.0	467	1 KCHUN	neutrophil collage
2	233	75.9	468	1 KCRBI	interstitial colla
3	231	75.2	469	1 KCRGI	interstitial colla
4	221	72.0	469	1 KCHUI	interstitial colla
5	218	71.0	469	1 KCOBI	interstitial colla
6	201.5	65.6	384	2 I51267	collagenase (EC 3.
7	196	63.8	477	1 KCHUS1	stromelysin 1 (EC
8	195	63.5	476	1 KCHUS2	stromelysin 2 (EC
9	193	62.9	476	1 JC6505	stromelysin 2 (EC
10	193	62.9	477	1 KMS51	stromelysin 1 (EC
11	192	62.5	478	1 KCRBS1	stromelysin 1 (EC
12	190	61.9	476	1 KCRTS2	stromelysin 2 (EC
13	189	61.6	466	2 A23685	interstitial colla
14	189	61.6	472	2 S29243	interstitial colla
15	188	61.2	471	2 A53711	collagenase 3 (EC
16	188	61.2	475	1 KCRTHH	stromelysin 1 (EC
17	183	59.6	483	2 JC5743	matrix metalloprot
18	163	53.1	267	2 A57490	matrilysin (EC 3.4
19	160	52.1	267	1 KCHUM	matrilysin (EC 3.4
20	160	52.1	470	2 A49499	metalloelastase HM
21	160	52.1	663	1 S46492	gelatinase A (EC 3
22	155	50.5	662	2 S70365	gelatinase A (EC 3
23	153	49.8	660	1 A28153	gelatinase A (EC 3
24	153	49.8	662	2 A24496	gelatinase A (EC 3
25	153	49.8	662	2 S34780	gelatinase A (EC 3
26	139.5	45.4	669	2 I38029	matrix metalloprot
27	138	45.0	662	2 A42401	macrophage elastat
28	134.5	43.8	582	2 I38028	matrix metalloprot
29	134.5	43.8	582	2 I84471	matrix metalloprot

30	134	43.6	707	1 A53796	gelatinase B (EC 3
31	132	43.0	708	2 S62907	gelatinase B (EC 3
32	131	42.7	712	1 I46031	gelatinase B (EC 3
33	129.5	42.2	582	2 I48673	matrix metalloprot
34	129	42.0	707	1 A34458	gelatinase B (EC 3
35	127	41.4	708	2 JC4364	gelatinase B (EC 3
36	120	39.1	82	2 PW0052	pro-matrix metallo
37	118.5	38.6	730	1 I52580	gelatinase B (EC 3
38	118.5	38.6	730	2 JC1456	gelatinase B (EC 3
39	111	36.2	521	2 T37252	probable matrix me
40	108	35.2	341	2 T51957	metalloproteinase
41	108	35.2	342	2 G84885	probable metallopr
42	104	33.9	364	2 Z71433	probable metallopr
43	90	29.3	377	2 T08643	zinc metalloprotei
44	89.5	29.2	305	2 T08836	probable metallopr
45	89.5	29.2	378	2 E96724	hypothetical prote

ALIGNMENTS

RESULT 1

KCHUN
neutrophil collagenase (EC 3.4.24.34) precursor [validated] - human
N:Alternate names: matrix metalloproteinase 8
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text change 09-Jul-2004
C:Accession: A37073; A61175; B61175; A36230; S09680; S11026; S19576; S27225; S32527; S6
R:Hasty, K.A.; Pourmotabbed, T.F.; Goldberg, G.I.; Thompson, D.G.; Spinnella, D.G.; Stev
J. Biol. Chem. 265, 11421-11424, 1990
A:Title: Human neutrophil collagenase. A distinct gene product with homology to other m
A:Reference number: A37073; MUID:90307647; PMID:2164002
A:Accession: A37073
A:Molecule type: mRNA
A:Residues: 1-467 <HAS>
A:Cross-references: UNIPROT:P22894; GB:J05556; NID:G180617; PIDN:AAA88021.1; PID:G18061
R:Devaxajan, P.; Mookhtiar, K.; Van Wart, H.; Berliner, N.
Blood 77, 2731-2738, 1991
A:Title: Structure and expression of the cDNA encoding human neutrophil collagenase.
A:Reference number: A61175; MUID:91255696; PMID:1646048
A:Accession: A61175
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-31, 'I', 33-86, 'E', 88-467 <DEV>
A:Accession: B61175
A:Molecule type: protein
A:Residues: 263-264, 'X', 266-270, 'X', 272-273, 'X', 275, 'X', 277 <DE2>
R:Mallya, S.K.; Mookhtiar, K.A.; Gao, Y.; Brew, K.; Dioszegi, M.; Birkedal-Hansen, H.;
Biochemistry 29, 10628-10634, 1990
A:Title: Characterization of 58-kilodalton human neutrophil collagenase: comparison wit
A:Reference number: A36230; MUID:91104978; PMID:2176876
A:Accession: A36230
A:Molecule type: protein
A:Residues: 'X', 86-87, 'X', 89-90, 'X', 92-97, 'X', 99-111, 'X', 113-120 <VAL>
R:Knaeuper, V.; Kraemer, S.; Reinke, H.; Tschesche, H.
Eur. J. Biochem. 189, 295-300, 1990
A:Title: Characterization and activation of procollagenase from human polymorphonuclear
A:Reference number: S09680; MUID:90249372; PMID:2159879
A:Accession: S09680
A:Molecule type: protein
A:Residues: 21-31, 'I', 33-39, 'I', 41-47, 'V', 49-53, 'I', 55-72, 'G', 74-86, 'E', 88-111, 'X', 113-
A>Note: 67-Lys was also found
R:Knaeuper, V.; Kraemer, S.; Reinke, H.; Tschesche, H.
Biol. Chem. Hoppe-Seyler 371, 733, 1990
A:Title: Corrigendum. Partial amino-acid sequence of human PMN leukocyte procollagenase
A:Reference number: S11026; MUID:91000455; PMID:2169766
A>Note: Original publication was Biol. Chem. Hoppe-Seyler 371 (Suppl.), 295-304, 1990
A:Accession: S11026
A:Molecule type: protein
A:Residues: 21-31, 'I', 33-53, 'I', 55-72, 'G', 74-111, 'X', 113-140; 183-203, 'X', 205-209; 248-26
A>Note: 87-Glu was also found
R:Blasner, J.; Knaeuper, V.; Osthus, A.; Reinke, H.; Tschesche, H.
Eur. J. Biochem. 202, 1223-1230, 1991

tion peptide by other proteinases.

C;Comment: Procollagenase is found in glycosylated and unglycosylated forms, both of which

C;Genetics:

A;Gene: GDB:MMP1; CLG

A;Cross-references: GDB:119783; OMIM:120353

A;Map position: 11q22.2-11q22.3

C;Function:

A;Description: hydrolyzes collagens, in particular types I, II, III, and X, serpins, and

C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloproteinase

C;Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metalloprotein

F;1-19/Domain: signal sequence #status predicted <SIG>

F;20-469/Product: procollagenase #status experimental <PRO>

F;20-99/Domain: activation peptide #status experimental <ACT>

F;60-261/Domain: matrix metalloproteinase homology <MMP>

F;90-97/Region: autoinhibitory

F;100-469/Product: interstitial collagenase #status experimental <MAT>

F;272-466/Domain: hemopexin repeat homology <PXN>

F;92-218,222,228/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status

F;120,143/Binding site: carboxylate (Asn) (covalent) #status predicted

F;218,228,228/Binding site: zinc, catalytic (His) (active) #status predicted

F;219/Active site: Glu #status predicted

F;269-270/Cleavage site: Pro-Ile (autolytic) #status experimental

F;278-466/Disulfide bonds: #status experimental

Query Match 72.0%; Score 221; DB 1; Length 469;

Best Local Similarity 70.9%; Pred. No. 5.2e-20;

Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 MQRFFGLNVTGKPNBETLDMKKPCGVPDPSGGFMTLPGNPKWERTNLTIRNY 55

Db 67 MQEFGKLVTKGRPDATLTKMKQPCGVPDVAQFVLTEGNFRWEQTHLTIRNY 121

RESULT 5

KCBOI

Interstitial collagenase (EC 3.4.24.7) precursor - bovine

N;Alternate names: fibroblast collagenase; matrix metalloproteinase 1 (MMP1); tissue col

C;Species: Bos primigenius taurus (Cattle)

C;Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text_change 09-Jul-2004

C;Accession: S14654; S20336; S14655

C;Tamura, M.; Shimokawa, H.; Sasaki, S.

submitted to the EMBL Data Library, March 1991

A;Reference number: S14654

A;Accession: S14654

A;Molecule type: mRNA

A;Residues: 1-469 <MAT>

A;Cross-references: UNIPROT:P28053; EMBL:X58256; NID:9259; PIDN:CAA41210.1; PID:9260

R;Subbeck, B.D.; Jeffrey, J.J.; Welgus, H.G.; Mecham, R.P.; McCourt, D.; Parks, W.C.

Arch. Biochem. Biophys. 293, 370-376, 1992

A;Title: Purification and characterization of bovine interstitial collagenase and tissue

A;Reference number: S20336; MUID:92161820; PMID:1311165

A;Accession: S20336

A;Molecule type: protein

A;Residues: 19-21, 'FP', 24-29, 'L', 31-34, 'LL', 37-39, 'F', 86-105, 'NPR', 109-112, 'D', 114-125 <

C;Comment: This enzyme cleaves collagens of types I, II, and III at a Gly-Ile site in th

C;Comment: Procollagenase can be activated without removal of the activation peptide. St

tion peptide by other proteinases.

C;Function: Procollagenase is found in glycosylated and unglycosylated forms, both of whi

A;Description: hydrolyzes collagens, in particular types I, II, III, and X, serpins, and

C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotein

C;Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo

F;1-18/Domain: signal sequence #status predicted <SIG>

F;19-469/Product: procollagenase #status predicted <PRO>

F;19-99/Domain: activation peptide #status predicted <ACT>

F;60-261/Domain: matrix metalloproteinase homology <MMP>

F;90-97/Region: autoinhibitory

F;100-469/Product: interstitial collagenase #status predicted <MAT>

F;272-466/Domain: hemopexin repeat homology <PXN>

F;92,218,222,228/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status

F;120,143/Binding site: carboxylate (Asn) (covalent) #status predicted

F;218,222,228/Binding site: zinc, catalytic (His) (active) #status predicted

F;219/Active site: Glu #status predicted

F;278-466/Disulfide bonds: #status predicted

Query Match 71.0%; Score 218; DB 1; Length 469;

Best Local Similarity 70.9%; Pred. No. 1.3e-19;

Matches 39; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 1 MQRFFGLNVTGKPNBETLDMKKPCGVPDPSGGFMTLPGNPKWERTNLTIRNY 55

Db 67 MQEFGKLVTKGRPDATLTKMKQPCGVPDVAQFVLTEGNFRWEQTHLTIRNY 121

RESULT 6

151267

collagenase (EC 3.4.24.-) - bullfrog

C;Species: Rana catesbeiana (bullfrog)

C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004

C;Accession: I51267

R;Oofusa, K.; Yomori, S.; Yoshizato, K.

Int. J. Dev. Biol. 38, 345-350, 1994

A;Title: Regionally and hormonally regulated expression of genes of collagen and collage

A;Reference number: I51267; MUID:95071832; PMID:7981043

A;Accession: I51267

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-384 <COF>

A;Cross-references: UNIPROT:Q11133; GB:S75623; NID:9913070; PIDN:AAB32661.1; PID:9913071

C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotei

C;Keywords: hydrolase; metalloproteinase; zinc; zymogen

F;53-231/Domain: matrix metalloproteinase homology <MMP>

F;236-381/Domain: hemopexin repeat homology <PXN>

F;81,189,193,199/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status

F;189,193,199/Binding site: zinc, catalytic (His) (active) #status predicted

F;190/Active site: Glu #status predicted

Query Match 65.6%; Score 201.5; DB 2; Length 384;

Best Local Similarity 65.5%; Pred. No. 1.2e-17;

Matches 36; Conservative 10; Mismatches 8; Indels 1; Gaps 1;

QY 1 MQRFFGLNVTGKPNBETLDMKKPCGVPDPSGGFMTLPGNPKWERTNLTIRNY 55

Db 57 LKQFGLKVTGKPDATLTKMKQPCGVPDVAQFVLTEGNFRWEQTHLTIRNY 110

RESULT 7

KCHUS1

stromelysin 1 (EC 3.4.24.17) precursor [validated] - human

N;Alternate names: angiotensin-converting enzyme; collagenase activating protein; matrix

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1992 #sequence_revision 08-May-1998 #text_change 09-Jul-2004

C;Accession: A28156; C29157; A28399; A60964; S15427

R;Saus, J.; Quinones, S.; Otani, Y.; Nagase, H.; Harris Jr., E.D.; Kurkinen, M.

J. Biol. Chem. 263, 6742-6745, 1988

A;Title: The complete primary structure of human matrix metalloproteinase-3. Identity wi

A;Reference number: A28156; MUID:88198243; PMID:3360803

A;Accession: A28156

A;Molecule type: mRNA

A;Residues: 1-44, 'E', 46-477 <SAU>

A;Cross-references: UNIPROT:P08254; GB:J03209; NID:G188618; PIDN:AAA36321.1; PID:G188619

R;Wilhelm, S.E.; Murphy, G.; Angel, P.; Rahmsdorf, H.J.; Smith, B.J.; Lyons, A.; Harris,

Biochem. J. 240, 913-916, 1986

A;Title: Comparison of human matrix metalloproteinase and collagenase by cloning and sequence analysi

A;Reference number: A90336; MUID:87156645; PMID:3030290

A;Accession: C29157

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-477 <WH1>

A;Cross-references: EMBL:X05232; NID:936632; PIDN:CAA28859.1; PID:936633

R;Wilhelm, S.E.; Collier, I.E.; Kronberger, A.; Eisen, A.Z.; Marmer, B.L.; Grant, G.A.;

Proc. Natl. Acad. Sci. U.S.A. 84, 6725-6729, 1987

A;Title: Human skin fibroblast stromelysin: structure, glycosylation, substrate specific

A;Reference number: A28399; MUID:88016164; PMID:3477804

A;Accession: A28399

A;Status: nucleic acid sequence not shown; not compared with conceptual translation

F;219/Active site: Glu #status predicted
F;290-477/Disulfide bonds: #status predicted

Query Match 63.8%; Score 196; DB 1; Length 477;
Best Local Similarity 63.6%; Pred. No. 7.8e-17;
Matches 35; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 MQRFFGLVNTGKNEETLDMMKPRGVPDSDGGFMLTPGNPKWERTNLTIRINY 55
DB 67 MQRFLGLEVTGKLDSTLEVMKPRGVPDVGHFRTFFGIPKWKTHLTIRINY 121

RESULT 8
KCHUS2

stromelysin 2 (EC 3.4.24.22) precursor [validated] - human
N/Alternate names: matrix metalloproteinase 10 (MMP10); transin-2
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
C/Accession: A28816; A47496
R/Muller, J.; Quantin, B.; Genet, M.C.; Millon-Collard, R.; Abecassis, J.; Breathnach, P.
Biochem. J. 253, 187-192, 1988
A/R116: the collagenase gene family in humans consists of at least four members.
A/Reference number: A90339; MUID:88339885; PMID:2844164
A/Accession: A28816
A/Molecule type: mRNA
A/Residues: 1-476 <MUL>
A/Cross-references: UNIPROT:P09239; EMBL:X07820; NID:q36628; PIDN:CAA30679.1; PID:g36622
A/Note: mRNA for this protein was detected in several human tumors
R/Windsor, L.J.; Grenett, R.; Birkedal-Hansen, B.; Bodden, M.K.; Engler, J.A.; Birkedal
J. Biol. Chem. 268, 17341-17347, 1993
A/R116: Cell type-specific regulation of SL-1 and SL-2 genes. Induction of the SL-2 gene
A/Reference number: A47496; MUID:93352520; PMID:8349617
A/Accession: A47496
A/Molecule type: protein
A/Residues: 17-33 <WIN>
C/Comment: This enzyme degrades various extracellular matrix proteins, including fibron
C/Genetics:
A/Gene: GDB:MMP10; STMY2
A/Cross-references: GDB:120392; OMIM:185260
A/Map position: 11q22.3-11q23
C/Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprote
C/Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo
F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-476/Product: stromelysin 2 #status experimental <PRO>
F;17-98/Domain: activation peptide #status predicted <ACT>
F;59-263/Domain: matrix metalloproteinase homology <MMP>
F;89-96/Region: autoinhibitory
F;99-476/Product: stromelysin 2 #status predicted <MAT>
F;283-476/Domain: hemopexin repeat homology <PXN>
F;917,217,221,227/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
F;119/Binding site: carboxylate (Asn) (covalent) #status predicted
F;17,221,227/Binding site: zinc, catalytic (His) (active) #status predicted
F;218/Active site: Glu #status predicted
F;289-476/Disulfide bonds: #status predicted

Query Match 63.5%; Score 195; DB 1; Length 476;
Best Local Similarity 63.6%; Pred. No. 1e-16;
Matches 35; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 MQRFFGLVNTGKNEETLDMMKPRGVPDSDGGFMLTPGNPKWERTNLTIRINY 55
DB 66 MQRFLGLEVTGKLDSTLEVMKPRGVPDVGHFSSFFGPKWKTHLTIRINY 120

RESULT 9
JC6505

stromelysin 2 (EC 3.4.24.22) precursor - mouse
N/Alternate names: matrix metalloproteinase 10
C/Species: Mus musculus (house mouse)
C/Date: 16-Oct-1998 #sequence_revision 16-Oct-1998 #text_change 09-Jul-2004
C/Accession: JC6505
R/Madlener, M.; Werner, S.
Gene 202, 75-81, 1997

A:Gene: GDB:MPI13; CLG3
A:Cross-references: GDB:373966; OMIM:600108
A:Map position: 11q22.2-11q22.3
C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloproteinase; zinc; zymogen
F:Keywords: hydrolase; metalloproteinase; zinc; zymogen
F:64-267/Domain: matrix metalloproteinase homology <MMP>
F:278-471/Domain: hemopexin repeat homology <PXN>
F:96-222,226,232/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
F:222,226,232/Binding site: zinc, catalytic (His) (active) #status predicted
F:223/Active site: Glu #status predicted

Query Match 61.2%; Score 188; DB 2; Length 471;
Best Local Similarity 63.6%; Pred. No. 7.9e-16;
Matches 35; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

QY 1 MQRFFGLNVTGKNEBETLDMKKPCGVPDSCGFMLTSCNPKWERTNLTIRNY 55
Db 71 MOSFFGLEVTGKLDNDTLDMKKPCGVPDVGGEYNVFPRTLKWSKQNLTYRINY 125

Search completed: October 13, 2004, 15:15:45
Job time : 20.8013 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 13, 2004, 15:00:44 ; Search time 112.821 Seconds
(without alignments)
280.495 Million cell updates/sec

Title: US-10-032-376A-10

Perfect score: 307

Sequence: 1 MQRFFGLNVTKPNEETLDM.....LTPGNPKWERTNLTYLRNY 55

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: UniProt_02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	ID	Description
1	307	100.0	467	1 MM08_HUMAN	P22894 homo sapien
2	233	75.9	468	1 MM01_RABIT	P13943 oryctolagus
3	231	75.2	469	1 MM01_PIG	P21692 sus scrofa
4	223	72.6	466	1 MM08_RAT	O88766 rattus norv
5	222	72.3	469	1 MM01_HORSE	Q9X825 equus cabal
6	221	72.0	469	1 MM01_HUMAN	P03956 homo sapien
7	221	72.0	469	2 AAP35520	AAP35520 homo sapi
8	218	71.0	469	1 MM01_BOVIN	P28053 bos taurus
9	201.5	65.6	384	1 MM01_RANCA	Q11133 rana catesb
10	198	64.5	465	2 Q8C209	Q8C209 mus muscu
11	198	64.5	465	2 Q8C230	Q8C230 mus muscu
12	198	64.5	465	2 AAH42742	AAH42742 mus muscu
13	198	64.5	465	2 BAC40805	BAC40805 mus muscu
14	198	64.5	478	2 Q6Y4Q5	Q6Y4Q5 canis fami
15	198	64.5	478	2 ARO63580	ARO63580 canis fam
16	196	63.8	469	1 MM13_XENLA	Q10835 xenopus lae
17	196	63.8	472	2 Q93342	Q93342 gallus gall
18	196	63.8	472	2 Q10833	Q10833 xenopus lae
19	196	63.8	477	1 MM03_HUMAN	P09254 homo sapien
20	196	63.8	477	2 AAH69716	AAH69716 homo sapi
21	196	63.8	477	2 AAH69716	AAH69716 homo sapi
22	195	63.5	476	1 MM10_HUMAN	P09238 homo sapien
23	195	63.5	476	2 AAP36110	AAP36110 homo sapi
24	194	63.2	145	2 Q9N283	Q9N283 bos taurus
25	194	63.2	452	2 Q9Y182	Q9Y182 canis fami
26	193	62.9	476	1 MM10_MOUSE	O55123 mus muscu
27	193	62.9	477	1 MM03_MOUSE	P28862 mus muscu
28	193	62.9	479	2 Q922W6	Q922W6 mus muscu
29	192	62.5	478	1 MM03_RABIT	P28863 oryctolagus
30	190	61.9	465	1 MM08_MOUSE	O70138 mus muscu
31	190	61.9	476	1 MM10_RAT	P07152 rattus norv

32	189	61.6	466	1 MM13_RAT	P23097 rattus norv
33	189	61.6	472	1 MM13_MOUSE	P33435 mus muscu
34	188	61.2	383	2 Q7Z5M0	Q7Z5M0 homo sapien
35	188	61.2	393	2 Q8MI18	Q8MI18 felis silve
36	188	61.2	471	1 MM13_HUMAN	P45452 homo sapien
37	188	61.2	471	2 Q6NWN6	Q6NWN6 homo sapien
38	188	61.2	471	2 AAH67522	AAH67522 homo sapi
39	188	61.2	471	2 AAH67523	AAH67523 homo sapi
40	188	61.2	475	1 MM03_RAT	P03957 rattus norv
41	188	61.2	489	2 Q7Z5M1	Q7Z5M1 homo sapien
42	187	60.9	472	1 MM13_HORSE	O18927 equus cabal
43	185	60.3	139	2 Q9GM58	Q9GM58 sus scrofa
44	185	60.3	471	1 MM13_BOVIN	O76656 bos taurus
45	184	59.9	259	2 Q6DF35	Q6DF35 xenopus tro

ALIGNMENTS

RESULT 1

MM08_HUMAN

ID MM08_HUMAN STANDARD; PRT; 467 AA.

AC P22894;

DT 01-AUG-1991 (Rel. 19, Last sequence update)

DT 01-AUG-1991 (Rel. 19, Last sequence update)

DE Neutrophil collagenase precursor (EC 3.4.24.34) (Matrix metalloproteinase-8) (MMP-8) (PMNL collagenase) (PMNL-CL).

DE Name=MMP8; Synonyms=CLG1;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

CX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A., AND SEQUENCE OF 314-337; 347-363 AND 424-441.

RC TISSUE=Neutrophils;

RX MEDLINE=90307547; PubMed=2164002;

RA Hasty K.A., Pourmotabbed T.F., Goldberg G.I., Thompson J.P., Spinella D.G., Stevens R.M., Mainardi C.L.;

RT "Human neutrophil collagenase. A distinct gene product with homology to other matrix metalloproteinases.";

RL J. Biol. Chem. 265:11421-11424(1990).

RN [2]

RP SEQUENCE OF 21-140.

RC TISSUE=Neutrophils;

RX MEDLINE=90249372; PubMed=2159879;

RA Knauper V., Kraemer S., Reinke H., Tschesche H.;

RT "Characterization and activation of procollagenase from human polymorphonuclear leucocytes. N-terminal sequence determination of the proenzyme and various proteolytically activated forms.";

RL Eur. J. Biochem. 189:295-300(1990).

RN [3]

RP SEQUENCE OF 21-103.

RC TISSUE=Neutrophils;

RX MEDLINE=92111500; PubMed=1662606;

RA Blaesser J., Knauper V., Osthus A., Reinke H., Tschesche H.;

RT "Mercurial activation of human polymorphonuclear leucocyte procollagenase.";

RL Eur. J. Biochem. 202:1223-1230(1991).

RN [4]

RP SEQUENCE OF 85-120, AND CHARACTERIZATION.

RC TISSUE=Neutrophils;

RX MEDLINE=91104978; PubMed=2176876;

RA Mallya S.K., Mookthiar K.A., Gao Y., Brew K., Dioszegi M., Birkedal-Hansen H., van Wart H.E.;

RT "Characterization of 58-kilodalton human neutrophil collagenase: comparison with human fibroblast collagenase.";

RL Biochemistry 29:10628-10634(1990).

RN [5]

RP PARTIAL SEQUENCE.

RC MEDLINE=90380298; PubMed=2169256;

RX Knauper V., Kraemer S., Reinke H., Tschesche H.;

RT "Partial amino acid sequence of human PMN leukocyte procollagenase.";

RL Biol. Chem. Hoppe-Seyler 371:295-304(1990).
RN [6]
RP ERRATUM.
RX MEDLINE=91000455; PubMed=2169766;
RA Knauper V., Kraemer S., Reinke H., Tschesche H.;
RL Biol. Chem. Hoppe-Seyler 371:733-733(1990).
RN [7]
RP CYS-STEIN-SWITCH MECHANISM.
RC TISSUE-NEUTROPHILS;
RA MEDLINE=93050220; PubMed=1330697;
RX Blaaser J., Triebel S., Reinke H., Tschesche H.;
RT "Formation of a covalent Hg-Cys-bond during mercurial activation of
PMNL procollagenase gives evidence of a cysteine-switch mechanism.";
RL FEBS Lett. 313:59-61(1992).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 100-262.
RX MEDLINE=94185631; PubMed=8137810;
RA Bode W., Reinemer P., Huber R., Klein T., Schnierer S., Tschesche H.;
RT "The X-ray crystal structure of the catalytic domain of human
neutrophil collagenase inhibited by a substrate analogue reveals the
essentials for catalysis and specificity.";
RL EMBO J. 13:1263-1269(1994).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 100-262.
RX MEDLINE=94139330; PubMed=8307185;
RA Reinemer P., Grams F., Huber R., Kleine T., Schnierer S., Piper M.,
RA Tschesche H., Bode W.;
RT "Structural implications for the role of the N terminus in the
'superactivation' of collagenases. A crystallographic study.";
RL FEBS Lett. 338:227-233(1994).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 100-262.
RX MEDLINE=95384762; PubMed=7656015;
RA Stams T., Spurlino J.C., Smith D.L., Wahl R.C., Ho T.F.,
RA Oronfleh M.W., Banks T.M., Rubin B.;
RT "Structure of human neutrophil collagenase reveals large S1'
specificity pocket.";
RL Nat. Struct. Biol. 1:119-123(1994).
RN [11]
RP X-RAY CRYSTALLOGRAPHY (1.81 ANGSTROMS) OF 100-262.
RX MEDLINE=97390108; PubMed=9249047;
RA Betz M., Huxley P., Davies S.J., Mushtaq Y., Pieper M., Tschesche H.,
RA Bode W., Gomis-Ruth F.-X.;
RT "1.8-A crystal structure of the catalytic domain of human neutrophil
collagenase (matrix metalloproteinase-8) complexed with a
peptidomimetic hydroxamate primed-side inhibitor with a distinct
selectivity profile.";
RL Eur. J. Biochem. 247:356-363(1997).
RN [12]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 105-262.
RX MEDLINE=98318039; PubMed=9655333;
RA Brandstetter H., Engh R.A., von Roeder E.G., Moroder L., Huber R.,
RA Bode W., Grams F.;
RT "Structure of malonic acid-based inhibitors bound to human neutrophil
collagenase. A new binding mode explains apparently anomalous data.";
RL Protein Sci. 7:1303-1309(1998).
CC -!- FUNCTION: Can degrade fibrillar type I, II, and III collagens.
CC -!- CATALYTIC ACTIVITY: Cleavage of interstitial collagens in the
triple helical domain. Unlike EC 3.4.24.7, this enzyme cleaves
type III collagen more slowly than type I.
CC -!- COFACTOR: Binds 2 zinc ions and 3 calcium ions per subunit.
CC -!- ENZYME REGULATION: Cannot be activated without removal of the
activation peptide.
CC -!- SUBCELLULAR LOCATION: Stored in intracellular granules.
CC -!- TISSUE SPECIFICITY: Neutrophils.
CC -!- SIMILARITY: Belongs to peptidase family M10A.
CC -!- SIMILARITY: Contains 1 hemopexin-like domain.

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CC -----
CC EMBL: J05556; AAA88021.1; -.
DR PIR: A37073; KCHUN.
DR PDB: 1A85; X-ray; A=105-262.
DR PDB: 1A86; X-ray; A=105-262.
DR PDB: 1BZS; X-ray; A=99-263.
DR PDB: 1I73; X-ray; A=100-262.
DR PDB: 1I76; X-ray; A=100-262.
DR PDB: 1JAN; X-ray; A=99-262.
DR PDB: 1JAO; X-ray; A=100-262.
DR PDB: 1JAP; X-ray; A=100-262.
DR PDB: 1JQA; X-ray; A=100-262.
DR PDB: 1JH1; X-ray; A=105-262.
DR PDB: 1JH9; X-ray; A=100-262.
DR PDB: 1KBC; X-ray; A/B=99-262.
DR PDB: 1MNB; X-ray; A=100-262.
DR PDB: 1MNC; X-ray; A=100-262.
DR MEROPS: M10.002; -.
DR Genew; HGNC:7175; MMP8.
DR MIM: 120355; -.
DR GO: GO:0005615; C:extracellular space; TAS.
DR GO: GO:0008130; F:neutrophil collagenase activity; TAS.
DR GO: GO:0008270; F:zinc ion binding; TAS.
DR GO: GO:0006508; P:proteolysis and peptidolysis; TAS.
DR InterPro: IPR000585; Hemopexin.
DR InterPro: IPR001818; Pept_M10A_M12B.
DR InterPro: IPR006025; Pept_M_Zn_BS.
DR InterPro: IPR009070; PGSD_like.
DR Pfam: PF00445; Hemopexin; 4.
DR Pfam: PF00413; Peptidase M10; 1.
DR Pfam: PF03933; Peptidase M10_N; 1.
DR PRINTS: PR00138; MATRINX.
DR PROSITE: PS00546; CYSTEINE SWITCH; 1.
DR PROSITE: PS00024; HEMOPEXIN; 1.
DR PROSITE: PS00142; ZINC PROTEASE; 1.
DR 3D-structure; Calcium-binding; Collagen degradation;
KW Direct protein sequencing; Extracellular matrix; Glycoprotein;
KW Hydrolyase; Metal-binding; Metalloprotease; Signal; Zinc; Zymogen.
FT SIGNAL 1 20 Activation peptide.
FT PROPEP 21 100 Neutrophil collagenase.
FT CHAIN 101 467 Hemopexin-like.
FT DOMAIN 276 467 Cysteine switch.
FT SITE 91 91 Calcium 1.
FT METAL 157 157 Zinc 1.
FT METAL 169 169 Zinc 1.
FT METAL 174 174 Calcium 2.
FT METAL 175 175 Calcium 2 (via carbonyl oxygen).
FT METAL 177 177 Calcium 2 (via carbonyl oxygen).
FT METAL 179 179 Calcium 2 (via carbonyl oxygen).
FT METAL 182 182 Zinc 1.
FT METAL 189 189 Calcium 1.
FT METAL 191 191 Calcium 1.
FT METAL 193 193 Zinc 1.
FT METAL 195 195 Calcium 2.
FT METAL 197 197 Zinc 2 (catalytic).
FT METAL 200 200 Zinc 2 (catalytic).
FT METAL 217 217 Zinc 2 (catalytic).
FT ACT_SITE 218 218 Calcium 3 (via carbonyl oxygen) (By
FT METAL 221 221 similarity).
FT METAL 227 227 Calcium 3 (via carbonyl oxygen) (By
FT METAL 286 286 similarity).
FT METAL 378 378 Calcium 3 (via carbonyl oxygen) (By
FT METAL 425 425 similarity).
FT CARBOHYD 54 54 N-linked (GlcNAc...) (Probable).
FT CARBOHYD 73 73 N-linked (GlcNAc...) (Probable).
FT CARBOHYD 112 112 N-linked (GlcNAc...)
FT CARBOHYD 204 204 N-linked (GlcNAc...)
FT

FT CARBOHYD 246 246 N-linked (GlcNAc...) (Potential).
 FT DISULFID 279 464 Probable.

Query Match 100.0%; Score 307; DB 1; Length 467;
 Best Local Similarity 100.0%; Pred. No. 3.1e-26; Indels 0; Gaps 0;
 Matches 55; Conservative 0; Mismatches 0;

QY 1 MQRFFGLNVTGKPNBETLDMKKPCRGVDSGGFMTLPGNPKWERTNLTIRNY 55
 |||||
 DB 66 MQRFFGLNVTGKPNBETLDMKKPCRGVDSGGFMTLPGNPKWERTNLTIRNY 120
 |||||

RESULT 2

MM01_RABIT STANDARD; PRT; 468 AA.

ID MM01_RABIT
 AC P13943;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Interstitial collagenase precursor (EC 3.4.24.7) (Matrix
 metalloproteinase-1) (MMP-1).
 GN Name=MMPI;
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Synovial cell;
 RX MEDLINE=88077876; PubMed=2825772;
 RA Fini M.E., Plucinska I.M., Mayer A.S., Gross R.H., Brinckerhoff C.E.;
 RT "A gene for rabbit synovial cell collagenase: member of a family of
 metalloproteinases that degrade the connective tissue matrix.";
 RL Biochemistry 26:6156-6165 (1987).
 RN [2]
 RP SEQUENCE OF 449-468 FROM N.A.
 RC STRAIN=New Zealand white;
 RX MEDLINE=87029174; PubMed=3021384;
 RA Fini M.E., Austin S.D., Holt P.T., Ruby P.L., Gross R.H., White H.D.,
 RA Brinckerhoff C.E.;
 RT "Homology between exon-containing portions of rabbit genomic clones
 for synovial cell collagenase and human foreskin and synovial cell
 mRNAs.";
 RL Coll. Relat. Res. 6:239-248 (1986).
 CC -!- FUNCTION: Cleaves collagens of types I, II, and III at one site in
 the helical domain. Also cleaves collagens of types VII and X.
 CC -!- CATALYTIC ACTIVITY: Cleaves preferentially one bond in native
 collagen. Cleavage of the triple helix of collagen at about three-
 quarters of the length of the molecule from the N-terminus, at
 775-Gly-Ile-776 in the alpha-1(I) chain. Cleaves synthetic
 substrates and alpha-macroglobulins at bonds where P1' is a
 hydrophobic residue.
 CC -!- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit (By
 similarity).
 CC -!- ENZYME REGULATION: Can be activated without removal of the
 activation peptide.
 CC -!- SIMILARITY: Belongs to peptidase family M10A.
 CC -!- SIMILARITY: Contains 1 hemopexin-like domain.
 CC -----
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 CC -----
 CC EMBL; M17823; AAB88016.1; --
 CC EMBL; M17820; AAB88016.1; JOINED.
 CC EMBL; M17821; AAB88016.1; JOINED.
 CC EMBL; M17822; AAB88016.1; JOINED.
 CC EMBL; M19240; AAB88016.1; JOINED.
 CC EMBL; M19240; AAB88016.1; JOINED.
 CC EMBL; M25663; AAB31203.1; --

DR PIR; A27500; KCRBI.
 DR HSP; P03956; IGLL.
 DR MEROPS; M10_001; --
 DR InterPro; IPR000585; Hemopexin.
 DR InterPro; IPR006026; Peptidase_M.
 DR InterPro; IPR001818; Pept_M10A_M12B.
 DR InterPro; IPR006025; Pept_M_Zn_BS.
 DR InterPro; IPR009070; PQBD_like.
 DR Pfam; PF00045; Hemopexin; 4.
 DR Pfam; PF00413; Peptidase_M10; 1.
 DR Pfam; PF03933; Peptidase_M10_N; 1.
 DR PRINTS; PRO0138; MAIRIXIN.
 DR SMART; SM00120; HX; 4.
 DR SMART; SM00235; ZmC; 1.
 DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
 DR PROSITE; PS00024; HEMOPEXIN; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 KW Calcium-binding; Collagen degradation; Extracellular matrix;
 KW Glycoprotein; Hydrolase; Metal-binding; Metalloprotease; Signal; Zinc;
 KW Zymogen.

FT SIGNAL 1 18
 FT PROPEP 19 98 Activation peptide.
 FT CHAIN 99 468 Interstitial collagenase.
 FT DOMAIN 274 468 Hemopexin-like.
 FT SITE 91 91 Cysteine switch (Potential).
 FT METAL 123 123 Calcium 1 (By similarity).
 FT METAL 157 157 Calcium 2 (By similarity).
 FT METAL 167 167 Zinc 1 (By similarity).
 FT METAL 169 169 Zinc 1 (By similarity).
 FT METAL 174 174 Calcium 3 (By similarity).
 FT METAL 175 175 Calcium 3 (via carbonyl oxygen) (By
 similarity).
 FT METAL 177 177 Calcium 3 (via carbonyl oxygen) (By
 similarity).
 FT METAL 179 179 Calcium 3 (via carbonyl oxygen) (By
 similarity).
 FT METAL 182 182 Zinc 1 (By similarity).
 FT METAL 189 189 Calcium 2 (via carbonyl oxygen) (By
 similarity).
 FT METAL 191 191 Calcium 2 (via carbonyl oxygen) (By
 similarity).
 FT METAL 193 193 Calcium 2 (By similarity).
 FT METAL 195 195 Zinc 1 (By similarity).
 FT METAL 197 197 Calcium 3 (By similarity).
 FT METAL 198 198 Calcium 1 (By similarity).
 FT METAL 200 200 Calcium 3 (By similarity).
 FT METAL 217 217 Zinc 2 (catalytic) (By similarity).
 FT ACT_SITE 218 218 By similarity.
 FT METAL 221 221 Zinc 2 (catalytic) (By similarity).
 FT METAL 227 227 Zinc 2 (catalytic) (By similarity).
 FT METAL 284 284 Calcium 4 (via carbonyl oxygen) (By
 similarity).
 FT METAL 328 328 Calcium 4 (via carbonyl oxygen) (By
 similarity).
 FT METAL 377 377 Calcium 4 (via carbonyl oxygen) (By
 similarity).
 FT METAL 426 426 Calcium 4 (via carbonyl oxygen) (By
 similarity).
 FT CARBOHYD 119 119 N-linked (GlcNAc...) (Probable).
 FT DISULFID 277 465 By similarity.
 SQ SEQUENCE 468 AA; 53739 MW; DA90538919952B8C CRC64;

Query Match 75.9%; Score 233; DB 1; Length 468;
 Best Local Similarity 74.5%; Pred. No. 4.3e-20;
 Matches 41; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 MQRFFGLNVTGKPNBETLDMKKPCRGVDSGGFMTLPGNPKWERTNLTIRNY 55
 |||||
 DB 66 MQRFFGLNVTGKPNBETLDMKKPCRGVDSGGFMTLPGNPKWERTNLTIRNY 120
 |||||

RESULT 3
 MM01_PIG


```
FT STRAND 293 298
FT TURN 299 300
FT STRAND 301 305
FT STRAND 313 316
FT HELIX 317 320
FT STRAND 330 334
FT TURN 335 338
FT STRAND 339 344
FT TURN 345 346
FT STRAND 347 352
FT TURN 353 354
FT STRAND 355 356
FT TURN 358 359
FT STRAND 362 363
FT HELIX 364 368
FT TURN 372 373
FT STRAND 379 383
FT TURN 384 387
FT STRAND 388 393
FT TURN 394 395
FT STRAND 396 401
FT TURN 402 405
FT STRAND 406 407
FT STRAND 413 414
FT HELIX 415 418
FT TURN 420 421
FT STRAND 428 432
FT TURN 433 434
FT STRAND 435 440
FT TURN 441 442
FT STRAND 443 448
FT TURN 449 452
FT STRAND 453 459
FT TURN 460 461
FT HELIX 462 464
FT TURN 465 465
SQ SEQUENCE 469 AA; 53666 MW; 7952D72B2753F682 CRC64;

Query Match 75.2%; Score 231; DB 1; Length 469;
Best Local Similarity 72.7%; Pred. No. 7.6e-20;
Matches 40; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 1 MOREFLGNTGKNEETLDMKKPCGVPDSGFMILTCGNPKWERTNLTIRNY 55
DB 67 MQQFFGLKVTGRPDATLNVNKKPCGVPDVAEFVLTCGNPRWENTHLYRIENY 121

RESULT 4
MM08 RAT
ID MM08 RAT STANDARD; PRT; 466 AA.
AC O88766;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Neutrophil collagenase precursor (EC 3.4.24.34) (Matrix metalloproteinase-8) (MMP-8).
GN Name=Mmp8;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Lewis;
RA Overall C.M., Lowe D., Wells G., Burel S., Clements J.M.;
RT "Cloning, expression, characterization and activation properties of rat neutrophil collagenase (MMP-8).";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Can degrade fibrillar type I, II, and III collagens.
CC -!- CATALYTIC ACTIVITY: Cleavage of interstitial collagens in the triple helical domain. Unlike EC 3.4.24.7, this enzyme cleaves type III collagen more slowly than type I.
CC -!- COFACTOR: Binds 2 zinc ions and 3 calcium ions per subunit (By
```

```
CC similarity).
CC -!- ENZYME REGULATION: Cannot be activated without removal of the activation peptide (By similarity).
CC -!- SUBCELLULAR LOCATION: Stored in intracellular granules.
CC -!- SIMILARITY: Belongs to peptidase family M10A.
CC -!- SIMILARITY: Contains 1 hemopexin-like domain.
CC
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CC
CC -----
CC EMBL; AJ007288; CAA07432.1; -.
CC HSSP; P22894; 1BZS.
CC
CC DR MEROPS; M10.002; -.
CC DR InterPro; IPR000585; Hemopexin.
CC DR InterPro; IPR001818; Pept_M10A_M12B.
CC DR InterPro; IPR006025; Pept_M_Zn_BS.
CC DR InterPro; IPR009070; PGSD_Like.
CC DR Pfam; PF00045; Hemopexin; 4.
CC DR Pfam; PF00413; Peptidase M10; 1.
CC DR PRINTS; PR0138; MATRIXIN.
CC DR PROSITE; PS00546; CYSTEINE SWITCH; 1.
CC DR PROSITE; PS00024; HEMOPEXIN; 1.
CC DR PROSITE; PS00142; ZINC_PROTEASE; 1.
CC KW Calcium-binding; Collagen degradation; Extracellular matrix; Glycoprotein; Hydrolase; Metal-binding; Metalloprotease; Signal; Zinc; Zymogen.
FT SIGNAL 1 20 By similarity.
FT PROPEP 21 101 Activation peptide (By similarity).
FT CHAIN 102 466 Neutrophil collagenase.
FT DOMAIN 277 466 Hemopexin-like.
FT SITE 92 92 Cysteine switch (By similarity).
FT METAL 158 158 Calcium 1 (By similarity).
FT METAL 168 168 Zinc 1 (By similarity).
FT METAL 170 170 Zinc 1 (By similarity).
FT METAL 175 175 Calcium 2 (By similarity).
FT METAL 176 176 Calcium 2 (via carbonyl oxygen) (By similarity).
FT METAL 178 178 Calcium 2 (via carbonyl oxygen) (By similarity).
FT METAL 180 180 Calcium 2 (via carbonyl oxygen) (By similarity).
FT METAL 183 183 Zinc 1 (By similarity).
FT METAL 190 190 Calcium 1 (via carbonyl oxygen) (By similarity).
FT METAL 192 192 Calcium 1 (via carbonyl oxygen) (By similarity).
FT METAL 194 194 Calcium 1 (By similarity).
FT METAL 196 196 Zinc 1 (By similarity).
FT METAL 198 198 Calcium 2 (By similarity).
FT METAL 201 201 Calcium 2 (By similarity).
FT METAL 218 218 Zinc 2 (catalytic) (By similarity).
FT ACT SITE 219 219 By similarity.
FT METAL 222 222 Zinc 2 (catalytic) (By similarity).
FT METAL 228 228 Zinc 2 (catalytic) (By similarity).
FT METAL 287 287 Calcium 3 (via carbonyl oxygen) (By similarity).
FT METAL 379 379 Calcium 3 (via carbonyl oxygen) (By similarity).
FT METAL 426 426 Calcium 3 (via carbonyl oxygen) (By similarity).
FT DISULFID 280 465 Probable.
FT CARBOHYD 56 56 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 113 113 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 466 AA; 53277 MW; 8B9DE97576E76C90 CRC64;

Query Match 72.6%; Score 223; DB 1; Length 466;
Best Local Similarity 70.9%; Pred. No. 7.3e-19;
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	DOMAIN	275	469	Hemopexin-like.
T	SITE	322	92	Cysteine switch (Potential).
T	METAL	124	124	Calcium 1 (By similarity).
T	METAL	158	158	Calcium 2 (By similarity).
T	METAL	168	168	Zinc 1 (By similarity).
T	METAL	170	170	Zinc 1 (By similarity).
T	METAL	175	175	Calcium 3 (By similarity).
T	METAL	176	176	Calcium 3 (via carbonyl oxygen) (By similarity).
T	METAL	178	178	Calcium 3 (via carbonyl oxygen) (By similarity).
T	METAL	180	180	Calcium 3 (via carbonyl oxygen) (By similarity).
T	METAL	183	183	Zinc 1 (By similarity).
T	METAL	190	190	Calcium 2 (via carbonyl oxygen) (By similarity).
T	METAL	192	192	Calcium 2 (via carbonyl oxygen) (By similarity).
T	METAL	194	194	Calcium 2 (By similarity).
T	METAL	196	196	Zinc 1 (By similarity).
T	METAL	198	198	Calcium 3 (By similarity).
T	METAL	199	199	Calcium 1 (By similarity).
T	METAL	201	201	Calcium 3 (By similarity).
T	METAL	218	218	Zinc 2 (catalytic) (By similarity).
T	ACT_SITE	219	219	By similarity.
T	METAL	222	222	Zinc 2 (catalytic) (By similarity).
T	METAL	228	228	Zinc 2 (catalytic) (By similarity).
T	METAL	285	285	Calcium 4 (via carbonyl oxygen) (By similarity).
T	METAL	329	329	Calcium 4 (via carbonyl oxygen) (By similarity).
T	METAL	378	378	Calcium 4 (via carbonyl oxygen) (By similarity).
T	METAL	427	427	Calcium 4 (via carbonyl oxygen) (By similarity).
T	DISULFID	278	466	By similarity.
CSQ	SEQUENCE	469 AA; 54001 MW; AE6760A82C529CA CRC64;		
Query Match		72.3%; Score 222; DB 1; Length 469;		
Best Local Similarity		70.9%; Pred. No. 9.8e-19;		
Matches 39; Conservative		7; Mismatches -9; Indels 0; Gaps		
QY		1 MQEFGLVGTGENEETLDMMKKPRGVPDSSGGFMLTGPNPKWERTNLTIVRIINY 55		
DBD		67 MQEFGFLKVLTKPDAETLNMVAKPGCGVDPAEFVLTEGNPRWNTHLTRIENY 121		
RESULT 6				
ID_1_HUMAN				
ID_2_HUMAN	STANDARD;	PRT; 469 AA.		
AC P03956; F08156;				
CD 23-OCT-1986 (Rel. 02, Created)				
DT 01-DEC-1992 (Rel. 24, Last annotation update)				
DD 01-OCT-2004 (Rel. 45, Last sequence update)				
DE Interstitial collagenase precursor (EC 3.4.24.7) (Matrix metalloproteinase-1) (MMP-1) (fibroblast collagenase).				
EN Name=MMP1; Synonyms=CLG;				
GN Homo sapiens (human).				
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX NCBI_TaxId=9606;				
RP [1]				
RPP SEQUENCE FROM N.A.				
RRP MEDLINE=90352587; PubMed=2167156;				
RT Templeton N.S.; Brown P.D.; Levy A.T.; Margulies I.M.K.; Liotta L.A.				
RA Stetler-Stevenson W.G.;				
RC "Cloning and characterization of human tumor cell interstitial collagenase.";				
RL Cancer Res. 50:5431-5437(1990).				
[2]				
RP SEQUENCE FROM N.A.				
RRP MEDLINE=87156645; PubMed=3030290;				
RA Whitham S.E.; Murphy G.; Angel P.; Rahmsdorf H.J.; Smith B.; Lyons A.				

RA Harris T.J.R., Reynolds J.J., Herrlich P., Docherty A.J.P.;
RT "Comparison of human stromelysin and collagenase by cloning and
RL sequence analysis.",
RN Biochem. J. 240:913-916(1986).
RN [3]
RN SEQUENCE FROM N.A.
RP MEDLINE=86196089; PubMed=3009463;
RX Goldberg G.I., Wilhelm S.M., Kronberger A., Bauer E.A., Grant G.A.,
RA Eisen A.Z.;
RT "Human fibroblast collagenase. Complete primary structure and homology
RL to an oncogene transformation-induced rat protein.",
RN J. Biol. Chem. 261:6600-6605(1986).
RN [4]
RN SEQUENCE FROM N.A.
RP Lin D., Duncan M., Allen E., Araujo R., Aparicio A., Chai A.,
RA Chung E., Davis K., Federspiel N., Hyman R., Kalman S., Komp C.,
RA Kurdi O., Lashkari D., Lew H., Namath A., Oefner P., Roberts D.,
RA Heller R., Davis R.W.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
RN [5]
RN SEQUENCE FROM N.A.
RP TISSUE=Ovary;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan A., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.",
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RN SEQUENCE OF 1-35 FROM N.A.
RX MEDLINE=87257941; PubMed=3037355;
RA Angel P., Baumann I., Stein B., Delius H., Rahmsdorf H.J.,
RA Herrlich P.;
RT "12-O-tetradecanoyl-phorbol-13-acetate induction of the human
RL collagenase gene is mediated by an inducible enhancer element located
RL in the 5'-flanking region.",
RN Mol. Cell. Biol. 7:2256-2266(1987).
RN [7]
RN SEQUENCE OF 1-70 FROM N.A.
RX TISSUE=Synovial cell;
RN MEDLINE=87109799; PubMed=3027129;
RA Brinckerhoff C.E., Ruby P.L., Austin S.D., Fini M.E., White H.D.;
RT "Molecular cloning of human synovial cell collagenase and selection of
RL a single gene from genomic DNA.",
RN J. Clin. Invest. 79:542-546(1987).
RN [8]
RN SEQUENCE OF 100-112 AND 270-287.
RX TISSUE=Fibroblast;
RN MEDLINE=90104231; PubMed=2557822;
RA Clark I.M., Cawston T.E.;
RT "Fragments of human fibroblast collagenase. Purification and
RL characterization.",
RN Biochem. J. 263:201-206(1989).
RN [9]
RN SIMILARITY TO THERMOLYSIN TYPE PROTEASES.
RX MEDLINE=87194799; PubMed=3032950;
RA McKerrow J.H.;
RT "Human fibroblast collagenase contains an amino acid sequence
homologous to the zinc-binding site of Serratia protease.",
RN J. Biol. Chem. 262:5943-5943(1987).
RN [10]
RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 100-269.
RX MEDLINE=95384760; PubMed=7656013;
RA Borkakoti N., Winkler F.K., Williams D.H., D'Arcy A., Broadhurst M.J.,
RA Brown P.A., Johnson W.H., Murray E.J.;
RT "Structure of the catalytic domain of human fibroblast collagenase
RL complexed with an inhibitor.",
RN Nat. Struct. Biol. 1:106-110(1994).
RN [11]
RN X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 102-269.
RX MEDLINE=94304829; PubMed=8031754;
RA Lovejoy B., Hassell A.M., Luther M.A., Weigl D., Jordan S.R.;
RT "Crystal structures of recombinant 19-kDa human fibroblast collagenase
RL complexed to itself.",
RN Biochemistry 33:8207-8217(1994).
RN [12]
RN X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 102-269.
RX MEDLINE=94105765; PubMed=8278810;
RA Lovejoy B., Cleasby A., Hassell A.M., Longley K., Luther M.A.,
RA Weigl D., McGeehan G., McElroy A.B., Drewry D., Lambert M.H.,
RA Jordan S.R.;
RT "Structure of the catalytic domain of fibroblast collagenase complexed
RL with an inhibitor.",
RN Science 263:375-377(1994).
RN [13]
RN X-RAY CRYSTALLOGRAPHY (1.56 ANGSTROMS) OF 101-269.
RX MEDLINE=94377426; PubMed=8090713;
RA Spurlino J.C., Smallwood A.M., Carlton D.D., Banks T.M., Vavra K.J.,
RA Johnson J.S., Cook E.R., Falvo J., Wahl R.C., Pulvino T.A., Et A.L.;
RT "1.56-A structure of mature truncated human fibroblast collagenase.",
RN Proteins 19:98-109(1994).
RN [14]
RN STRUCTURE BY NMR OF 101-269.
RX MEDLINE=98145213; PubMed=9484219;
RA Moy F.J., Chanda P.K., Cosmi S., Pisano M.R., Urbano C., Wilhelm J.,
RA Powers R.;
RT "High-resolution solution structure of the inhibitor-free catalytic
RL fragment of human fibroblast collagenase determined by
RL multidimensional NMR.",
RN Biochemistry 37:1495-1504(1998).
RN [15]
RN FUNCTION: Cleaves collagens of types I, II, and III at one site in
CC the helical domain. Also cleaves collagens of types VII and X.
CC
CC CATALYTIC ACTIVITY: Cleaves preferentially one bond in native
CC collagen. Cleavage of the triple helix of collagen at about three-
CC quarters of the length of the molecule from the N-terminus, at
CC 775-Gly-Ile-776 in the alpha-1(I) chain. Cleaves synthetic
CC substrates and alpha-macroglobulins at bonds where p1' is a
CC hydrophobic residue.
CC
CC COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit.
CC
CC ENZYME REGULATION: Can be activated without removal of the
CC activation peptide.
CC
CC DOMAIN: There are two distinct domains in this protein; the
CC catalytic N-terminal, and the C-terminal which is involved in
CC substrate specificity and in binding TIMP (tissue inhibitor of
CC metalloproteinases).
CC
CC PFM: Undergoes autocatalytic cleavage to two major forms (22 kDa and
CC 27 kDa). A minor form (25 kDa) is the glycosylated form of the 22
CC kDa form. The 27 kDa form has no activity while the 22/25 kDa form
CC can act as activator for collagenase.
CC
CC SIMILARITY: Belongs to peptidase family M10A.
CC
CC SIMILARITY: Contains 1 hemoexin-like domain.
CC
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CC
CC EMBL; X05233; CAA28858.1; -.


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DR EMBL; M13509; AAA35699.1; -
DR EMBL; M16567; AAA52033.1; -
DR EMBL; U78045; AAB36941.1; -
DR EMBL; BC013875; AAH13875.1; -
DR EMBL; M15996; AAA35700.1; -
DR EMBL; X54925; CAA38691.1; -
DR PIR; A37308; KCHUL
DR PDB; 1AYK; NMR; @=101-269.
DR PDB; 1CGE; X-ray; @=102-269.
DR PDB; 1CGF; X-ray; A/B=102-269.
DR PDB; 1CGL; X-ray; A/B=101-269.
DR PDB; 1HFC; X-ray; @=101-269.
DR PDB; 2AYK; NMR; @=101-269.
DR PDB; 2TCL; X-ray; @=101-269.
DR PDB; 3AYK; NMR; A=101-269.
DR PDB; 4AYK; NMR; A=101-269.
DR MEROPS; M10.001; -
DR GlycosuiteDB; P03956; -
DR Genew; HGNC:7155; MMP1.
DR MIM; 120353; -; F.collagenase activity; TAS.
DR GO; GO:0008133; F.zinc ion binding; TAS.
DR GO; GO:0008270; F.zinc ion binding; TAS.
DR GO; GO:0006508; P.proteolysis and peptidolysis; TAS.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR006026; Peptidase M.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR009070; PGSD_like.
DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF00413; Peptidase_M10; 1.

Query Match 72.0%; Score 221; DB 1; Length 469;
Best Local Similarity 70.9%; Pred. No. 1.3e-18;
Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 MQRFFGLVTGKNEETLDMKKPRCGVDPDSCGFMLTGPNKWTNLTIRNY 55
DB 67 MQEFFGLKVTGKPDATLTKVMKQRCGVDPDVAQFVLTEGNPRWEQTHLTIRNY 121

RESULT 7
AAP35520 PRELIMINARY; PRT; 469 AA.
AC AAP35520;
DT 02-MAR-2004 (T-EMBLrel. 27, Created)
DT 02-MAR-2004 (T-EMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (T-EMBLrel. 27, Last annotation update)
DE Matrix metalloproteinase 1 (interstitial collagenase).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kainine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
RA Phelan M., Farmer A.;
RT "Cloning of human full-length cDNAs in BD Creator(TM) System Donor
vector."
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
RW EMBL; BT006874; AAP35520.1; -
KW Collagen.
SQ SEQUENCE 469 AA; 54007 MW; 4B1361DCF4C54B20 CRC64;

Query Match 72.0%; Score 221; DB 2; Length 469;
Best Local Similarity 70.9%; Pred. No. 1.3e-18;
Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 MQRFFGLVTGKNEETLDMKKPRCGVDPDSCGFMLTGPNKWTNLTIRNY 55
DB 67 MQEFFGLKVTGKPDATLTKVMKQRCGVDPDVAQFVLTEGNPRWEQTHLTIRNY 121

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RESULT 8
MM01_BOVIN STANDARD; PRT; 469 AA.
ID MM01_BOVIN
AC P28053;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interstitial collagenase precursor (EC 3.4.24.7) (Matrix
DE metalloproteinase-1) (MMP-1) (Fibroblast collagenase).
GN Name=MMP1; Synonyms=CLG;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Periosteum fibroblast;
RC MEDLINE=95201294; PubMed=7894061;
RA Tamura M., Shimokawa H., Sasaki S.;
RT "Primary structure of bovine interstitial collagenase deduced from
RT cDNA sequence."
RL DNA Seq. 5:63-66(1994).
RN [2]
RP SEQUENCE OF 19-39 AND 85-125.
RX PubMed=1311165;
RX Sudbeck B.D., Jeffrey J.J., Welgus H.G., Mecham R.P., McCourt D.,
RA Parks W.C.;
RT "Purification and characterization of bovine interstitial collagenase
RT and tissue inhibitor of metalloproteinases."
RL Arch. Biochem. Biophys. 293:370-376(1992).
CC -!- FUNCTION: Cleaves collagens of types I, II, and III at one site in
CC the helical domain. Also cleaves collagens of types VII and X.
CC -!- CATALYTIC ACTIVITY: Cleaves preferentially one bond in native
CC collagen. Cleavage of the triple helix of collagen at about three-
CC quarters of the length of the molecule from the N-terminus, at
CC 775-Gly-Ile-776 in the alpha-1(I) chain. Cleaves synthetic
CC substrates and alpha-macroglobulins at bonds where P1' is a
CC hydrophobic residue.
CC -!- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit (By
CC similarity).
CC -!- ENZYME REGULATION: Can be activated without removal of the
CC activation peptide.
CC -!- SIMILARITY: Belongs to peptidase family M10A.
CC -!- SIMILARITY: Contains 1 hemopexin-like domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X58256; CAA41210.1; -
DR PIR; S14554; KCBO1.
DR HSRF; P03956; LHFC.
DR MEROPS; M10.001; -
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR006026; Peptidase_M.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR009070; PGSD_like.
DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF00413; Peptidase_M10; 1.
DR Pfam; PF03933; Peptidase_M10_N; 1.
DR PRINTS; PR00138; MATRININ.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZnMc; 1.
DR PROSITE; PS00546; CYSTEINE SWITCH; 1.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00144; ZINC_PROTEASE; 1.
KW Calcium-binding; Collagen degradation; Direct protein sequencing;

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Query Match      64.5%; Score 198; DB 2; Length 465;
Best Local Similarity 85.5%; Pred. No. 9e-16;
Matches 36; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

QY   1  MQRFFGLNVITGKNEETLDMMKIKPCGVDPDSGGFMLTGCNPKWERTNTLYIRNY 55
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Db   66  MQRFESLAETGKLDAAATMGIMEMPCGVDPDSGDFLLTGSPKWHTNTLYRIINH 120
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RESULT 13
BAC40805
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Search completed: October 13, 2004, 15:14:41
Job time : 112.821 secs

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